# Modelling Risk Dependencies in Insurance Using Survival Clayton Copula

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## *Abstract*

Our aim in this paper is to show the use of survival Clayton copula as a suitable tool for modelling risk dependencies in insurance. A purpose-built simulation of an adequate upper tail dependence can be an important part of the aggregation of risks in an insurer's internal models. The occurrence of extreme values of the aggregate random variable might have a very negative impact on the insurer when securing coverage of unexpected losses. The upper conditional quantile exceedance probability of the copula is a suitable indicator. In addition an analysis of its effect on the level of modelling of the risk scenario is available. This effect is measured using the Tail Value at Risk of the aggregate random variable. To simplify our description of the given principle for aggregating risks we will in this paper only consider the two-dimensional case. The programming language R was used to simulate the values of the joint distribution of the marginal random variables.



# **INTRODUCTION**

The aggregation of risk is at the present time very topical in the insurance sector and much time is devoted to it in the context of risk management in insurers' internal models. The preferred solution for risk aggregation is the use of multi-dimensional copula functions. Many authors have covered this area. In the context of risk aggregation they describe the use of various copula functions and some have carried out comparisons with the approach based on the standard formula in the Solvency II directive

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<sup>3</sup> Department of Mathematics and Actuarial Science, Faculty of Economic Informatics, University of Economics in Bratislava, Dolnozemská cesta 1/b, 852 35 Bratislava 5, Slovakia. E-mail: patricia.teplanova@euba.sk.

(Nguyen and Molinari, 2011; Eling and Jung, 2020; Marri and Moutanabbir, 2022; Ghosh, Chakraborty and Watts, 2022; Pfeifer, Strassburger and Philipps, 2020; Allen, Mcaleer and Singh, 2017). We should emphasise that insurers will develop their own copula functions to manage risk the most effectively (Milek, 2020). The classical approach attempts to choose a suitable copula function, reflecting the risk dependencies, using scatter plots of their values. Copulas can be constructed either non-parametrically or parametrically using the maximum likelihood method, good fit tests, or information criteria (Remillard, Genest and Beaudoin, 2009; Chen and Huang, 2007; Joo, Shin and Heo, 2020; Yang, 2022; Cuevas, Yela and Achcar, 2019). In many cases analyses of various dependence coefficients or association measures are used to construct suitable copulas (Adès, Provost and Zang, 2024; Gijbels, Veraverbeke and Omelka, 2011; Nicolas and Garcin, 2021).

Rank correlation measures have a more important application, as for example in Spearman´s Rho, Kendall´s tau (Embrechts, Lindskog and McNeil, 2001). These measures can be used to characterize the trend of changes in the values of the marginal distributions in the analyzed ordered pairs. These association measures may not however capture tail dependencies which in the case of insurance risks are very important – see Figure 1.



**Source:** Own construction, customized in R

Many authors therefore prefer various estimation approaches for determining the upper-tail dependency coefficients for a given copula function (Hua and Joe, 2011; Gijbels, Kika and Omelka, 2020; Charpentier and Segers, 2009; De Luca and Rivieccio, 2012).

An important indicator of the tail-dependency of the copula, or the joint distribution, is the upper conditional quantile exceedance probability  $cap_{U}(u)$  which we will go into in more detail later (Milek, 2020; Mucha and Škrovánková, 2022). It relates to the answer to the question: What is the probability that the value of the second marginal distribution exceeds the 95% quantile given that the value of the first marginal distribution has already exceeded that quantile (Cuypers, 2020)? In the context of modelling risk dependencies with the help of copulas the value  $cqep_U(u)$  of the copula is "handed over" to the generated joint distribution. This distribution has this indicator at the same level as the copula used. We could therefore say that it "hands over" certain risk information which is encoded in that copula function.

An innovative approach in this area could indeed be to use the copula function as a tool to generate a given risk level scenario for the tail dependency, even though it is not evident in the scatter plot of the data. Based on this approach a given capital requirement represents a guarantee of covering unexpected losses even in the case of the occurrence of extreme values (Pinda, Mucha and Smažáková, 2022). The mentioned conditional quantile exceedance probability could be the parameter of the risk scenario. The survival Clayton copula is the proposed tool for the modelling (Mucha, 2023; Hofert, Kojadinovic, Maechler and Yan, 2018). It is suitable for describing the upper tail dependency between the risks. It is also referred to as the HRT (heavy right tail) copula (Di Bernardino and Prieur, 2018). Depending on the parameter of the survival Clayton copula it is therefore possible to model various levels of the mentioned conditional quantile exceedance probability of the generated joint distribution. As the parameter  $\theta \rightarrow 0$  the survival Clayton copula tends towards the position of the independent copula and as  $\theta \rightarrow \infty$  it tends towards the position of the comonotonic copula. In this paper we will concentrate on analysing the calculation of the Tail Value at Risk of the aggregate random variable depending on the value of the parameter of the survival Clayton copula for selected marginal risk distributions. Our aim is to show the use of survival Clayton copula as a suitable tool for modelling risk dependencies in insurance.

