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Estimation of Contagion: Bayesian Model Averaging on Tail Dependence of Mixture Copula

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Abstract: This study introduces a novel approach to estimate tail dependence in financial contagion using mixture copulas. Addressing the challenges of weight parameter estimation in conventional models, we propose a Bayesian model averaging method to determine optimal copula weights. Through both simulations and empirical studies, the proposed method demonstrates improved robustness and accuracy, particularly when handling extreme weight scenarios. These advancements offer more reliable measurements of financial contagion, contributing to enhanced risk management and policy-making in interconnected financial markets.

Keywords: Bayesian model averaging; contagion; copula; tail dependence

MSC: 37M10; 62P05; 62H12



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1. Introduction

Financial contagion, the spread of economic crises across markets or regions, has been a critical concern in the global financial landscape since the Asian financial crisis of 1997 [1,2]. Accurate measurement of contagion is crucial for policymakers and investors to understand and mitigate systemic risks in interconnected financial systems [3]. Despite its importance, quantifying contagion remains challenging due to the complex, non-linear relationships between financial markets [4].

This study proposes a novel approach to measure financial contagion using tail dependence, which can be determined through copula functions. We focus on estimating tail dependence within the framework of mixture copulas, specifically combining lower tail copula dependence models such as Clayton, Gumbel, survival Clayton, and survival Gumbel copulas. While conventional mixed copula models have demonstrated potential in providing reliable tail dependence measurements [5], they often face challenges related to the estimation of weight parameters. These parameters are typically treated as unknown variables to be estimated, which can lead to local optimization issues [6,7].

To address these limitations, our study introduces a Bayesian Model Averaging (BMA) method for selecting optimal weights. This approach aims to produce more reliable estimated weight results, thereby enhancing the accuracy of tail dependence measurements. By employing this method, our research contributes to the existing contagion literature by offering a potentially more robust and accurate technique for measuring contagion compared to conventional approaches.

Traditionally, several methods have been used to measure contagion in financial markets. King and Wadhwani [8] and Calvo and Reinhart [9] applied a correlation-based

approach, demonstrating the presence of contagion during the U.S. market crash in 1987 and the Mexican crisis in 1994. However, Forbes and Rigobon [1] later challenged this, providing evidence that there was no contagion in these events. A key limitation of the correlation-based method is its focus on linear dependence, which fails to capture nonlinear relationships that may exist during extreme market events. To address this, Patton [6] introduced a copula-based approach that allows for the estimation of tail dependence, effectively capturing nonlinear dependence in the tails of distributions. The coefficients of tail dependence are measures of pairwise dependence that are derived from the copula of two random variables with continuous marginal distributions [10]. These coefficients are particularly useful as they provide insight into extremal dependence, or the strength of dependence in the tails of a bivariate distribution.

In tail dependence analysis, various copulas can be employed to capture different types of dependence structures between variables. The accurate estimation of tail dependence is crucial, especially in fields like finance, where extreme events (such as financial crises) can have significant impacts. Copula models, first introduced by Sklar, provide a flexible framework for modeling dependence structures that go beyond simple linear correlation, making them particularly useful for understanding tail dependencies in multivariate distributions [11]. To enhance the accuracy of tail dependence estimation, mixture copula models, which combine multiple copulas, have been found to be particularly effective as they can capture more complex dependency structures than any single copula can [6,12].

In this study, we consider several copulas, including the Clayton copula, Gumbel copula, survival Clayton copula, and survival Gumbel copula [13]. Each copula serves a specific purpose: the Clayton copula is adept at capturing lower tail dependence, which is important for modeling joint downside risks (such as simultaneous downturns in financial markets); the Gumbel copula, on the other hand, is designed to model upper tail dependence, making it useful for capturing joint extreme positive events [14]. Survival copulas are often used to model tail dependencies in survival analysis contexts but also find application in finance, where they capture tail dependencies involving extreme risks of asset survival or market collapse [15].

A key challenge in using copula models, particularly mixture copulas, is the simultaneous optimization of copula weights and parameters. While traditional methods for optimizing copula parameters such as maximum likelihood estimation (MLE) are widely used [16], the optimization of weights in a mixture copula is more complex due to the lack of a closed-form solution for the weight parameter, which is critical in calculating the expected tail dependence across multiple copulas. Patton [6] demonstrated that selecting a single best-fitting copula for tail dependence estimation can sometimes fail to capture the full complexity of dependencies in real-world data, advocating for mixture copulas. The mixture copula model integrates different copulas to better capture complex dependence structures and is particularly useful in the context of financial contagion, where multiple markets or assets exhibit different dependency patterns under various conditions [17]. However, mixture copulas pose challenges not only due to the need for complex optimization but also due to model uncertainty—the fact that it is difficult to ascertain a prior for which copula (or combination thereof) will best capture the true underlying dependency structure [10]. One conventional solution is to select the single best copula using information criteria, such as the Bayesian Information Criterion (BIC) or Akaike Information Criterion (AIC), but these methods may overlook the benefits of blending multiple models [18].

BMA offers an elegant solution to these issues by incorporating model uncertainty into the estimation process. BMA provides a robust framework for averaging across multiple candidate models, assigning posterior probabilities to each model based on how well it fits the data. This avoids the need to commit to a single model, allowing for better estimation of tail dependencies by capturing the strengths of multiple copulas [19]. By averaging over models, BMA ensures that the models contributing more to explaining the data receive higher weights, resulting in more stable and reliable tail dependence estimates, especially in extreme market conditions [20]. Furthermore, BMA incorporates the

posterior distributions of parameters, which allows for a wider exploration of the parameter space. This broader exploration helps avoid overfitting and increases the robustness of tail dependence estimates, which is particularly crucial in financial markets where model overfitting can lead to misleading predictions of extreme events [21]. By penalizing overly complex models, BMA strikes a balance between model fit and complexity, leading to better generalizability in new data scenarios [22]. This is particularly useful in applications such as financial contagion modeling, where the accuracy of tail dependence estimation is essential for understanding systemic risks and extreme events, such as during a market crash or financial crisis [4]. BMA's ability to better estimate tail dependence when extreme dependencies are present, compared to traditional optimization-based approaches, makes it a valuable tool in this domain [23].

The primary contribution of this study is the development and application of an advanced approach to estimating tail dependence in financial markets using copulas. Unlike traditional methods that rely on a single copula or simplistic linear dependence measures, our study integrates bivariate copulas to capture a broader range of dependence structures. We specifically utilize Clayton copula, Gumbel copula, survival Clayton copula, and survival Gumbel copula, each selected for their ability to model different aspects of tail dependence. Our approach incorporates a mixture copula model to blend these copulas, offering a more nuanced understanding of dependence dynamics. This method enhances the estimation of tail dependence by addressing complex, non-linear relationships that traditional models might miss. Furthermore, we tackle the challenge of optimizing the weights in mixture copulas, which traditionally lacks a closed-form solution. By employing BMA, we account for model uncertainty and robustly average across different copulas, leading to more accurate and reliable estimates of tail dependence. The study also advances the field by addressing the limitations of conventional optimization methods for mixture copulas, providing a more effective framework for capturing extreme dependence in financial markets. This improved methodology offers valuable insights for risk management and policy formulation, particularly in understanding and managing financial contagion and systemic risk.

The paper is organized as follows: Section 2 presents the Materials and Methods; Section 3 discusses the Simulation Study; Section 4 focuses on the Application Study; Section 5 provides the Discussion and concludes with the Conclusion.

2. Materials and Methods

2.1. Copulas

A copula function is the joint distribution of the uniform distributions. Copulas are used to describe the dependence between random variables. It shows the connection between each marginal distribution, which shows as the joint distribution.

Definition 1 ([24]). *A two-dimensional copula C is the function from $[0,1]^2$ to $[0,1]$ with the following properties:*

1. *For every $v, z \in [0,1]$,*
$$C(v,0) = 0 = C(0,z)$$
and
$$C(v,1) = v \text{ and } C(1,z) = z.$$
2. *For every $v_1, v_2, z_1, z_2 \in [0,1]$ such that $v_1 \leq v_2$ and $z_1 \leq z_2$,*
$$C(v_2,z_2) - C(v_2,z_1) - C(v_1,z_2) + C(v_1,z_1) \geq 0.$$

Theorem 1 (Sklar's Theorem [11]). *Let $F(x), G(y)$ be marginal distribution functions of random variables X and Y, respectively. Then, for every $(x,y) \in \mathbb{R}^2$, we have the following:*

1. *If $\mathcal{C}$ is any subcopula whose domain contains Range $F \times$ Range G,*

$$\mathcal{C}(F(x), G(y))$$

is a joint distribution function with margins $F(x)$ and $G(y)$.
2. *Conversely, if $H(x, y)$ is a joint distribution function with margins $F(x)$ and $G(y)$, there exists a unique subcopula $\mathcal{C}$, with domain Range $F \times$ Range G, such that*

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

If $F(x)$ and $G(y)$ are continuous, the subcopula is a copula. Otherwise, there exists a copula C such that

$$C(v, z) = \mathcal{C}(v, z)$$

for every $(v, z) \in$ Range $F \times$ Range G.

Sklar's theorem shows the connection between two or more joint distributions by a copula function. It also shows that we can form them into the joint distribution function using a copula function. This results in the various application of copula function.

