RELIABILITY ANALYSIS OF NETWORKS INTERCONNECTED WITH COPULAS

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ABSTRACT

With the increasing size and complexity of modern infrastructure networks rises the challenge of devising efficient and accurate methods for the reliability analysis of these systems. Special care must be taken in order to include any possible interdependencies between networks and to properly treat all uncertainties. This work presents a new approach for the reliability analysis of complex interconnected networks through Monte Carlo Simulation and survival signature. Application of the survival signature is key in overcoming limitations imposed by classical analysis techniques and facilitating the inclusion of competing failure modes. The (inter)dependencies are modelled using vine copulas while the uncertainties are handled by applying probability-boxes and imprecise copulas. The proposed method is tested on a complex scenario based on the IEEE reliability test system, proving it's effectiveness and highlighting the ability to model complicated scenarios subject to a variety of dependent failure mechanisms.

INTRODUCTION

Reliability analysis of complex networks is an important task in the field of risk analysis. This importance is a result of the ever increasing size and complexity of modern critical infrastructure.

At the same time, society is becoming increasingly reliant on the availability of these critical infrastructures such as water supply networks, electrical distribution networks or the internet. A breakdown of any of these systems can have a drastic impact on people's lives, as evident from the aftermath of recent natural disasters (UN-OCHA 2013). As a result, efficient and accurate methods for the reliability of these complex systems are required. However, history has shown that it is not sufficient to analyse these networks as individual units because the systems are often subject to complex interdependencies between one another. That is, failure in one network can potentially cascade into another network (Buldyrev et al. 2010; Leavitt and Kiefer 2006). For example, failures in a power grid due to natural disasters will drastically effect the communication network which in turn will inhibit the coordination of emergency personnel (Comfort and Haase 2006). Therefore, it is of paramount importance to include and accurately model these interdependencies when analysing the reliability of networks.

Behrensdorf et al. (2017) presented a novel approach to the numerical reliability analysis of interdependent networks based on Monte Carlo simulation and survival signature. The survival signature (Coolen and Coolen-Maturi 2012) has the capability to fully separate the structure of a network from its probabilistic characteristics, allowing for efficient simulation while modelling dependencies in a probabilistic way. Due to these characteristics it has constantly increased in popularity since its development, with new simulations techniques based on the signature being constantly developed (see for example Patelli et al. 2017). In the previous the modelling of interdependencies between networks was limited to simple deterministic unidirectional causal links where failure of one component would result in the immediate failure of all dependent components. However, this approach lacks flexibility and does not allow to accurately capture the complex interdependencies between real world networks. As a result, a new methodology to model these interdependencies is required. Copulas have been successfully used to model dependence in enterprise risk management (Schirmacher and Schirmacher 2008), finance (Cherubini et al. 2004), insurance (Goodwin and Hungerford 2014), and environmental studies (Zhang and Singh 2006). Modelling dependencies with copulas is especially powerful as multivariate copulas allow to separate modelling of the marginal distributions from modelling the dependence structure (Joe 2014). Though the popularity of copulas for engineering applications has increased in the recent years (Yan 2006; Ram and Singh 2009), literature is still scarce.

This work extends the previously developed method to allow for complex dependencies between nodes and networks as well as competing failure modes using multivariate copulas. This work is focused on using appropriate copulas to represent realistic dependency structures between different networks. The goal is to find a single dependency structure containing the complete dependency information. For this reason, different types of multivariate copulas such as hierarchical Archimedean copulas and vine copulas are investigated. The copula models are usually inferred from data or expert knowledge, both of which are subject to two types of uncertainty, namely aleatory and epistemic uncertainty. Aleatory uncertainty represents the natural randomness in process while epistemic uncertainty results from vagueness or lack of information (Beer et al. 2013). Dealing with these uncertainties by imprecise reliability analysis results in bounds on the obtained survival function.

The remainder of this paper is outlined as follows. First, the basic notations and required definitions of copulas including measures of dependence is presented followed by an discussion of copula construction methods. Then, the numerical method used to compute the network reliability is introduced. After discussing the modelling of dependencies and handling of uncertainties, the proposed method is applied to a complex numerical example. Finally, the paper closes with some concluding remarks and an outlook into future works.