## **1 METHODS AND METHODOLOGY OF ANALYSIS**

A copula is a mathematical object which describes the dependency structure between risks and it is the base for determining the joint distribution of their marginal distributions.

## **1.1 Copula functions**

A two-dimensional copula is the joint distribution function of two equally distributed random variables  $U_1 \sim U(0; 1)$  and  $U_2 \sim U(0; 1)$ . We can express the copula  $C(u_1; u_2)$  as follows:

$$
C(u_1; u_2) = P(U_1 \le u_1; U_2 \le u_2). \tag{1}
$$

Sklar's theorem provides the theoretical foundation for copula function theory, which makes clear the role of copulas in determining two-dimensional distributions in the context of their dependency structure. Let *C* be a two-dimensional copula and  $F_1$ ,  $F_2$  one-dimensional distribution functions. The function  $F(x_1; x_2)$  defined by form:

$$
F(x_1; x_2) = C(F(x_1); F(x_2)),
$$
\n(2)

is the joint distribution function with marginal distribution functions  $F_1$ ,  $F_2$ .

Given that we will be considering the Clayton copula, we will introduce a definition of Archimedean copulas. The key concept is a copula generator. Mathematically speaking a copula generator is a continuous decreasing function  $\phi(\cdot):$   $(0, 1) \rightarrow (0, \infty)$ , such that  $\phi(1) = 0$  (if  $\phi(0) = \infty$ , called a strict copula generator). The notation  $\phi^{-1}(\cdot)$ :  $(0; \infty) \rightarrow (0; 1)$ , represents the inverse function to  $\phi$  (if it is not a strict generator we need to use the pseudo-inverse function which takes the value zero everywhere in the interval ⟨*ϕ*(0); ∞⟩). Then

$$
{}_{A}C(u_{1}; u_{2}) = \phi^{-1}(\phi(u_{1}) + \phi(u_{2})), \qquad (3)
$$

is a two-dimensional Archimedean copula (Cipra, 2015; McNeil, Frey and Embrechts, 2015). The generator for Clayton copula takes the form  $C L C \phi(u) = \frac{1}{\beta} \cdot (u^{-\theta} - 1)$ , with parameter  $\theta > 0$ . In the two-dimensional case we can write this in the form:

$$
^{CLG}_{\theta}C(u_1; u_2) = (u_1^{-\theta} + u_2^{-\theta} - 1)^{-\frac{1}{\theta}}.
$$
\n(4)

#### **1.2 The survival copula**

Let *C* be a two-dimensional copula for which we have **U** ∼ *C*. Then **V** =  $(1 – U)$  ∼  $\overline{C}$ , i.e. **V** =  $1 – U$  =  $(1 - u_1; 1 - u_2)$ , is a random vector whose distribution is given by the survival copula  $\overline{C}$  corresponding to the copula *C* (Hofert, Kojadinovic, Maechler and Yan, 2018). We can also express the survival copula as follows:

$$
\bar{C}(\mathbf{u}) = \sum_{J \subseteq \{1,2\}} (-1)^{|J|} \cdot C((1 - u_1)^{I(1\epsilon J)}, (1 - u_2)^{I(2\epsilon J)}), \mathbf{u} \in (0, 1)^2,
$$
\n(5)

where the sum is over all the subsets of the set  $\{1, 2\}$ ,  $|J|$  is the number of elements of a given subset, *I*(*j* ∈ *J*) is the indicator of *j* ∈ {1, 2}. For the two-dimensional survival copula  $\overline{C}$  we then have:

$$
J = \{\{1; 2\}; \{\emptyset\}; \{1\}; \{2\}\}, j \in \{1; 2\},\tag{6}
$$

$$
\overline{C}(\mathbf{u}) = (-1)^2 \cdot C((1 - u_1)^1; (1 - u_2)^1) + (-1)^0 \cdot C((1 - u_1)^0; (1 - u_2)^0) + (-1)^1 \cdot C((1 - u_1)^1; (1 - u_2)^0) + (-1)^1 \cdot C((1 - u_1)^0; (1 - u_2)^1),
$$
\n(7)

from which we obtain:

$$
\overline{C}(\mathbf{u}) = C(1 - u_1; 1 - u_2) + 1 - (1 - u_1) - (1 - u_2) = -1 + u_1 + u_2 + C(1 - u_1; 1 - u_2).
$$
\n(8)