The class of copulas that we are interested in in this work is the Archimedean copula, which is defined as follows:

Definition 2 ([24]). *Let ϕ be a continuous strictly decreasing function from $[0, 1]$ to $[0, \infty]$ such that $\phi(1) = 0$, and let $\phi^{[-1]}$ denotes the pseudo-inverse of ϕ—that is, $\phi^{[-1]}(t) = \phi^{-1}(t)$ for $t \in [0, \phi(0)]$ and $\phi^{[-1]} = 0$ for $t \geq \phi(0)$. Then, $C(v, z) = \phi^{[-1]}(\phi(v) + \phi(z))$ is a copula and called **Archimedean copula**.*

Clayton copula and Gumbel copula are Archimedean copula generated by these generators.

1. Clayton copula is generated by $\phi(t) = (t^{-\theta} - 1)/\theta$, $\theta \in [-1, \infty)$, i.e.,

$$C_\theta(v, z) = \max\left[(v^{-\theta} + z^{-\theta} - 1)^{-\frac{1}{\theta}}, 0\right]. \tag{1}$$

2. Gumbel–Hougaard copula is generated by $\phi(t) = (-\ln t)^\theta$, $\theta \in [1, \infty)$, i.e.,

$$C_\theta(v, z) = \exp\left(-\left((-\ln v)^\theta + (-\ln z)^\theta\right)^{\frac{1}{\theta}}\right). \tag{2}$$

Definition 3 ([24]). *Let C be a copula function. The survival copula function $\hat{C}$ of C is the function from $[0, 1]^2$ to $[0, 1]$ if, for every $v, z \in [0, 1]$,*

$$\hat{C}(v, z) = v + z - 1 + C(1 - v, 1 - z).$$

When there are multiple copulas that all show similar goodness of fit, usually only a single best copula is selected and treated as the true copula. This approach ignores model uncertainty resulting in under- or over-estimation. An alternative way is to combine the selected copulas.

Lemma 1 ([24]). *Let $C_1(v, z)$ and $C_2(v, z)$ be 2-dimensional copula and $w_1, w_2 \in [0, 1]$, where $w_1 + w_2 = 1$. Then,*

$$C_{mix}(v, z) = w_1 C_1(v, z) + w_2 C_2(v, z)$$

is also a copula.

2.2. Tail Dependence

Definition 4 ([10]). *Let X and Y be random variables with distribution functions F and G, respectively. The coefficient of lower tail dependence (TDCL, λ_L) is*

$$\lambda_L = \lim_{v \to 0^+} \mathbb{P}(Y \leq G^{-1}(v) | X \leq F^{-1}(v)),$$

provided the limit $\lambda_L \in [0,1]$ exists. If $\lambda_L \in (0,1]$, then X and Y are said to show lower tail dependence. It $\lambda_L = 0$, they are asymptotically independent in the lower tail.

From Definition 4, the lower tail dependence coefficient (TDCL) can be derived to the form of the copula function.

$$\begin{aligned} \lambda_L &= \lim_{v \to 0^+} \mathbb{P}(Y \leq G^{-1}(v) | X \leq F^{-1}(v)) \\ &= \lim_{v \to 0^+} \frac{C(v,v)}{v} \end{aligned}$$

If we have a copula, we can calculate its TDC by the copula function and the above equation.

1. Clayton copula:
$$\lambda_L = 2^{-\frac{1}{\theta}}.$$
2. Survival Clayton copula:
$$\lambda_L = 0.$$
3. Gumbel copula:
$$\lambda_L = 0.$$
4. Survival Gumbel copula:
$$\lambda_L = 2 - 2^{\frac{1}{\theta}}.$$

From Lemma 1, the coefficient of lower tail dependence can also be written as follows:

$$\lambda_{L_{C_{mix}}} = w_1 \lambda_{L_{C_1}} + w_2 \lambda_{L_{C_2}}.$$

In this study, we are interested in 3 combination of mixture copula as follow;

1. Mixture of Clayton copula and Gumbel copula (C-G):
$$\lambda_L = w_1 2^{-\frac{1}{\theta}}.$$
2. Mixture of Clayton copula and survival Gumbel copula (C-SG):
$$\lambda_L = w_1 2^{-\frac{1}{\theta}} + w_2(2 - 2^{\frac{1}{\theta}}).$$
3. Mixture of survival Clayton copula and survival Gumbel copula (SC-SG):
$$\lambda_L = w_2(2 - 2^{\frac{1}{\theta}}).$$

There are several methods to estimate the copula function. For non-parametric estimation, the empirical copula method can be used [25]. This approach allows for the estimation of the copula by assigning discrete values based on the observed data, without making any assumptions about the underlying distribution. However, for parametric inference, maximum likelihood estimation (MLE) is a more commonly used approach [12]. MLE estimates the parameters of the copula by fitting them to the data under a specified parametric family, ensuring a more precise and structured estimation. This study employs

the MLE method to estimate the copula function as it provides a more robust framework for capturing the dependence structure between variables in a parametric setting.

2.3. BMA for Selecting the Optimal Weight

To select the optimal weight parameter for our mixed copula model, we employ a BIC-based BMA approach. BMA helps in weight selection by considering a set of candidate weights and averaging over them based on their posterior probabilities. This approach accounts for the uncertainty in the model selection process and ensures that the final weight selection balances the complexity of the copula model with its fit to the data.

The mixed copula model combines two copula functions, C_1 and C_2, to capture the joint dependence structure between two random variables. The mixed copula is defined as

$$C_{\text{mix}}(u, v; \theta, w) = wC_1(u, v; \theta_1) + (1 - w)C_2(u, v; \theta_2), \tag{3}$$

where $w \in [0, 1]$ represents the weight parameter and $\theta = (\theta_1, \theta_2)$ denotes the parameters associated with each copula.

We specified a grid of candidate weight parameters $\{w_i\}$ across the range $[0, 1]$. For each candidate weight w_i, the parameters θ_1 and θ_2 are estimated using MLE.

2.3.1. Derivation of Posterior Weights

According to the Bayesian framework, the posterior probability of a model (or weight parameter) w_i, given the data, is proportional to the likelihood of the data under that model, multiplied by the prior probability of the model. Mathematically, this is expressed as

$$p(w_i \mid \text{data}) = \frac{p(\text{data} \mid w_i) \cdot p(w_i)}{p(\text{data})} \tag{4}$$

where $p(w_i \mid \text{data})$ is the posterior probability of the weight w_i given the data.$p(\text{data} \mid w_i)$ is the likelihood of the data given the weight w_i. $p(w_i)$ is the prior probability of weight w_i. $p(\text{data})$ is the marginal likelihood (evidence), which normalizes the posterior distribution.

Given the absence of strong prior information about the weights, we assume a uniform prior distribution over the candidate weights. Therefore, the posterior becomes proportional to the likelihood:

$$p(w_i \mid \text{data}) \propto p(\text{data} \mid w_i) \tag{5}$$

The posterior probability is normalized by summing over all candidate weights:

$$p(w_i \mid \text{data}) = \frac{p(\text{data} \mid w_i)}{\sum_{j=1}^{N} p(\text{data} \mid w_j)} \tag{6}$$

2.3.2. BIC for Likelihood Approximation

Direct computation of the likelihood $p(\text{data} \mid w_i)$ is often computationally expensive, particularly in high-dimensional copula models. To simplify this, we approximate the likelihood using BIC, a common model selection criterion that balances goodness of fit with model complexity. BIC is defined as follows:

The BIC for each model is computed as

$$\text{BIC}(w_i) = -2 \cdot L(w_i, \theta|\text{data}) + d_i \cdot \log(n), \tag{7}$$

where $L(w_i, \theta|\text{data})$ is the log-likelihood of the mixed copula model with weight w_i, d_i represents the number of estimated parameters, and n is the number of observations.

$$L(w_i \mid \text{data}) \propto \exp\left(-\frac{1}{2} BIC(w_i)\right) \tag{8}$$

2.3.3. Posterior Weight Calculation

From Equation (6), we can calculate the posterior probability of each candidate weight using two approaches:

1. Original BIC-Based BMA:
   The posterior probability for each weight parameter w_i is approximated using the BIC values:
   $$p(w_i|\text{data}) \approx \frac{\exp\left(-\frac{1}{2}\text{BIC}(w_i)\right)}{\sum_{j=1}^{N}\exp\left(-\frac{1}{2}\text{BIC}(w_j)\right)}, \tag{9}$$
   assuming equal prior probabilities for all candidate weights. The BMA estimate of the optimal weight parameter $\hat{w}_{\text{BMA}}$ is then obtained as
   $$\hat{w}_{\text{BMA}} = \sum_{i=1}^{N} w_i \cdot p(w_i|\text{data}). \tag{10}$$
2. Alternative BMA with Sample Size Adjustment ($\text{BMA}_{\log}$):
   However, traditional BMA can sometimes over-penalize models with extreme weights because the BIC imposes penalties based on model complexity. BIC might consider a model with an extreme weight more complex, especially in cases with smaller sample sizes, leading to suboptimal weight selection. To account for potential biases due to sample size, an alternative weighting method, $\text{BMA}_{\log}$, is applied. This approach adjusts the BIC by incorporating the logarithm of the sample size n, providing a more balanced penalty for model complexity. The transformed weight $p_{\log,i}$ is computed as
   $$p_{\log,i} = \frac{\exp\left(-\frac{1}{2}\frac{\text{BIC}(w_i)}{\log(n)}\right)}{\sum_{j=1}^{N}\exp\left(-\frac{1}{2}\frac{\text{BIC}(w_j)}{\log(n)}\right)}. \tag{11}$$
   The alternative $\text{BMA}_{\log}$ estimate of the optimal weight parameter $\hat{w}_{\text{BMA}_{\log}}$ is then calculated as
   $$\hat{w}_{\text{BMA}_{\log}} = \sum_{i=1}^{N} w_i \cdot p_{\log,i}. \tag{12}$$

This adjustment reduces the complexity penalty for extreme weights, allowing the model to focus more on the fit to the data rather than over-penalizing the model's complexity. As a result, $\text{BMA}_{\log}$ performs better in selecting extreme weights when they are necessary for capturing the underlying dependency structure, particularly in situations where strong tail dependence is present.