COPULAS

This chapter introduces the basic theory on copulas as well as how they can be used to model dependencies in high dimensions. An overview of different parametric copula families is given. Additionally, measurements of dependence are introduced. For a comprehensive discussion of copulas, see for example Nelson (2007) or Joe (2014).

Copulas (from the Latin for “bond“ or “tie“) are functions that couple multivariate distribution functions to their one-dimensional marginal distributions functions (Nelson 2007) and as such allow to separate modelling of the dependence structure from modelling the univariate marginals. The foundation of the theory of copulas lies in what is known as Sklar's theorem (Sklar 1959). It states, that any multivariate distribution H can always be separated into its marginal distributions F_i and a copula function C. The theorem is valid in all dimensions $d \geq 2$.

Theorem 2.1 (Sklar's theorem) *Let H be an d-dimensional distribution function with margins $F_1, \ldots, F_d$. There exists an d-dimensional copula C such that for all $\mathbf{x}$ in $\mathbb{R}^d$*

$$H(\mathbf{x}) = C(F_1(x_1), \ldots, F_d(x_d)). \tag{1}$$

If the marginals $F_1, \ldots, F_d$ are continuous, then C is unique; otherwise, C is unique on Range(F_1) $\times \cdots \times$ Range(F_d). Conversely, if C is an d-copula and $F_1, \ldots, F_d$ are distribution functions, then the function H defined by Eq. 1 is an d-dimensional distribution function with margins $F_1, \ldots, F_d$.

Probabilistically, if C is a joint cumulative distribution function of a d-dimensional random vector on the unit cube $[0, 1]^d$ with uniform marginals, then $C : [0, 1]^d \rightarrow [0, 1]$ is a copula. It is noteworthy, that copulas are invariant under strictly increasing transformations, as stated by Theorem 2.2 (Nelson 2007).

Theorem 2.2 *For $d \geq 2$ let $X_1, \ldots, X_d$ be random variables with continuous distribution functions $F_1, \ldots, F_d$, joint distribution function H and copula C. Let $f_1, \ldots, f_d$ be strictly increasing functions from $\mathbb{R}$ to $\mathbb{R}$. Then $f_1(X_1), \ldots, f_d(X_d)$ are random variables with continuous distribution functions and copula C. Thus, C is invariant under strictly increasing transformation of $X_1, \ldots, X_d$.*

As such, any property of the joint distribution function that is invariant under strictly increasing transformation is in fact a property of the copula. As a result, This means, one can study dependence between random variables by studying the copula (Schirmacher and Schirmacher 2008). There exist multiple copula families with different dependence structures of which some of the most popular are presented in the following.

The Gaussian Copula

The d-dimensional Gaussian copula with positive definite correlation Matrix $\mathbf{R} \in [-1, 1]^{d \times d}$ is defined by

$$C_R(u_1, \ldots, u_d) = \Phi_d(\Phi^{-1}(u_1), \ldots, \Phi^{-1}(u_d)), \tag{2}$$

where $\Phi_d(\cdot; \mathbf{R})$ is the d-variate cumulative distribution of a $\mathbb{N}_d(0, \mathbf{R})$ random vector and Φ^{-1} denotes the inverse of the univariate standard Gaussian cumulative distribution function (Joe 2014).

Archimedean Copulas

Archimedean copulas are an important class of copulas. Their popularity stems from a variety of reasons: They are easily constructed, the class holds a great number of different families and the copulas posses many excellent properties (Nelson 2007). Additionally, the bivariate Archimedean copulas can be used in multivariate construction methods based on pairs of bivariate copulas (Joe 2014). A d-dimensional copula C_φ is classified as *Archimedean* if it admits to the representation

$$C_\varphi(u_1, \ldots, u_d) := \varphi(\varphi^{-1}(u_1) + \cdots + \varphi^{-1}(u_d)), \tag{3}$$

where the function $\varphi : [0, \infty] \to [0, 1]$ is called the *generator* of C_φ , φ^{-1} denotes its inverse and $u_1, \ldots, u_d \in [0, 1]$ (Mai and Scherer 2012). Table 1 shows some of the most popular one-parameter (governing the strength of dependence) Archimedean copula families with their generators, inverses and parameter domains.