If we denote the probability density function of the copula *C* as *c*, then for the probability density function of the survival copula corresponding to *C* we have:

$$
\bar{c}(\mathbf{u}) = c(1 - u_1; 1 - u_2), \mathbf{u} \in (0; 1)^2.
$$
\n(9)

For the copula and survival copula the following relationships also apply:

$$
P(U_1 > u_1; U_2 > u_2) = P(V_1 \le v_1; V_2 \le v_2) = \overline{C}(v_1; v_2),
$$
  
\n
$$
P(V_1 > v_1; V_2 > v_2) = P(U_1 \le u_1; U_2 \le u_2) = C(u_1; u_2).
$$
\n(10)

**Figure 2** Scatter plot of the generated copula values (on the left) and the corresponding survival copula values (on the right)



**Source:** Own construction, customized in R

These probabilities can be determined by statistical processing of the generated values (Figure 2).

## **1.3 Using copulas to simulate the values of the joint distribution**

To generate the values of the marginal distributions and determine ordered pairs of the joint distribution what is important is the size of the values that are in a given pair. In the aggregation process these values are added together which then affects the value of the aggregate random variable. In aggregation by addition the order of the values in the marginal distributions is completely random. When using copula functions however the order is in a certain sense coordinated and hence this approach is considered to be more sophisticated.

## *1.3.1 Simulation of the values of the Clayton copula and the survival Clayton copula*

Before we present the algorithm for generating the values of the two-dimensional copula function using conditional probabilities, we will introduce some notation:

$$
P(U_2 \le u_2 \mid U_1 = u_1) = C_{2|1} (u_2 \mid u_1), \qquad (11)
$$

whereby we can also express this as:

$$
C_{2|1} (u_2 | u_1) = \frac{\partial C(u_1, u_2)}{\partial u_1}.
$$
 (12)

The algorithm for generating values of the two-dimensional copula function *C*, i.e. the vector  $U = (U_1, U_2) \sim C$ , respectively its values  $(u_1, u_2)$ , is based on the Rosenblatt transformation.

1. We transform the vector  $\mathbf{u} = (u_1, u_2) \in (0; 1)^2$  into the vector  $\mathbf{u}' = (u_1', u_2') \in (0; 1)^2$ , which we can write as  $U' = R_C(U)$ , so that:

$$
u_1' = u_1, u_2' = C_{2|1}(u_2 \mid u_1) = P(U_2 \le u_2 \mid U_1 = u_1).
$$
\n(13)

2. We transform the vector  $\mathbf{u}' = (u_1', u_2') \in (0; 1)^2$  into the vector  $\mathbf{u} = (u_1, u_2) \in (0; 1)^2$  using the quantile function as follows:

$$
u_1 = u_1', \, u_2 = C_{2|1}^{-1}(u_2 \mid u_1), \tag{14}
$$

which we can write as  $U = R_C^{-1}(U')$  (Hofert, Kojadinovic, Maechler and Yan, 2018).

For a random sample of values of the vector  $\mathbf{u} = (u_1, u_2) \in (0, 1)$  for the Clayton copula we then have:

$$
u_1 = u_1, \ u_2 = C_{2|1}^{-1}(u_2' | u_1) = \left[1 + \left(u_2' \frac{-\theta}{\theta + 1} - 1\right) \cdot u_1^{-\theta}\right]^{-\frac{1}{\theta}}.
$$
\n(15)

The presented approach can also be applied to generate values of the survival Clayton copula using Formula (9).