3. Simulation Study

To evaluate the performance of the BMA method, we conduct a simulation study focusing on three possible combinations of mixture copulas: (1) the Clayton copula and the Gumbel copula, (2) the Clayton copula and the survival Gumbel copula, and (3) the survival Clayton copula and the survival Gumbel copula [26]. The procedure involves the following steps:

1. Generate Datasets: Simulate 1000 pairs of data from the mixture copula for different parameter settings. The parameters (θ_1, θ_2) are set to $(2, 2)$, $(2, 6)$, $(6, 2)$, and $(6, 6)$. The weights (w_1, w_2) for the mixtures are varied as $(0.1, 0.9)$, $(0.3, 0.7)$, $(0.5, 0.5)$, $(0.7, 0.3)$, and $(0.9, 0.1)$.
2. Estimate Using Mixture Copula Method:
   (a) Estimate the parameters of the datasets. Obtain the estimates $(\hat{\theta_1}, \hat{\theta_2})$ and the weights $(\hat{W}_1, \hat{W}_2)$ for the first and second copulas, respectively.

(b) Calculate the Tail Dependence Coefficient of the mixture copula using the parameter estimates from (a) and apply Equations (5) and (6).

3. Estimate using BMA and BMAlog Methods:
   (a) Estimate the parameters of the datasets using the maximum likelihood estimator (MLE). Obtain the estimates $(\hat{\theta_1}, \hat{\theta_2})$.
   (b) Use the BIC from the parameter estimation to determine the weights for the BMA approach, resulting in weights (W_{C_1}, W_{C_2}) for BMA and (W_{Clog_1}, W_{Clog_2}) for BMAlog.
   (c) Calculate the TDC using the weights and parameter estimates from (a) and (b) with Equations (5) and (6).
4. Estimate using Nonparametric Methods: Estimate the tail dependence coefficient directly from the datasets using the estimator from Schmidt and Stadtmuller [27].
5. Repeat Steps 1–4: Perform steps 1 to 3 for 100 iterations.
6. Bias Analysis: Determine the bias of each estimator and compare them to assess performance.

The criteria for comparing the mixture copula method and the BMA method in TDC estimation is the Root Mean Square Error (RMSE). The RMSE evaluates the error between the estimated TDC $(\hat{\lambda}_i)$ and the true TDC (λ) over 100 iterations:

$$RMSE = \sqrt{\frac{1}{100}\sum_{i=1}^{100}(\hat{\lambda}_i - \lambda)^2}. \tag{13}$$

3.1. Simulation Result of Mixture of Clayton and Gumbel Copulas

The simulation results for the Mixture Clayton and Gumbel copulas are presented in Table 1 and illustrated in Figure 1. Table 1 provides a detailed comparison of the estimated Tail Dependence Coefficients obtained using the Mixture Copula method, and BMA and BMAlog methods, under various parameter and weight settings. Figure 1 visually represents the performance of these methods across different scenarios, highlighting differences in RMSE between the approaches.

For the mixture of Clayton and Gumbel copulas, the results presented in Figure 1a–d show that the Mixture Copula method consistently performs well across all parameter settings, as evidenced by its relatively low RMSE values in all cases. This indicates that the Mixture Copula method provides robust estimates of the Tail Dependence Coefficients regardless of the weight combinations or parameter settings used in the simulation.

Table 1. RMSE of mixture of Clayton and Gumbel copulas.

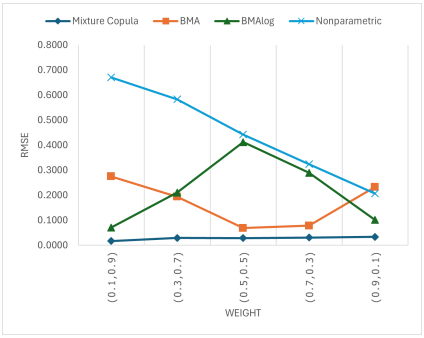
Parameter	Weight	Mixture	BMA	BMAlog	Nonpara
$\theta_1 = 2, \theta_2 = 2$	$(w_1 = 0.1, w_2 = 0.9)$	0.0285	0.2446	0.0707	0.2498
	$(w_1 = 0.3, w_2 = 0.7)$	0.0386	0.1191	0.2121	0.2843
	$(w_1 = 0.5, w_2 = 0.5)$	0.0407	0.0106	0.2998	0.2178
	$(w_1 = 0.7, w_2 = 0.3)$	0.0371	0.1319	0.2063	0.2491
	$(w_1 = 0.9, w_2 = 0.1)$	0.0287	0.2533	0.0745	0.2236
$\theta_1 = 2, \theta_2 = 6$	$(w_1 = 0.1, w_2 = 0.9)$	0.0166	0.2747	0.0707	0.6702
	$(w_1 = 0.3, w_2 = 0.7)$	0.0289	0.1936	0.2103	0.5831
	$(w_1 = 0.5, w_2 = 0.5)$	0.0285	0.0684	0.4115	0.4422
	$(w_1 = 0.7, w_2 = 0.3)$	0.0308	0.0782	0.2894	0.3240
	$(w_1 = 0.9, w_2 = 0.1)$	0.0331	0.2328	0.1009	0.2068
$\theta_1 = 6, \theta_2 = 2$	$(w_1 = 0.1, w_2 = 0.9)$	0.0305	0.2305	0.0891	0.2396
	$(w_1 = 0.3, w_2 = 0.7)$	0.0353	0.0831	0.2673	0.2437
	$(w_1 = 0.5, w_2 = 0.5)$	0.0336	0.0586	0.4365	0.2230
	$(w_1 = 0.7, w_2 = 0.3)$	0.0269	0.1885	0.2142	0.2091
	$(w_1 = 0.9, w_2 = 0.1)$	0.0218	0.2991	0.0730	0.1620

Table 1. *Cont.*

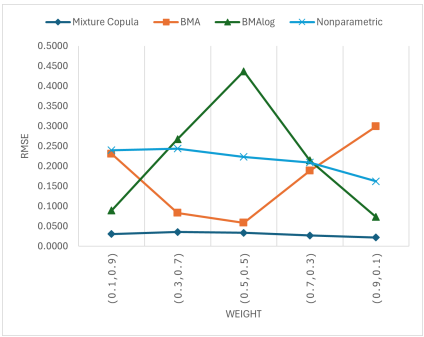
Parameter	Weight	Mixture	BMA	BMAlog	Nonpara
$\theta_1 = 6, \theta_2 = 6$	$(w_1 = 0.1, w_2 = 0.9)$	0.0225	0.2384	0.0891	0.6859
	$(w_1 = 0.3, w_2 = 0.7)$	0.0338	0.1372	0.2673	0.5257
	$(w_1 = 0.5, w_2 = 0.5)$	0.0332	0.0198	0.4111	0.3983
	$(w_1 = 0.7, w_2 = 0.3)$	0.0349	0.1185	0.2774	0.2627
	$(w_1 = 0.9, w_2 = 0.1)$	0.0303	0.2669	0.0922	0.1591



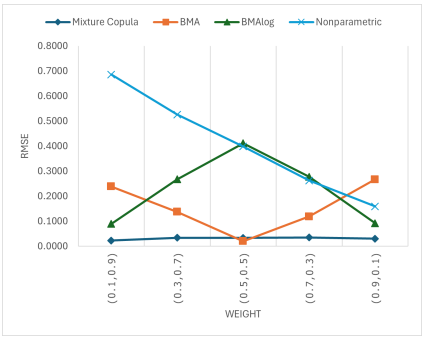
(**a**) Parameter $(\theta_1 = 2, \theta_2 = 2)$



(**b**) Parameter $(\theta_1 = 2, \theta_2 = 6)$



(**c**) Parameter $(\theta_1 = 6, \theta_2 = 2)$



(**d**) Parameter $(\theta_1 = 6, \theta_2 = 6)$

Figure 1. RMSE of mixture of Clayton and Gumbel copulas.

In contrast, the performance of the BMA method varies depending on the weight combination and parameter settings. The BMA method shows good performance, with lower RMSE values when the weights are balanced, particularly at (0.5, 0.5), and when the parameters are (2, 2) or (6, 6). In these scenarios, the BMA method even outperforms the Mixture Copula method, indicating its effectiveness in scenarios where the true dependence structure might be more evenly mixed between the two copulas. However, as the weight distribution becomes more extreme (i.e., closer to (0.1, 0.9) or (0.9, 0.1)), the performance of the BMA method declines, resulting in higher RMSE values. This suggests that the BMA method is less effective when the underlying dependence is dominated by one copula over the other.