Random Variable Generation

There exists a general algorithm for sampling from bivariate copulas. The methodology known as *conditional sampling* (Mai and Scherer 2012) is based on computing the partial derivatives of copulas to obtain conditional distribution functions. For an arbitrary bivariate copula $C : [0,\ 1]^2 \to [0,\ 1]$:

1. Simulate two independent variates $U_2 \sim U[0,\ 1]$ and $V \sim U[0,\ 1]$

2. Compute the conditional distribution function

$$F_{U_1|V_2}(u_1) := \frac{\partial}{\partial u_2} C(u_1, u_2)\Big|_{u_2=U_2}, \quad u_1 \in [0, 1] \tag{4}$$

and the generalized inverse

$$F^{-1}_{U_1|U_2}(v) := \inf\{u_1 > 0 : F_{U_1|U_2}(u_1) \geq v\}, \quad v \in (0, 1). \tag{5}$$

3. Set $U_1 := F^{-1}_{U_1|U_2}(V)$ and return $(U_1, U_2) \sim C$.

The algorithm is valid for all classes of copulas. However, in many cases an easier algorithm can be found for a specific copula. Figure 1 shows four example scatter plots of samples generated from different bivariate copulas, highlighting the individual dependence structure.

While this algorithm can be extended to higher dimensions $d > 2$, this requires the computation of conditional distribution functions, which in high dimensions can be challenging or even impossible. Therefore, other techniques are usually applied in higher dimensions.

Dependence

The study of dependence among random variables requires some form of dependence measurement. Typically, "correlation" is used to describe different forms of dependence. However, in its technical meaning as the *linear correlation coefficient* ρ it is not "scale-invariant" and as such does not remain unchanged under strictly increasing transformation (Schirmacher and Schirmacher 2008). Therefore, the more modern term "association" is used instead of correlation. Two well known scale-invariant measures of association are the population versions of Kendall's tau and Spearman's rho. In this work, Kendall's tau is applied in all cases.

Kendall's tau is a measure of association based on *concordance*. A pair of random variables is concordant if "large" values of one are associated with "large" values of the other and the same holds for "small" values. Formally, two observations (x_i, y_i) and (x_j, y_j) from a vector (X, Y) are *concordant* if $x_i < x_j$ and $y_i < y_j$, or *discordant* if $x_i > x_j$ and $y_i > y_j$. Alternatively, concordance can be expressed as $(x_i - x_j)(y_i - y_j) > 0$ and discordance as $(x_i - x_j)(y_i - y_j) < 0$.

Let (X, Y) denote a vector of continuous random variables and $\{(x_i, y_i), \ldots, (x_n, y_n)\}$ a sample of n observations from said vector. With c as the number of concordant pairs and d the number of discordant pairs among all possible $\binom{n}{2}$ pairs of observations (x_i, y_i) and (x_j, y_j), Kendall's tau for the sample is defined as

$$t = \frac{c-d}{c+d} = (c-d) \bigg/ \binom{n}{2}. \tag{6}$$

The value t may also be interpreted as the probability of concordance minus the probability of discordance for a random pair of observations (x_i, y_i) and (x_j, y_j) chosen from the sample. In turn, this can be applied to define the population version of Kendall's tau for random variables X and Y

$$\tau(X, Y) = P\left[(X - \widetilde{X})(Y - \widetilde{Y}) > 0\right] - P\left[(X - \widetilde{X})(Y - \widetilde{Y}) < 0\right], \tag{7}$$

where $(\widetilde{X}, \widetilde{Y})$ is an independent copy of (X, Y) (Schirmacher and Schirmacher 2008).

COPULA CONSTRUCTION METHODS

Modelling dependencies inside and between networks requires a flexible dependence structure. Using one distinct copula family to sample failure times for all components in one or multiple networks is never precise enough. Therefore, the ability to combine different copula families in one structure is of utmost importance. This section presents two copula construction methods capable of this. These methods possess different modelling capabilities and strengths. For a discussion of additional methods and further details, see Joe (2014).