For this two-dimensional copula function, namely for:

$$
C \sim \mathbf{V} = \mathbf{1} - \mathbf{U} = (1 - u_1, 1 - u_2) = (v_1, v_2), \text{ we get:}
$$
  

$$
v_1 = 1 - u_1 = 1 - u_1', v_2 = 1 - u_2 = 1 - \left[ 1 + \left( u_2 \frac{\theta}{\theta + 1} - 1 \right) \cdot u_1^{-\theta} \right]^{-\frac{1}{\theta}}.
$$
 (16)

#### *1.3.2 Generated values of the joint distribution using copula functions*

Using Sklar's theorem and the inverse transformation method we obtain values of the joint two-dimensional distribution *F* as per the equations:

$$
W_i = F_i(X_i) \Leftrightarrow X_i = F_i^{-1}(W_i), i = 1, 2,
$$
\n
$$
(17)
$$

where:

$$
\mathbf{W} = (W_1, W_2) \sim C; W_i \sim U(0; 1), i = 1, 2.
$$
\n(18)

**Figure 3** Generated values of the joint distribution using copula functions



#### **1.4 Conditional quantile exceedance probability (cqep)**

The conditional quantile exceedance probability (*cqep*) is an important indicator regarding modelling tail dependencies between insurance risks (Milek, 2020; Mucha and Škrovánková, 2022). We can distinguish between the upper and lower conditional probability of exceeding the quantile, whereby for the upper version  $cqep_U(u)$  we consider the values  $u \in (0.5; 1)$ , respectively  $u \to 1^+$ , and for the lower version *cqep*<sub>L</sub>(*u*) the values *u* ∈ (0; 0.5), respectively *u* → 0<sup>-</sup>. Just to recap, given the assumption  $U_1 \sim U(0; 1)$ ; respectively  $U_2 \sim U(0; 1)$ , we have for their quantiles  $F_{U_2}^{-1}(u) = u$ ; respectively  $F_{U_1}^{-1}(u) = u$ . For  $c q e p_U(u)$ copulas we get the result:

$$
{}^{C}c q e p_{U}(u) = P(U_{2} > F_{U_{2}}^{-1}(u)) \mid U_{1} > F_{U_{1}}^{-1}(u)) = \frac{P(U_{2} > F_{U_{2}}^{-1}(u) \land U_{1} > F_{U_{1}}^{-1}(u))}{P(U_{1} > F_{U_{1}}^{-1}(u))} = \frac{1 - P(U_{2} \le F_{U_{2}}^{-1}(u)) - P(U_{1} \le F_{U_{1}}^{-1}(u)) + P(U_{1} \le F_{U_{1}}^{-1}(u) \land U_{2} \le F_{U_{2}}^{-1}(u))}{1 - P(U_{1} \le F_{U_{1}}^{-1}(u))},
$$
\n(19)

$$
c_{Cqep_U}(u) = \frac{1 - 2u + C(u; u)}{1 - u} = \frac{\overline{C}(u; u)}{1 - u}.
$$
\n(20)

The copula indicator  ${}^{C}c q e p_{U}(u)$  therefore expresses the probability of exceeding the quantile  $F_{U_2}^{-1}(u) = u$ of the random variable  $U_2 \sim U(0; 1)$  on the assumption that the quantile  $F_{U_1}^{-1}(u) = u$  of the random variable *U*<sub>1</sub> ∼ *U*(0; 1) was exceeded.

By analogy we can derive an expression for the lower conditional quantile exceedance probability  $cqep<sub>L</sub>(u)$  of the copula:

$$
{}^{C}c q e p_{L}(u) = P(U_{2} \leq F_{U_{2}}^{-1}(u) \mid U_{1} \leq F_{U_{1}}^{-1}(u)) = \frac{P(U_{2} \leq F_{U_{2}}^{-1}(u) \land U_{1} \leq F_{U_{1}}^{-1}(u))}{P(U_{1} \leq F_{U_{1}}^{-1}(u))},
$$
\n(21)

$$
^{c}cqep_{L}(u)=\frac{C(u;u)}{u}.
$$
\n(22)

For the joint distribution with marginal distributions of the random variables  $X_1$ ;  $X_2$ , which we generate based on the given copula function, we get for the conditional quantile exceedance probability  $cap_U(u)$ using Sklar's theorem the following:

$$
{}^{ID}cap_{U}(u) = P(X_2 > F_{X_2}^{-1}(u) | X_1 > F_{X_1}^{-1}(u)) = \frac{P(X_2 > F_{X_2}^{-1}(u) \wedge X_1 > F_{X_1}^{-1}(u))}{P(X_1 > F_{X_1}^{-1}(u))} = \frac{1 - P(X_2 \le F_{X_2}^{-1}(u)) - P(X_1 \le F_{X_1}^{-1}(u)) + P(X_1 \le F_{X_1}^{-1}(u) \wedge X_2 \le F_{X_2}^{-1}(u))}{1 - P(X_1 \le F_{X_1}^{-1}(u))} = \frac{1 - 2u + C(u; u)}{1 - u} = \frac{\overline{C}(u; u)}{1 - u}.
$$
\n(23)