On the other hand, the BMA with log-transformed weights (BMAlog) method displays a contrasting performance pattern. The BMAlog method performs worse than the BMA method when the weights are balanced at (0.5, 0.5), showing higher RMSE values. However, its performance improves when the weights become more extreme, suggesting that the log transformation adjusts better to scenarios where the dependence structure is heavily skewed towards one copula. Despite this improvement in more extreme cases, the BMAlog method does not outperform the Mixture Copula method in any scenario, indicating its limitations in providing more accurate TDC estimates than the Mixture Copula method.

Overall, the Mixture Copula method proves to be the most reliable across all cases, with consistently low RMSE values. The BMA method shows potential advantages in

balanced scenarios but suffers from decreased accuracy when the dependence is highly skewed. Meanwhile, the BMAlog method seems to adjust better in these skewed scenarios but still falls short of the Mixture Copula method's accuracy. These findings suggest that while BMA methods can offer some benefits, particularly in balanced dependence structures, they may not always outperform traditional methods in cases with extreme dependence weightings.

The contrasting performance of the BMA and BMAlog methods highlights the impact of the weighting strategy on the estimation accuracy of the TDC. The BMA method uses standard BIC-based weights, which seem to work well when there is no clear dominance of one copula over the other. In contrast, the BMAlog method, which adjusts weights based on a log transformation, may be better suited for cases where there is an imbalance in the contributions of each copula. However, the inability of the BMAlog method to surpass the Mixture Copula method suggests that the log transformation does not fully compensate for the complexities introduced by extreme weight distributions.

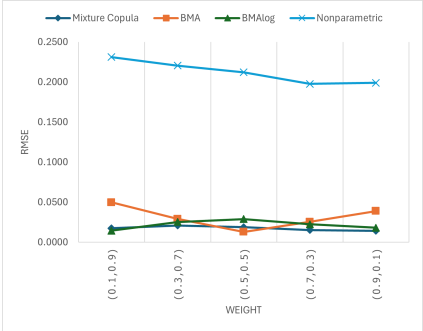
These results imply that the choice between using a Mixture Copula method or a BMA approach should be guided by the characteristics of the dependence structure in the data. For data with a more balanced dependence structure, the BMA method may provide advantages. However, for data with an extreme dependence on one copula, the Mixture Copula method remains the more reliable choice. Future research could explore alternative weighting schemes or adjustments to the Bayesian averaging methods to further enhance their performance in diverse scenarios.

3.2. Simulation Result of Mixture of Clayton and Survival Gumbel Copula

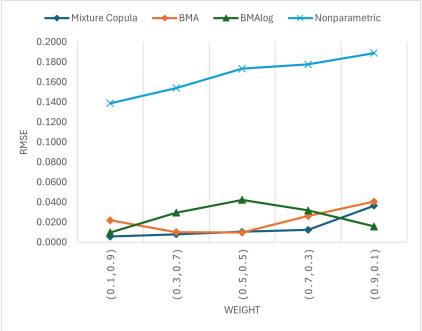
The simulation results for the Mixture Clayton and survival Gumbel copula are presented in Table 2 and illustrated in Figure 2.

Table 2. RMSE of mixture of Clayton and survival Gumbel copulas.

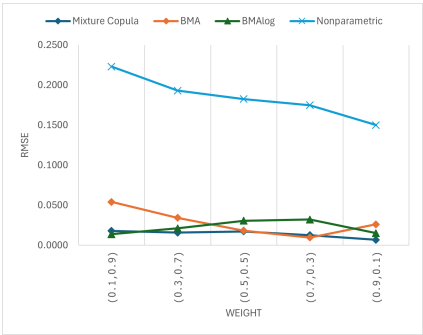
Parameter	Weight	Mixture	BMA	BMAlog	Nonpara
$\theta_1 = 2, \theta_2 = 2$	$(w_1 = 0.1, w_2 = 0.9)$	0.0173	0.0497	0.0144	0.2311
	$(w_1 = 0.3, w_2 = 0.7)$	0.0209	0.0291	0.0253	0.2204
	$(w_1 = 0.5, w_2 = 0.5)$	0.0187	0.0130	0.0289	0.2122
	$(w_1 = 0.7, w_2 = 0.3)$	0.0153	0.0253	0.0224	0.1977
	$(w_1 = 0.9, w_2 = 0.1)$	0.0142	0.0389	0.0181	0.1990
$\theta_1 = 2, \theta_2 = 6$	$(w_1 = 0.1, w_2 = 0.9)$	0.0057	0.0219	0.0098	0.1388
	$(w_1 = 0.3, w_2 = 0.7)$	0.0080	0.0101	0.0296	0.1539
	$(w_1 = 0.5, w_2 = 0.5)$	0.0104	0.0097	0.0423	0.1733
	$(w_1 = 0.7, w_2 = 0.3)$	0.0123	0.0262	0.0317	0.1776
	$(w_1 = 0.9, w_2 = 0.1)$	0.0365	0.0406	0.0157	0.1889
$\theta_1 = 6, \theta_2 = 2$	$(w_1 = 0.1, w_2 = 0.9)$	0.0179	0.0540	0.0137	0.2230
	$(w_1 = 0.3, w_2 = 0.7)$	0.0157	0.0342	0.0211	0.1929
	$(w_1 = 0.5, w_2 = 0.5)$	0.0172	0.0182	0.0306	0.1825
	$(w_1 = 0.7, w_2 = 0.3)$	0.0126	0.0095	0.0321	0.1749
	$(w_1 = 0.9, w_2 = 0.1)$	0.0067	0.0261	0.0152	0.1500
$\theta_1 = 6, \theta_2 = 6$	$(w_1 = 0.1, w_2 = 0.9)$	0.0050	0.0203	0.0081	0.1379
	$(w_1 = 0.3, w_2 = 0.7)$	0.0056	0.0081	0.0208	0.1320
	$(w_1 = 0.5, w_2 = 0.5)$	0.0042	0.0067	0.0190	0.1380
	$(w_1 = 0.7, w_2 = 0.3)$	0.0057	0.0185	0.0150	0.1365
	$(w_1 = 0.9, w_2 = 0.1)$	0.0109	0.0302	0.0068	0.1683



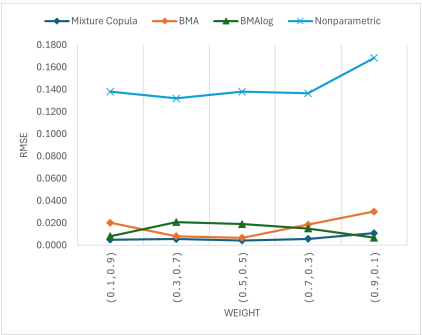
(**a**) Parameter ($\theta_1 = 2, \theta_2 = 2$)



(**b**) Parameter ($\theta_1 = 2, \theta_2 = 6$)



(**c**) Parameter ($\theta_1 = 6, \theta_2 = 2$)



(**d**) Parameter ($\theta_1 = 6, \theta_2 = 6$)

Figure 2. RMSE of mixture of Clayton and survival Gumbel copulas.

For the mixture of Clayton and survival Gumbel copulas, the results depicted in Figure 2a–d show a pattern similar to the previous case with the Clayton and Gumbel copulas. The BMA method tends to perform better when the weights are more balanced (e.g., at $(0.5, 0.5)$), as evidenced by lower RMSE values in these scenarios. However, as the weight distribution becomes more extreme (e.g., at $(0.1, 0.9)$ or $(0.9, 0.1)$), the BMA method's performance declines, resulting in higher RMSE values. This suggests that BMA is more suited to situations where there is a more equal contribution from both copulas.

Conversely, the BMAlog method shows improved performance in cases with extreme weight distributions. The BMAlog achieves lower RMSE values when one copula dominates (e.g., weights closer to $(0.1, 0.9)$ or $(0.9, 0.1)$), indicating that the log transformation effectively adjusts for scenarios with skewed dependence structures. Notably, unlike the previous case with the Clayton and Gumbel copulas, BMAlog outperforms the Mixture Copula method in every scenario presented in Figure 2a–d. This result suggests that BMAlog is more robust in handling extreme weight settings when the survival Gumbel copula is involved.

The comparison highlights the differences in performance between BMA and BMAlog when applied to a mixture of Clayton and survival Gumbel copulas. The BMA method shows its strength in scenarios where the weights are balanced, suggesting that it is suitable for cases where the true underlying dependence structure is a more equal mix of the two copulas. However, its performance deteriorates when the structure becomes more skewed, indicating a limitation in handling cases where one copula dominates.

In contrast, BMAlog's consistent superiority across all scenarios in this case demonstrates its effectiveness in adjusting to various dependence structures, especially when there is an extreme imbalance between the copulas. The log transformation seems to provide a significant advantage when dealing with skewed weight distributions, allowing BMAlog to outperform not only BMA but also the Mixture Copula method in every scenario tested.

The fact that BMAlog performs better than the Mixture Copula method across all cases suggests that it may be more adaptable to changes in the underlying copula structure,

particularly when the survival Gumbel copula is one of the components. This could be due to the unique properties of the survival Gumbel copula, which may require a more nuanced adjustment for extreme weights—a scenario where BMAlog excels.