Hierarchical Archimedean Copulas

Hierarchical (alternatively: nested) Archimedean copulas are a class of copulas where groups of variables are connected by Archimedean copulas and these groups themselves are then coupled with another copula from one of the Archimedean families. This nesting structure may be repeated up to an arbitrary number of nesting levels. Figure 2 shows a visual representation of a hierarchical Archimedean copula with six variables in four groups as a dendrogram. Formally, hierarchical

Archimedean copulas are defined by

$$C_{\varphi_0}(C_{\varphi_1}(u_{1,1}, \ldots, u_{1,d_1}), \ldots, C_{\varphi_J}(u_{J,1}, \ldots, u_{J,d_J})) \tag{8}$$

where further nesting levels are defined recursively (Mai and Scherer 2012). However, not all arbitrary combinations of $J + 1$ generators lead to Eq. 8 defining a valid copula.

The dependence in every group in this structure is governed by one parameter and variables that are close to each other (e.g, in the same group) share the same dependence (Joe 2014). This reduces the modelling flexibility substantially. An implementation of hierarchical Archimedean copulas can be found in the package `nacopula` for the statistical programming language **R** (Hofert and Mächler 2011).

Pair Copula Construction

The goal of pair copula constructions (PCCs) is to build high-dimensional copulas from combinations of bivariate copulas and as such use the extensive theory on bivariate copulas to overcome limitations in the available literature on multivariate copulas (Mai and Scherer 2012).

Consider a vector of d random variables $\mathbf{X} = (X_1, \ldots, X_d)$ with joint density function denoted by $f_{1:d}(x_1, \ldots, x_d)$. The density can then be represented as a factorization of conditional densities:

$$f_{1:d}(x_1, \ldots, x_d) = f_1(x_1) \cdot f_{2|1}(x_2|x_1) \cdot f_{3|2,1}(x_3|x_2, x_1) \cdot \cdots \cdot f_{d|1:(d-1)}(x_d|x_1, \ldots, x_{d-1}) \tag{9}$$

In the next step Sklar's theorem is applied to the conditional densities effectively splitting a multivariate density into bivariate copula densities and densities of univariate margins. Differentiating Eq. 1 with respect to a distribution with joint density $f(x_1, \ldots, x_d)$, marginals f_j and marginal cdfs F_j, $j = 1, \ldots, d$ leads to

$$f_{1:d}(x_1, \ldots, x_d) = c_{1:d}(F_1(x_1), \ldots, F_d(x_d)) \cdot f_1(x_1) \cdot \cdots \cdot f_d(x_d), \tag{10}$$

where $c_{1:d}(\cdot)$ is the d-variate copula density. The bivariate case with pair-copula density $c_{1,2}(\cdot, \cdot)$

simplifies to

$$f_{1,2}(x_1, x_2) = c_{1,2}(F_1(x_1), F_2(x_2)) \cdot f_1(x_1) \cdot f_2(x_2), \tag{11}$$

which yields

$$f_{1|2}(x_1|x_2) = c_{1,2}(F_1(x_1), F_2(x_2)) \cdot f_1(x_1). \tag{12}$$

Equation 12 can be applied stepwise to Eq. 9 to fully decompose the multivariate density into bivariate copula densities and densities of univariate marginals. Note, that not all multivariate copulas can be modelled with this pair copula construction method.

Vine Copulas

Vines are a graphical representation of valid pair copula decompositions as sets of trees. Basic graph theory is used to define vines (Mai and Scherer 2012)

Definition 3.1 (Regular Vine) *A regular vine (R-Vine)* $\mathcal{V} = (T_1, \ldots, T_{d-1})$ *is defined as a tree sequence on d elements where:*

1. T_1 *is a tree with Nodes* $N1 = \{1, \ldots, d\}$ *and edges* E_1.
2. *For* $j \geq 2$, T_j *is a tree with nodes* $N_j = E_{j-1}$ *and edges* E_j.
3. *For* $j = 2, \ldots, d-1$ *and* $\{a, b\}$ *it must hold that* $|a \cap b| = 1$.

The so called *proximity property* (3) states that, if an edge exists in T_j, $j \geq 2$ connecting a and b, in turn a and b must share a common node in T_{j-1}. Figure 3 shows a regular vine representation of a 5-dimensional copula.

There exist a multitude of d-dimensional R-vines. However, two sub-classes called C- and D-Vines are used almost exclusively. A regular vine $\mathcal{V}$ is called a C-Vine if in each tree T_i there is one node that holds $n \in N_i$ such that $|\{e \in E_i | n \in e\}| \leq d - 1$. This condition states, that in each tree one node has the maximum degree (is connected to all other nodes). Alternatively, a D-Vine is characterised by each node $n \in N_i$ satisfying $|\{e \in E_i | n \in e\}| \leq 2$. Thus, any node may only have a maximum of two connections. Figure 4 shows the graphical structures of a five-dimensional C- and D-vine.