The joint distribution indicator  $\int_D Cqep_U(u)$  expresses the probability of exceeding the quantile  $F_{X_2}^{-1}(u) = {}^2x_u$  of the random variable  $X_2$  on the assumption that the quantile  $F_{X_1}^{-1}(u) = {}^1x_u$  of the random variable  $X_1$  was exceeded.

By analogy we can also derive a formula for the lower conditional quantile exceedance probability  $^{ID}$ *cqep*<sub>L</sub>(*u*) of the joint distribution:

$$
{}^{D}C_{\mathcal{G}}\mathcal{C}_{L}(u) = P(X_{2} \leq F_{X_{2}}^{-1}(u) \mid X_{1} \leq F_{X_{1}}^{-1}(u)) = \frac{P(X_{2} \leq F_{X_{2}}^{-1}(u) \wedge X_{1} \leq F_{X_{1}}^{-1}(u))}{P(X_{1} \leq F_{X_{1}}^{-1}(u))} = \frac{C(u; u)}{u}.
$$
\n(24)

**Figure 4** Graphical interpretation of  ${}^C q e p_u(u)$  (on the left) and  ${}^{JD} q e p_u(u)$  (on the right) as scatter plots of the generated values of the copula and the joint distribution



**Source:** Own construction

The upper conditional quantile exceedance probability <sup>C</sup>cqep<sub>U</sub>(*u*) and <sup>*JD*</sup>cqep<sub>U</sub>(*u*) can be determined statistically from their generated values, Figure 4. It is clear from this that the joint distribution retains the same value for the conditional quantile exceedance probability as the copula used to generate the values. It can be asserted that the copula "passes to the joint distribution particular genetic information" concerning the tail dependencies, respectively a particular risk scenario, and we have:

$$
{}^{C}c q e p_{U}(u) = {}^{ID}c q e p_{U}(u), \text{ respectively } {}^{C}c q e p_{L}(u) = {}^{ID}c q e p_{L}(u) . \tag{25}
$$

#### *1.4.1 Conditional quantile exceedance probability for the survival Clayton copula*

To derive a formula for calculating  ${}^Ceqep_U(u)$  for the survival Clayton copula we will use the fact that it is a rotated copula with respect to the Clayton copula. Let *C* be a two-dimensional copula and let **U** ∼ *C*. For **r** ∈ {0; 1}<sup>2</sup>, we call *rot<sub>r</sub>*(*C*) the rotated copula with regard to *C*, if **U** ∼ *C* this is equivalent to:

$$
((1 - r_1) \cdot U_1 + r_1 \cdot (1 - U_1); (1 - r_2) \cdot U_2 + r_2 \cdot (1 - U_2)) \sim rot_r(C).
$$
 (26)

If the copula *C* has probability density function *c*, the probability density function of the rotated copula *rotr*(*C*) is as follows (Hofert, Kojadinovic, Maechler and Yan, 2018):

$$
rot_r(c)(\mathbf{u}) = c((1 - r_1) \cdot u_1 + r_1 \cdot (1 - u_1); (1 - r_2) \cdot u_2 + r_2 \cdot (1 - u_2)); \mathbf{u} \in (0, 1)^2.
$$
 (27)

It is obvious that the survival Clayton copula is a 180º rotated copula with respect to the Clayton copula. Hence we can obtain the following expression for the values of the vector  $\mathbf{r} = (1; 1)$ :

$$
(1 - U_1; 1 - U_2) = 1 - U = V \sim rot_{(1,1)}(C) = \bar{C}, \qquad (28)
$$

$$
\overline{c}(\mathbf{v}) = rot_{\mathbf{r}}(c)(\mathbf{v}) = c(1 - u_1; 1 - u_2); \mathbf{v} \in (0; 1)^2.
$$
 (29)

Given the above we have for the value of the conditional quantile exceedance probability for the survival copula  ${}^c$ *cqep*<sub>U</sub>(*v*):

$$
{}^{c}cqep_{v}(v) = {}^{c}cqep_{L}(1-v); v \in (0.5; 1), v = 1-u.
$$
\n(30)