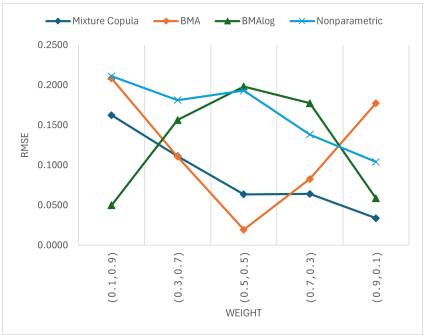
3.3. Simulation Result of Mixture of Survival Clayton and Survival Gumbel Copulas

For the last scenario, the simulation results for the Mixture survival Clayton and survival Gumbel copulas are presented in Table 3 and illustrated in Figure 3.

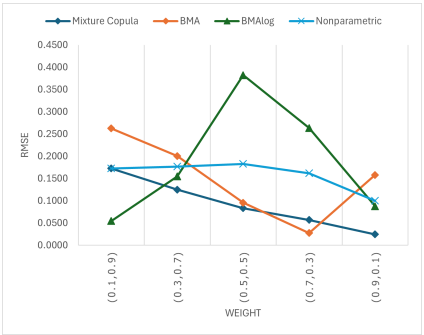
For the mixture of survival Clayton and survival Gumbel copulas, the results in Figure 3a–d show that there are cases where the BMAlog method outperforms the Mixture Copula method, particularly when the weight distribution is more extreme (e.g., at $(0.1, 0.9)$ or $(0.9, 0.1)$). This suggests that BMAlog is capable of providing better estimates of the Tail Dependence Coefficient (TDC) in scenarios where the underlying dependence structure is highly skewed towards one of the copulas.

Table 3. RMSE of mixture of survival Clayton and survival Gumbel copulas.

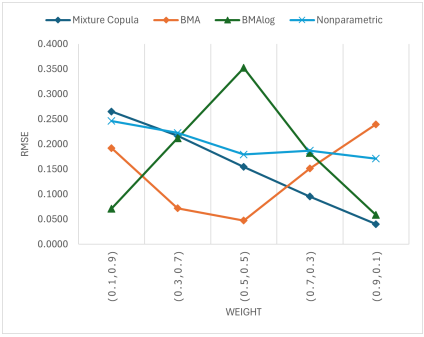
Parameter	Weight	Mixture	BMA	BMAlog	Nonpara
$\theta_1 = 2, \theta_2 = 2$	$(w_1 = 0.1, w_2 = 0.9)$	0.1622	0.2082	0.0499	0.2109
	$(w_1 = 0.3, w_2 = 0.7)$	0.1112	0.1105	0.1564	0.1811
	$(w_1 = 0.5, w_2 = 0.5)$	0.0636	0.0194	0.1981	0.1930
	$(w_1 = 0.7, w_2 = 0.3)$	0.0640	0.0827	0.1774	0.1381
	$(w_1 = 0.9, w_2 = 0.1)$	0.0337	0.1773	0.0586	0.1039
$\theta_1 = 2, \theta_2 = 6$	$(w_1 = 0.1, w_2 = 0.9)$	0.1726	0.2625	0.0545	0.1726
	$(w_1 = 0.3, w_2 = 0.7)$	0.1249	0.2005	0.1545	0.1766
	$(w_1 = 0.5, w_2 = 0.5)$	0.0833	0.0954	0.3821	0.1829
	$(w_1 = 0.7, w_2 = 0.3)$	0.0568	0.0275	0.2633	0.1617
	$(w_1 = 0.9, w_2 = 0.1)$	0.0245	0.1577	0.0878	0.1000
$\theta_1 = 6, \theta_2 = 2$	$(w_1 = 0.1, w_2 = 0.9)$	0.2650	0.1920	0.0710	0.2460
	$(w_1 = 0.3, w_2 = 0.7)$	0.2164	0.0719	0.2116	0.2224
	$(w_1 = 0.5, w_2 = 0.5)$	0.1544	0.0472	0.3522	0.1792
	$(w_1 = 0.7, w_2 = 0.3)$	0.0954	0.1512	0.1821	0.1871
	$(w_1 = 0.9, w_2 = 0.1)$	0.0402	0.2395	0.0586	0.1710
$\theta_1 = 6, \theta_2 = 6$	$(w_1 = 0.1, w_2 = 0.9)$	0.0270	0.2400	0.0719	0.1620
	$(w_1 = 0.3, w_2 = 0.7)$	0.0306	0.1499	0.2191	0.1956
	$(w_1 = 0.5, w_2 = 0.5)$	0.0344	0.0463	0.3696	0.1861
	$(w_1 = 0.7, w_2 = 0.3)$	0.0287	0.0766	0.2633	0.2128
	$(w_1 = 0.9, w_2 = 0.1)$	0.0285	0.2050	0.0878	0.1534



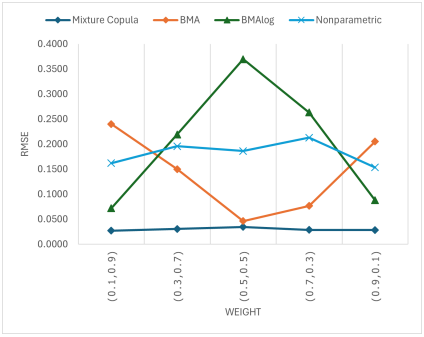
(**a**) Parameter $(\theta_1 = 2, \theta_2 = 2)$



(**b**) Parameter $(\theta_1 = 2, \theta_2 = 6)$



(**c**) Parameter ($\theta_1 = 6, \theta_2 = 2$)



(**d**) Parameter ($\theta_1 = 6, \theta_2 = 6$)

Figure 3. RMSE of mixture of survival Clayton and survival Gumbel copulas.

The BMA method, on the other hand, tends to perform better when the weights are more balanced (e.g., at $(0.5, 0.5)$), resulting in lower RMSE values. This indicates that BMA is more effective when there is a relatively equal contribution from both copulas. However, the performance of BMA declines as the weight distribution becomes more extreme, as seen by the increase in RMSE values, which aligns with its behavior in the previous cases.

In contrast, BMAlog demonstrates an advantage in scenarios with extreme weights, where it adjusts more effectively for the skewed dependence structure and outperforms the Mixture Copula method in several cases. This behavior is consistent with its performance in the earlier scenarios involving the survival Gumbel copula, reinforcing the observation that BMAlog's log-transformed weighting scheme is particularly suited to handling extreme dependencies.

These findings suggest that the effectiveness of each method depends heavily on the underlying distribution of weights between the two copulas. The Mixture Copula method generally maintains a stable performance across different settings, with consistently low RMSE values, making it a reliable choice overall. However, BMA shows its strength in cases where the mixture is balanced, while BMAlog demonstrates its robustness in handling scenarios with extreme weights.

The ability of BMAlog to outperform the Mixture Copula method in cases with extreme weights suggests that its log-transformed weighting scheme provides a significant adjustment that better captures the characteristics of the survival copulas involved. This is particularly relevant when the true data-generating process is heavily influenced by one copula, as BMAlog adapts to this skewness and offers more accurate TDC estimates.

3.4. Simulation Result: Extreme Weight Case

From the previous study, we observed that the BMAlog method can sometimes outperform the Mixture Copula method in cases with extreme weights. Therefore, we conduct further analysis to examine the performance of the proposed BMAlog method, specifically in scenarios with more extreme weight distributions. The simulation steps are as follows:

1. Generate the datasets of 1000 pairs of the mixture copula, where parameters (θ_1, θ_2) are (2, 2), (2, 6), (6, 2), and (6, 6) and weights are (0.01, 0.99), (0.02, 0.98), . . . , (0.1, 0.9) and (0.9, 0.1), (0.91, 0.09), . . . , (0.99, 0.01).
2. Estimate the datasets using Mixture Copula method.
   (a) Estimate the parameter of datasets. Obtain the $(\hat{\theta_1}, \hat{\theta_2})$ and $(\hat{W_1}, \hat{W_2})$ for first copula and second copula.
   (b) Calculate the TDC of the mixture copula from (a) using Equations (5) and (6).
3. Estimate the datasets using BMAlog method.
   (a) Estimate the parameter of datasets. Obtain $(\hat{\theta_1}, \hat{\theta_2})$ using maximum likelihood estimator.
   (b) Use the BIC from estimating the parameter to obtain the weight of BMA approach (W_{Clog_1}, W_{Clog_2}).

(c) Calculate the TDC from the weight and parameter values from (a) and (b) using Equations (5) and (6).

4. Determine the error for both the Mixture Copula method and the BMAlog method.
5. Compare the errors obtained in Step 1 and calculate the percentage of cases where the BMAlog method has a lower error than the Mixture Copula method.

Figure 4 shows the percentage of cases where the BMAlog method performs better than the Mixture Copula method for different weight settings in the mixture of Clayton and Gumbel copulas. The results suggest that the Mixture Copula method generally outperforms the BMAlog method across most scenarios, even when the weight distribution is extreme. This is indicated by the relatively low percentages, especially when the weights are closer to balanced (e.g., $(0.50, 0.50)$) or moderately skewed.