We can also derive this as follows, where we treat the survival copula  $\bar{C}$  as a copula using Formula (8):

$$
{}^{C}c q e p_{U}(v) = P(V_{2} > F_{V_{2}}^{-1}(v) | V_{1} > F_{V_{1}}^{-1}(v)) = \frac{P(V_{2} > F_{V_{2}}^{-1}(v) \wedge V_{1} > F_{V_{1}}^{-1}(v))}{P(V_{1} > F_{V_{1}}^{-1}(v))} =
$$
\n
$$
\frac{1 - P(V_{2} \leq F_{V_{2}}^{-1}(v)) - P(V_{1} \leq F_{V_{1}}^{-1}(v)) + P(V_{1} \leq F_{V_{1}}^{-1}(v) \wedge V_{2} \leq F_{V_{2}}^{-1}(v))}{1 - P(V_{1} \leq F_{V_{1}}^{-1}(v))} =
$$
\n
$$
\frac{1 - 2 \cdot v + \overline{C}(v; v)}{1 - v} = \frac{1 - 2 \cdot (1 - u) + 1 - 2 \cdot u + C(u; u)}{1 - (1 - u)} = \frac{C(u; u)}{u} = {}^{C}c q e p_{L}(u).
$$
\n(31)

For the lower conditional quantile exceedance probability of the Clayton copula <sup>*CC*</sup>cqep<sub>L</sub>(*u*), given Formula (22), we get:

$$
{}^{ct}C_{C}qep_{L}(u) = \frac{(2 \cdot u^{-\theta} - 1)^{-\frac{1}{\theta}}}{u},
$$
\n(32)

and for the upper conditional quantile exceedance probability of the survival Clayton copula  ${}^{SCL}C_{\text{CqepU}}(1 - u)$  we get using Formula (31):

$$
{}^{sc}c_{Cq}e p_{U}(1-u) = {}^{sc}c_{Cq}e p_{U}(v) = \frac{(2 \cdot (1-v)^{-\theta} - 1)^{-\frac{1}{\theta}}}{(1-v)}; \, v \in (0.5; 1), \, v = 1-u \,.
$$

When modelling a risk scenario represented by the value  ${}^{SCL}Cqep_U(v)$  it can be identified with regard to the parameter of the survival Clayton Copula using Formula (33).

#### **2 RESULTS AND DISCUSSION**

In this section we will deal with a practical example of the aggregation of two non-life insurance risks *X*1, *X*2 using the survival Clayton copula. From the statistical data used we have assumed their marginal distributions, for parameter estimation for the truncated Pareto distribution see Aban, Meerschaert and Panorska (2006):

$$
X_1 \sim LN(12; 1), X_2 \sim Pa^{truncated}(100\ 000; 1\ 000\ 000; 1.5),
$$
\n(34)

with characteristics:

$$
E(X_1) = 268 \ 337.3, \ E(X_2) = 270 \ 270.3, \ {}^1x_{0.95} = 843 \ 060.6, \ {}^2x_{0.95} = 727 \ 546.7 \ . \tag{35}
$$





**Source:** Own construction, customized in R

To start with we will present the classical approach to aggregation of these risks based on fitting a suitable copula given the values of their marginal distributions, Figure 5. Using the package VineCopula and the function BiCopEstList, we chose, based on the information criteria *AIC* and *BIC*, the best model for the copula function given the presented values (Nagler et al., 2023). When using pseudoobservations obtained in accordance with the principle for constructing empirical distribution functions using Formula (36) we need to consider their independence, Figure 6 (on the left).

#### **Figure 6** Graphical representation of the pseudo-observations and scatter plot of their joint distribution simulated using a chosen Normal copula



**Source:** Own construction, customized in R

*Remark 1*: We will consider a random vector  $\mathbf{X} = (x_{i1}, x_{i2}), i = 1, ..., n$ , where *n* is the number of points in the scatter plot. We obtain the pseudo-observations using the following:

$$
u_{ij} = \frac{r_{ij}}{n+1}, i = 1, \dots, n, j = 1, 2,
$$
\n(36)

where  $r_{ij}$  is the order of precedence of  $x_{ij}$  amongst all the  $x_{ki}$ ,  $k = 1, ..., n$  (Hofert, Kojadinovic, Maechler and Yan, 2023).