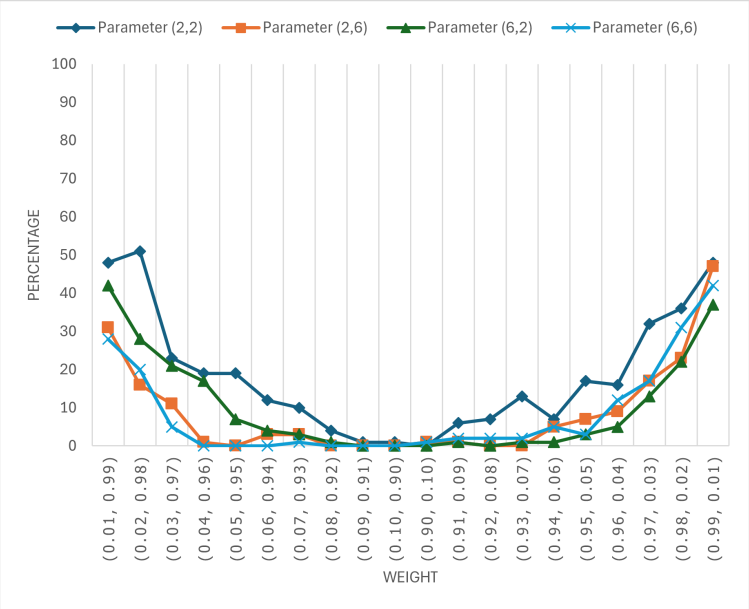


Figure 4. Percentage of BMAlog method better than Mixture Copula method for mixture of Clayton and Gumbel copulas.

However, the BMAlog method does show some advantages in very specific cases where the weight distribution is extremely imbalanced, particularly at $(0.02, 0.98)$. In this scenario, the BMAlog method outperforms the Mixture Copula method, achieving a higher percentage where it yields a lower error. This suggests that the BMAlog method may have an edge in scenarios where one copula almost entirely dominates the mixture.

The findings suggest that while the BMAlog method has some potential in handling extreme weight distributions, its performance is generally not superior to the Mixture Copula method in most cases. The BMAlog method's advantage appears limited to very specific situations where the weight is almost entirely skewed towards one component, as seen at $(0.02, 0.98)$. This could be due to the log-transformed weighting scheme in BMAlog, which might better adjust to scenarios with highly uneven contributions from the two copulas.

For the mixture of Clayton and survival Gumbel copulas, the BMAlog method shows good performance in certain cases (Figure 5). Specifically, for the parameter settings $(2, 2)$ and $(6, 2)$ with extreme weights favoring the survival Gumbel copula, the BMAlog method performs better than the Mixture Copula method more than 50% of the time. Additionally, for the parameter settings $(2, 2)$ and $(2, 6)$ with extreme weights favoring the Clayton copula, the BMAlog method performs comparably to the Mixture Copula method, with the BMAlog method showing better results roughly 50% of the time.

For the mixture of survival Clayton and survival Gumbel copulas, the results in Figure 6 reveal notable patterns in the performance of the BMAlog method compared

to the Mixture Copula method. The BMAlog method demonstrates strong performance when the weight is highly skewed towards the survival Gumbel copula (e.g., $(0.01, 0.99)$ or $(0.02, 0.98)$). In these scenarios, the BMAlog method consistently outperforms the Mixture Copula method, achieving better results in nearly all cases, as indicated by the percentage values close to 100%. This suggests that the BMAlog method is particularly effective in situations where the dependence structure is predominantly influenced by the survival Gumbel copula. However, as the weight distribution becomes more balanced or shifts towards the survival Clayton copula (e.g., $(0.99, 0.01)$ or $(0.98, 0.02)$), the performance of the BMAlog method declines. In these cases, the percentage of instances where the BMAlog method outperforms the Mixture Copula method drops significantly, reaching as low as 0% when the weight is most extreme towards the survival Clayton copula. This indicates that the BMAlog method is less effective when the dependence structure is dominated by the survival Clayton copula.

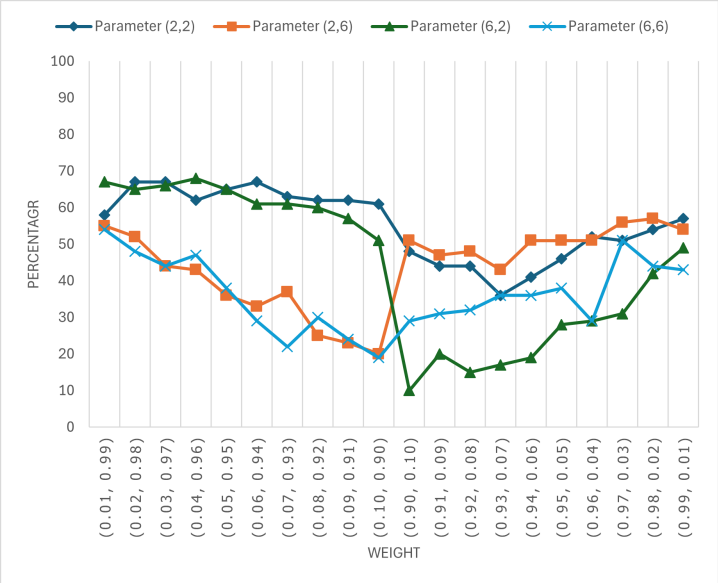


Figure 5. Percentage of BMAlog method better than Mixture Copula method for mixture of Clayton and survival Gumbel copulas.

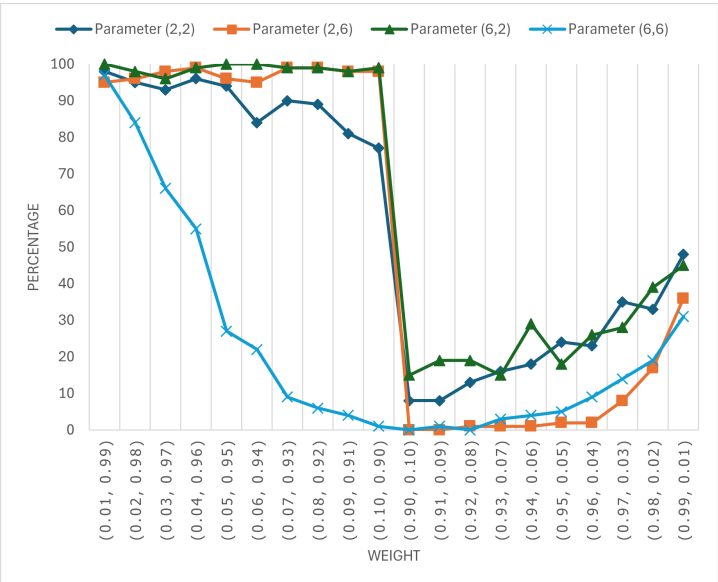


Figure 6. Percentage of BMAlog method better than Mixture Copula for mixture of survival Clayton and survival Gumbel copulas.

3.5. Asymptotic Properties

In this section, we are going to study the asymptotic properties of each estimator. We repeat the simulation study; however, this time, instead of varying the parameter and weight, we fix the parameter as $(2, 2)$ and weight as $(0.1, 0.9)$, where the numbers of datasets are 500, 1000, and 2000.

From Table 4, we observe that as the sample size n increases, the RMSE consistently decreases across all mixture copula combinations and estimation methods. This trend indicates that the estimators exhibit strong asymptotic properties. Notably, the BMA_{log} estimator consistently outperforms the standard BMA and Mixture estimators, particularly when dealing with extreme weights such as $w = 0.1$ or $w = 0.9$. In the C-SG and SC-SG copulas, BMA_{log} demonstrates the lowest RMSE values, especially as n increases, suggesting that it is more effective at capturing the underlying dependency structure in these scenarios. The adjustment for sample size in BMA_{log} helps reduce over-penalization for complexity, allowing it to handle extreme weights more effectively. This highlights the robustness of BMA_{log} in accurately estimating tail dependencies, making it particularly well-suited for modeling financial contagion and other complex dependency structures.

Table 4. RMSE of Mixture Copula with parameter $(2, 2)$, weight $(0.1, 0.9)$, and different numbers of datasets.

Mixture Copula	*n*	Mixture	BMA	BMAlog
C-G	$n = 500$	0.0491	0.2454	0.0707
	$n = 1000$	0.0311	0.2437	0.0707
	$n = 2000$	0.0241	0.2427	0.0707
C-SG	$n = 500$	0.0693	0.0531	0.0219
	$n = 1000$	0.0255	0.0530	0.0135
	$n = 2000$	0.0160	0.0505	0.0121
SC-SG	$n = 500$	0.1986	0.2074	0.0540
	$n = 1000$	0.1849	0.2065	0.0520
	$n = 2000$	0.1407	0.2045	0.0515

3.6. Misspecified Copula

For this section, we are going to explore the simulation study in the case when we misspecified the copula. In this case, we are going to repeat the simulation study but, this time, we will generate the mixture copula from three possible combinations and estimate those datasets using the different mixture copulas where the parameter is $(2, 2)$ and weight is $(0.1, 0.9)$.

From the simulation results presented in Table 5, we observe the impact of misspecifying the copula on the estimation of the tail dependence structure, as measured by RMSE. The study shows that when the true mixture copula is the combination of the Clayton and Gumbel (C-G) copulas, the RMSE values are relatively high for all methods when we estimate the model using the Clayton–survival Gumbel (C-SG) or survival Clayton–survival Gumbel (SC-SG) copulas. This indicates that misspecifying the mixture copula has a significant impact on the estimation accuracy of tail dependence, particularly when the true underlying model is a mixture of Clayton and Gumbel copulas.