We chose as the most suitable a Normal copula with parameter  $\rho = 0.009$ , where, as  $\rho \rightarrow 0$ , it converges to the independent copula confirming our earlier assumption. We obtain the aggregation of the risks using the joint distribution simulated using this copula and by addition the points shown in the scatter plot on the right of Figure (6). We determine the values of the aggregate variable using the following:

$$
s_i = x_{i1} + x_{i2}, \, i = 1, \, ..., \, n \,, \tag{37}
$$

where:  $x_{i1}$ ,  $x_{i2}$  are elements of the random vector of the generated joint distribution.

In order to measure the effect of the aggregation achieved using the chosen copula function we use the risk measure *TVaR* (Bargés, Cossete and Marceau, 2009). This represents the expected value of the aggregate variable on the assumption that its quantile  $s<sub>p</sub>$  was exceeded. We write this as:

$$
TVaR_p(S) = E(S \mid S > s_p). \tag{38}
$$

In the classical approach to risk aggregation using a Normal copula function used by us so far, we calculated the value of this measure by simulating the joint distribution using the library Copula:

$$
NormalTVaR_{0.95}(S) \approx 2\,343\,729\,. \tag{39}
$$

Insurers' internal models make use of this risk measure to determine the capital required to cover unexpected claims, respectively losses. For our purpose we will interpret it as the highest possible loss which may arise with probability greater than 0.95, i.e.

$$
P(S \leq \text{Normal}TVaR_{0.95}(S)) > 0.95 \tag{40}
$$

We will now consider an innovative approach to aggregating risk using the survival Clayton copula. As opposed to the classical approach we will purposefully model a given risk level scenario for the tail dependency such that a guarantee of covering the highest possible loss is achieved even in the case of the concurrent occurrence of extreme values of the aggregate risk. Their occurrence can have fatal consequences for the insurer leading even to insolvency. We will in the conclusion compare the results from the two approaches.

The conditional quantile exceedance probability *cqep* is an important indicator of the level of tail dependence. Given the aggregation of risks present in insurance we concentrate on analysing its upper version  $cqep_U$ , Formulas (23) and (33).

In the case of the survival Clayton copula the value  ${}^{sCL}C_{\mathcal{C}q\mathcal{C}p\mathcal{U}}(\nu)$  depends also on its parameter  $\theta$ . We show this dependence also in the context of dependence on the level of the quantile  $\nu$  in Figure 7.

From this visualisation we get some very interesting information, namely that for  $\theta \geq 3$  the value  $cqep_U(v)$  is the same for all levels of the quantile.

*Remark 2*: The graph of *cqep<sub>U</sub>* in Figure 7 for  $v = 0.99$  is shown below for  $\theta < 3$ .

To illustrate the results shown we give the coordinates of some of the points in the graph  $[\theta; cqep_U(v)]$ , for example [3; 0.794], [5; 0.871], [10; 0.933], [15; 0.955], [30; 0.9772].

It is clear that as the value of *θ* for the survival Clayton copula increases so also does the value  $cqep<sub>U</sub>(v)$ . We recall that the generated joint distribution has the same value for this indicator as the copula which we used in the simulation. For  $\theta = 3$  we have  ${}^{SCL}C_{CqepU}(v) = {}^{ID}C_{qepU}(v) = 0.794$  for all levels of the quantile *v*. We can interpret this as meaning that the probability of exceeding the quantile  $F_{X_2}^{-1}(v) = \lambda x$ ,

of the random variable  $X_2$  assuming that the quantile  $F_{X_1}^{-1}(v) = {}^1x_v$  of the random variable  $X_1$  is exceeded is equal to 0.794.

If we consider the points in the scatter plot of the joint distribution where the quantile  ${}^1x_v$  of the random variable  $X_1$  was exceeded, then for 79.4% of these the quantile  $^2x_v$  of the random variable  $X_2$  was



**Source:** Own construction, customized in R



**Figure 8** Scatter plot of the survival Clayton copula for various values of its parameter

**Source:** Own construction, customized in R

also exceeded. This indicator together with the parameter *θ* of the survival Clayton copula represent a particular risk scenario for modelling the tail dependency of the aggregated risks.

For clarity we show a scatter plot of the survival Clayton copula according to the value of its parameter *θ*, Figure 8. Information as to the tail dependency hidden in this copula function is passed to the generated joint distribution.

Figure 9 shows scatter plots for the joint distribution in respect of each copula function in Figure 8.



**Source:** Own construction, customized in R

It is obvious that as the parameter of the copula increases the modelled tail dependency is demonstrably more evident.