In contrast, when the true mixture copula is the C-SG copula, the RMSE values are lower compared to the C-G copula case, although misspecification still affects the results. Specifically, the RMSE for the BMA_{log} estimator is notably lower than for the other methods, particularly in the case where the estimator copula is SC-SG, where BMA_{log} performs best with an RMSE of 0.0175. This suggests that BMA_{log} is more robust when the mixture copula is misspecified, especially in capturing tail dependence.

For the SC-SG copula, the results show that estimation using the misspecified C-G and C-SG copulas produces relatively low RMSE values across all methods. Notably, BMA_{log}

once again outperforms the other methods, especially when the estimator is C-SG, with an RMSE of 0.0516.

Table 5. RMSE of estimating with the misspecified copula.

True Mixture Copula	Estimator Mixture Copula	Mixture	BMA	BMAlog
C-G	C-SG	0.4482	0.5477	0.4420
	SC-SG	0.2200	0.1972	0.1947
C-SG	C-G	0.0836	0.2308	0.1088
	SC-SG	0.1663	0.2624	0.0175
SC-SG	C-G	0.1130	0.1709	0.1033
	C-SG	0.1123	0.1129	0.0516

In summary, the simulations demonstrate that misspecifying the copula structure can have a considerable impact on the accuracy of tail dependence estimation, particularly when the true model involves the Clayton and Gumbel copulas. However, BMA_{log} shows better performance overall in handling misspecified models, consistently yielding lower RMSE values than the standard Mixture and BMA estimators, indicating its robustness in the presence of model misspecification.

4. Application on World Markets

To validate the performance of the proposed methods and highlight the potential occurrence of extreme weights in mixture copulas with real-world data, we conduct an application study. For this study, we selected 25 markets from a diverse range of developed and emerging countries across various regions, including Asia, Africa, the Americas, and Europe. The selection includes markets that hold significant value and influence within their respective regions. These markets represent a mix of both advanced economies and emerging markets, allowing for a more comprehensive examination of the contagion effect between the MSCI World Index and these selected regional markets. By including a broad spectrum of financial environments, we aim to demonstrate the robustness of our approach and its ability to capture extreme dependencies in a real-world financial context. The chosen markets are of high importance, both regionally and globally, due to their economic potential and the role they play in driving financial trends within their regions.

The dataset consists of daily returns of the markets and the MSCI World Index from 1 January 2021 to 31 December 2023. We apply four different mixture copulas to analyze these data. The best-fitting mixture copula was selected based on the AIC, with the lowest AIC value indicating the most suitable copula model (Table 6).

Table 6. Estimation results and AICs.

Country	Mixture Copula	W_1	W_2	θ_1	θ_2	AIC
Argentina (S&P Merval)	C-G	0.2528	0.7472	1.2482	1.3509	−80.81
	C-SG	0.0000	1.0000	2.2964	1.3595	−66.81
	SC-SG	0.5291	0.4709	0.6754	1.5152	−83.27
Australia (S&P ASX50)	C-G	0.3376	0.6624	1.5837	1.2223	−89.14
	C-SG	0.0514	0.9486	9.6021	1.3379	−88.42
	SC-SG	0.0781	0.9219	9.3779	1.3133	−96.69
Austria (ATX)	C-G	0.4321	0.5679	1.4161	2.2344	−335.53
	C-SG	0.1042	0.8958	0.2297	2.0739	−327.54
	SC-SG	0.2144	0.7856	3.2849	1.8369	−340.15
Belgium (BEL20)	C-G	0.2182	0.7818	3.0951	1.8612	−372.67
	C-SG	0.1062	0.8938	0.2099	2.1003	−353.00
	SC-SG	0.3711	0.6289	1.3537	2.1893	−373.01

Table 6. *Cont.*

Country	Mixture Copula	W_1	W_2	θ_1	θ_2	AIC
Bulgaria (BSE Sofix)	C-G	0.1109	0.8891	2.3156	1.1220	−19.15
	C-SG	0.0000	1.0000	0.8503	1.1771	−15.72
	SC-SG	0.7474	0.2526	0.1607	1.7299	−21.36
China (China A50)	C-G	0.0935	0.9065	6.2841	1.0956	−18.84
	C-SG	0.0755	0.9245	8.0869	1.1120	−20.26
	SC-SG	0.0617	0.9383	6.9020	1.1243	−18.57
Colombia (FTSE Colombia)	C-G	0.2334	0.7666	2.7399	1.2927	−117.01
	C-SG	0.1119	0.8881	5.2849	1.3225	−103.15
	SC-SG	0.5746	0.4254	0.2949	2.2448	−121.25
Czech Republic (FTSE Czech)	C-G	0.3712	0.6288	2.2477	1.0662	−68.14
	C-SG	0.3610	0.6390	2.4023	1.0535	−66.90
	SC-SG	0.1299	0.8701	6.5507	1.2252	−70.20
France (CAC40)	C-G	0.4445	0.5555	3.1371	2.0011	−480.74
	C-SG	0.1190	0.8810	0.2912	2.4798	−486.70
	SC-SG	0.1616	0.8384	0.7379	2.4958	−490.00
Hungary (Budapest)	C-G	0.4845	0.5155	1.6789	1.1830	−106.93
	C-SG	0.0618	0.9382	10.9017	1.3920	−112.68
	SC-SG	0.0542	0.9458	14.8193	1.4044	−113.40
India (Bombay SE)	C-G	0.2584	0.7416	1.9643	1.3794	−130.17
	C-SG	0.0000	1.0000	2.0265	1.4771	−118.13
	SC-SG	0.5126	0.4874	0.3662	2.0568	−134.03
India (NIFTY50)	C-G	0.2683	0.7317	1.8452	1.3739	−126.72
	C-SG	0.0003	0.9997	3.7944	1.4725	−116.66
	SC-SG	0.4976	0.5024	0.3421	2.0142	−130.90
Indonesia (Jarkata SE)	C-G	0.1559	0.8441	2.4181	1.1679	−44.54
	C-SG	0.0639	0.9361	4.8558	1.2070	−38.33
	SC-SG	0.6904	0.3096	0.2253	1.8604	−44.41
Israel (TA35)	C-G	0.4465	0.5535	1.8923	1.8469	−235.08
	C-SG	0.1974	0.8026	0.2135	2.2084	−236.00
	SC-SG	0.2223	0.7777	1.1402	2.0208	−239.22
Kazakhstan (Kase)	C-G	0.0461	0.9539	6.4843	1.1164	−14.12
	C-SG	0.0377	0.9623	8.1919	1.1143	−9.09
	SC-SG	0.2362	0.7638	0.9815	1.0922	−12.76
Korea (Kospe)	C-G	0.2479	0.7521	1.3420	1.3319	−89.97
	C-SG	0.0000	1.0000	3.3904	1.3882	−82.84
	SC-SG	0.5201	0.4799	0.3446	1.7888	−91.91
Mexico (Mexico SE)	C-G	0.2065	0.7935	2.6923	1.6543	−266.44
	C-SG	0.2406	0.7594	0.2015	2.0365	−245.32
	SC-SG	0.4988	0.5012	0.9565	2.1497	−265.52
New Zealand (DJ New Zealand)	C-G	0.3079	0.6921	1.0506	1.1595	−40.88
	C-SG	0.0000	1.0000	1.9398	1.2517	−38.99
	SC-SG	0.0514	0.9486	8.8096	1.2106	−43.24
Spain (IBEX)	C-G	0.4331	0.5669	1.7875	1.8206	−314.64
	C-SG	0.0366	0.9634	0.1141	1.9008	−318.54
	SC-SG	0.2006	0.7994	0.9619	1.9954	−323.60
Srilanka (CSE All Share)	C-G	0.1651	0.8349	1.7569	1.0570	−11.59
	C-SG	0.2314	0.7686	1.6679	1.0000	−8.11
	SC-SG	0.1285	0.8715	3.0778	1.0542	−12.07
Turkey (BIST100)	C-G	0.2860	0.7140	1.3663	1.1237	−34.70
	C-SG	0.0000	1.0000	0.3787	1.2504	−33.83
	SC-SG	0.0337	0.9663	20.0239	1.2185	−37.94

Table 6. *Cont.*

Country	Mixture Copula	W_1	W_2	θ_1	θ_2	AIC
UK (FTSE100)	C-G	0.4500	0.5500	2.5371	1.6090	−296.53
	C-SG	0.1273	0.8727	0.1988	2.0326	−298.41
	SC-SG	0.2321	0.7679	0.6676	2.1098	−303.89
USA (NASDAQ)	C-G	0.3395	0.6605	5.7938	4.7346	−1389.28
	C-SG	0.0095	0.9905	0.3854	4.4684	−1384.76
	SC-SG	0.1391	0.8609	7.0025	4.4606	−1395.53
Vietnam (VN30)	C-G	0.1129	0.8871	5.8028	1.0330	−12.86
	C-SG	0.1352	0.8648	5.4069	1.0000	−11.61
	SC-SG	0.1369	0.8631	4.6080	1.0000	−14.59
Zimbabwe (ZSE All Share)	C-G	0.0000	1.0000	1.5469	1.0819	2.16
	C-SG	0.0588	0.9412	4.9875	1.0000	4.00
	SC-SG	1.0000	0.0000	0.2057	1.0000	−0.85

The estimation results in Table 4 identify the best-fitting mixture copula for each of the 25 selected market pairs with the MSCI World Index, as determined by the lowest AIC value. Among these, five market pairs—Australia (S&P ASX50), Hungary (Budapest), New Zealand (DJ New Zealand), Turkey (BIST100), and China (A50)—are fitted by a mixture copula with extreme weight combinations. For Australia, the best-fitting copula is the survival Clayton–survival Gumbel (SC-SG) copula, with weights $W_1 = 0.0781$ and $W_2 = 0.9219$, indicating that the dependence structure is heavily influenced by the survival Gumbel component, which accounts for approximately 92.19% of the mixture, and is supported by a low AIC value of −96.69. Similarly, Hungary is best fitted by the SC-SG copula with weights $W_1 = 0.0542$ and $W_2 = 0.9458$, showing a dominance of the survival Gumbel copula with about 94.58% weight, confirmed by an AIC of −113.40.