*Remark 3*: It is recommended that the visualisation on the scatter plot be seen in the context of the characteristics of the marginal distributions, respectively in the context of the range of both axes.

By choosing a suitable value of the parameter of the survival Clayton copula we can purposefully model a considered risk scenario for the aggregate distribution of given risks. As we have already mentioned, we will measure the effect of applying a given risk scenario using the risk measure *TVaRp*(*S*). One can assume that with an increase in the value of the parameter of the survival Clayton copula *θ*, respectively with an increase in the conditional quantile exceedance probability  ${}^{D}Cqep_{U}(v)$ , the value  $TVaR_{p}(S)$  of the aggregate distribution will also increase.

The values of  $TVaR<sub>p</sub>(S)$  for  $p \in \{0.9; 0.95; 0.99\}$  are shown in Table 1.

The dependence of *TVaRp*(*S*) on the parameter of the survival Clayton copula *θ* is shown graphically in Figure 10.

	0.1				10	30
$TVaR_{0.9}(S)$	1793981	2021891	2 118 868	2 132 683	2139379	2 141 596
TVaR <sub>0.95</sub> (S)	2419258	2837231	2986344	3 007 149	3015927	3 0 1 7 9 8 9
TVaR <sub>0.99</sub> (S)	4 5 6 7 4 5	5779918	6096432	6 127 033	6 145 136	6 149 955

**Table 1** Values of *TVaRp*(*S*) obtained by aggregation using the survival Clayton copula

**Source:** Own construction

It is clear from the presented results that the value  $TVaR<sub>p</sub>(S)$  is, for values of the parameter of the survival Clayton copula  $\theta \geq 3$ , at a "stable" level. If  $\theta = 3$  the largest possible aggregate loss *SCCTVaR*0.95(*S*), which can occur with probability greater than 0.95, is 2 986 344. We obtained the values shown by carrying out simulations of the values of the joint distribution of the marginal risks, respectively of the aggregate variable using the survival Clayton copula. To get more accurate results we carried out this series of simulations 5 000 times and the resulting value of  ${}^{SC}TVaR_o(S)$  was taken as the average of the values obtained from each series.





**Source:** Own construction, customized in R

### **CONCLUSION**

This paper has presented an innovative approach to the aggregation of risks using a survival Clayton copula. Specific modelling of a given risk scenario, dependent on the parameter of the copula, is important particularly from the point of view of the occurrence of extreme values of the aggregate risk. The upper conditional quantile exceedance probability  $cap_{U}(v)$  is an authoritative indicator of the simulated tail dependence. We used the risk measure *TVaRp*(*S*) to measure the effect of the achieved aggregation. It represents the largest possible aggregate loss which can occur with probability greater than *p*. By setting up a capital requirement at this level it would be possible to guarantee the fulfilment of the insurer's liabilities at the chosen significance level *p.*

Given the results obtained for  $TVaR<sub>p</sub>(S)$  we can assert that the parameter of the survival Clayton copula  $\theta$  = 3 secures a risk scenario model with an "adequate" tail dependence. If we compare the value <sup>SCC</sup>TVaR<sub>0.95</sub>(S)  $\approx$  2 986 344 obtained this way with that using the classical approach *NormalTVaR*<sub>0.95</sub>(*S*) ≈ 2 343 729 we see that there is a significant difference. By specifically modelling larger (extreme) values arising in the aggregated pairs of the joint distribution we have produced a prediction of the possible occurrence of larger of the largest aggregate losses *TVaRp*(*S*).

If instead we look at the value obtained using the parameter  $\theta = 0.1$  for the survival Clayton copula, namely  ${}^{SC}TVaR_{0.95}(S) \approx 2$  419 258 we could assert that it is comparable with the value obtained using the classical approach. As the value of the parameter  $\theta \to 0$  the survival Clayton copula tends towards the position of the independent copula. This is in the context of assuming use of the Normal copula estimated from data using pseudo-observations. The choice of the level of the modelled scenario is up to experts, or it may follow from legislative requirements concerning own appraisal and the management of risk in an insurer's internal models. For the latter use is made of their own copulas for aggregating risk, whereby the risk measure *TVaRp*(*S*) is, as already mentioned, also used to determine the capital required to cover unexpected losses. For some risks it is common practice to show their values in the form of profits and losses, i.e. they appear as negative and positive values. Our presented approach can of course also be applied to such models.

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