For New Zealand, Turkey, and China, the best-fitting copulas are the Clayton–survival Gumbel (C-SG) copulas with extreme weight settings of $W_1 = 0.0000$ and $W_2 = 1.0000$, indicating a complete reliance on the survival Gumbel component (100% weight). This suggests that the dependence between these markets and the MSCI World Index is entirely described by the survival Gumbel copula, with AIC values of −38.89, −33.83, and −82.84, respectively. These findings suggest that in these five market pairs, the survival Gumbel copula often dominates, particularly in cases with extreme weight combinations, highlighting the importance of accounting for such structures when modeling market dependencies.

Overall, the consistent selection of copulas with extreme weights (either heavily or entirely favoring one component) highlights their relevance in capturing the co-movement and tail dependence between global markets and the MSCI World Index, especially during periods of extreme market conditions. This also indicates that these markets may exhibit stronger contagion effects or more significant dependencies with the global index, confirming the utility of using extreme weight mixture copulas to model complex dependence structures in real-world financial data.

This real data study provides evidence that extreme weight scenarios do occur in reality, underscoring the importance of measuring tail dependence, particularly lower tail dependence, when assessing contagion effects. Ignoring extreme dependencies may lead to an underestimation of the risk associated with market co-movements, as tail dependencies can significantly influence the propagation of shocks across markets [28]. Therefore, these five cases can serve as examples where the BMAlog method could be more appropriate for measuring tail dependence or contagion effects, rather than using conventional methods that treat parameters as unknowns and estimate them without considering the potential for extreme weights [6].

By applying BMAlog, which effectively incorporates model uncertainty and adjusts for the skewness in the dependence structure, we can achieve a more accurate understanding of the contagion dynamics, particularly in the lower tail, where extreme co-movements are

most impactful [22]. This approach could improve risk management strategies and provide a more realistic assessment of the interconnectedness of global financial markets (Table 7).

Table 7. Tail dependence measurement from the extreme weight mixture copula.

		RMSE of LTDC		
Country	**Mixture Type**	**BMA**	**BMAlog**	**Mixture**
Australia	SC-SG	0.3544	0.3019	0.2810
China	C-SG	0.1852	0.1543	0.1940
Hungary	SC-SG	0.3923	0.3839	0.3423
New Zealand	SC-SG	0.2598	0.1889	0.2155
Turkey	SC-SG	0.2592	0.2064	0.2259

To assess the lower tail dependence between the selected markets and the MSCI World Index, we calculate the lower tail dependence coefficients (LTDCs) using both the proposed BMAlog method and the conventional Mixture Copula method for 5 out of the 25 market pairs, as shown in Table 5. The results reveal slight differences in the LTDC values obtained by the two methods.

For example, for China, where the mixture type is Clayton and survival Gumbel (C-SG), the LTDC calculated using the BMAlog method is 0.1543, compared to 0.1940 using the conventional Mixture Copula method. Similarly, for Australia, Hungary, New Zealand, and Turkey, where the mixture type is survival Clayton and survival Gumbel (SC-SG), the BMAlog method provides LTDC values of 0.3019, 0.3839, 0.1889, and 0.2064, respectively, which differ from those obtained using the conventional method (0.2810, 0.3423, 0.2155, and 0.2259, respectively). These small differences in LTDC values suggest that relying solely on the conventional method to compute weights may introduce biases, particularly in scenarios involving extreme weights. Our previous simulation study demonstrates that the BMAlog method is more accurate in such cases. Therefore, these results confirm that using the conventional approach to compute tail dependence in mixture copulas can lead to biased estimates, as the conventional method does not adequately account for the effects of extreme weights.

5. Discussion and Conclusions

This study provides a comprehensive evaluation of the BMA and BMAlog methods compared to the conventional Mixture Copula method for measuring tail dependence and assessing contagion effects using both simulation and real-world application studies in global markets and the MSCI World Index.

Based on the our results, several key insights emerge regarding the performance of the BMA and BMAlog methods compared to the Mixture Copula method. Across various scenarios, the Mixture Copula method generally exhibits robust performance, maintaining consistently low RMSE values across different weight settings. This suggests that the Mixture Copula method is a reliable choice for a wide range of dependence structures, particularly when there is no significant skewness in the copula weights. However, the performance of the BMA and BMAlog methods depends heavily on the specific characteristics of the weight distribution and the underlying copula dynamics. The BMA method tends to perform well when the weights are more balanced, indicating that it effectively captures the dependence structure in scenarios where both copulas contribute equally. This aligns with findings from prior studies that suggest BMA approaches are beneficial when model uncertainty is evenly distributed across multiple candidate models [19]. In contrast, the BMAlog method demonstrates its strength in cases where the weight distribution is highly skewed towards one copula, particularly when the survival Gumbel copula dominates. The log-transformed weighting scheme in BMAlog appears to provide a significant adjustment for extreme dependence structures, allowing it to outperform the Mixture Copula method in scenarios where one copula heavily influences the mixture. This result is consistent with the theoretical advantages of log-transformed weights in accommodating skewed data

distributions, as suggested by [22]. Nonetheless, the BMAlog method does not consistently outperform the Mixture Copula method across all scenarios. When the survival Clayton copula dominates, the Mixture Copula method generally remains superior. This indicates that while BMAlog is effective in specific contexts, it may not always offer a universally better alternative. The findings suggest that the BMAlog method's performance is context-dependent and that its effectiveness is closely tied to the nature of the underlying copulas and their weight distributions.

The real data study further supports these findings. When evaluating the tail dependence between the selected markets and the MSCI World Index, we observe that the TDCL values calculated using the BMAlog method differ slightly from those obtained using the conventional Mixture Copula method. For instance, in the case of China, the TDCL calculated using BMAlog is 0.1543, while it is 0.1940 for the conventional method. Similarly, for Australia, Hungary, New Zealand, and Turkey, the BMAlog method provides TDCL values that are consistently closer to the BMA reference values than those from the Mixture Copula method. These small differences suggest that relying solely on the conventional method to compute weights may introduce biases, particularly when extreme weight distributions are present [29]. Our findings from the real data study confirm that extreme weight scenarios do occur in practice, reinforcing the need to consider lower tail dependence in contagion risk assessment. The BMAlog method, by incorporating model uncertainty and effectively adjusting for skewness in the dependence structure, provides more accurate estimates of tail dependence, especially in cases where extreme weights are observed. This demonstrates that the use of conventional methods might lead to biased results, while the BMAlog method offers a more reliable alternative for capturing contagion effects in global financial markets [30]. However, it is also noted that the BMAlog method does not consistently outperform the Mixture Copula method across all scenarios. For example, when the survival Clayton copula dominates, the Mixture Copula method generally proves to be superior. This suggests that while the BMAlog method is effective in specific contexts, it may not always offer a universally better alternative [24]. Overall, the findings indicate that the performance of the BMAlog method is context-dependent and closely related to the nature of the underlying copulas and their weight distributions. Thus, selecting the most appropriate method requires careful consideration of the specific dependence structure and the characteristics of the data involved [28].

Based on the findings of this study, we recommend adopting the BMAlog method for scenarios involving extreme weight distributions, particularly when one copula heavily dominates the mixture. This method has proven to provide more accurate measurements of tail dependence, which is critical for understanding contagion risks in financial markets. Additionally, it is advisable to use a combination of methods—such as BMA, BMAlog, and the conventional Mixture Copula method—to achieve a more robust analysis of dependence structures, as no single method universally outperforms the others across all scenarios. Finally, future research should explore alternative weighting schemes or modifications to the BMAlog method to enhance its adaptability and performance across a wider range of dependence structures, further refining tools for measuring contagion effects and tail dependence in complex financial environments.

For future study, BMA_{log} is proposed to be applied to additional stock markets and extended to time-varying mixture copula models. This will help validate its performance in more complex, dynamic financial environments. By considering time-varying dependencies, we can further assess the robustness of BMA_{log} in capturing evolving relationships between stock markets and improving tail dependence estimation, especially during periods of market instability or financial crises.

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Abbreviations

The following abbreviations are used in this manuscript:

TDC	Tail Dependence Coefficient
TDCL	Lower Tail Dependence Coefficient
TDCU	Upper Tail Dependence Coefficient
BMA	Bayesian Model Averaging
RMSE	Root Mean Square Error

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