Sampling of vine copulas is a non-trivial task. A regular vine on n variables possesses 2^{n-1} implied sampling orders (Mai and Scherer 2012). Therefore, C- and D-Vines, where sampling is easier, are applied in all examples of this work with sampling from the vines being performed by the MATLAB toolbox `VineCopulaMatlab` (Kurz 2016).

RELIABILITY ANALYSIS

This section recaps the numerical methodology used to compute the network reliability first introduced in Behrensdorf et al. (2017). It is based on the survival signature, an extension of the system signature, and Monte Carlo simulation.

Survival Signature

The survival signature (Coolen and Coolen-Maturi 2012) is a novel tool for the quantification of system and network reliability based on the system signature (Samaniego 2007). Both signatures allow for a separation of the system structure from its probabilistic characteristics such as component failure times. However, the system signature has a severe limitation in that it is only defined for systems made up of a single component type, which does not apply to complex networks. The survival signature addresses this drawback by generalizing the signature to systems with an arbitrary number of component types.

Consider a system with m components. The state vector is defined as $\underline{x} = (x_1, \ldots, x_m)$, where $x_i = 1$ indicates a component in working condition, while $x_i = 0$ indicates a component in a failed state. As such, the state vector represents the state of the individual components. The state of the full system is obtained by applying the structure function $\varphi(\underline{x})$ to the state vector. As before, $\varphi(\underline{x}) = 1$ indicates a working system and $\varphi(\underline{x}) = 0$ indicates that the system has failed. The structure function is defined based on the problem at hand. In this work, the structure function is assumed to return 1 if a path from any start node to any end node exists for the current network state. Calculating the survival signature for l out of m components working then becomes a combinatorial problem defined as

$$\Phi(l) = \binom{m}{l}^{-1} \sum_{\underline{x} \in S_l} \varphi(\underline{x}) \tag{13}$$

The survival signature is easily extended to systems with multiple component types. Consider a system with K component types, m_k components per type k ($k = 1, \ldots, K$) and l_k out of m_k components per type in a working state, the survival signature becomes

$$\Phi(l_1, \ldots, l_k) = \left[\prod_{k=1}^{K} \binom{m_k}{l_k}^{-1} \right] \times \sum_{\underline{x} \in S_{l_1,\ldots,l_k}} \varphi(\underline{x}) \tag{14}$$

As an example, consider a system with two component types and three components per type as illustrated in Fig. 5. Here, node 1 is selected to be the start node and nodes 5 and 6 represent the end nodes. The full survival signature for the network is show in Table 2.

While algorithms to calculate the survival signature have already been available for a number of years (Aslett 2012; Reed 2017), efficient computation of the signature for systems with large numbers of components and types still poses a numerical challenge. A new approach attempting to reduce the high computational demand of the survival signature using graph theory and Monte Carlo approximation can be found in (Behrensdorf et al. 2018).

Survival Function

Based on the survival signature, the survival function is defined as

$$P(T_s > t) = \sum_{l_1=0}^{m_1} \ldots \sum_{l_k=0}^{m_k} \Phi(l_1, \ldots, l_k) P\left(\bigcap_{k=1}^{K} \{C_t^k = l_k\} \right) \tag{15}$$

This function gives the probability that a network is still working at time t, in other words the reliability of the system. The equation clearly shows the separation of structural information (survival signature on the left) and probabilistic information about component failures (right). This is beneficial as it allows to analyze the network once ahead of the reliability analysis instead of having to re-evaluate the structure every step of the way as with traditional techniques such as fault tree analysis. Additionally, this makes it possible to efficiently run multiple failure scenarios against a network.

Simulation

Component failure times are sampled from the vine copula, after selecting the number of desired samples N_{MC} and a sufficiently small time step, and transformed to their respective marginals. Next, for all combinations $l_1, \dots, l_k$ from the survival signature and all time steps t the number of samples representing the exact same combination (amount of components still working at time t) are counted as $N_{l_1,\dots,l_k}(t)$. Then, the probabilistic part of the survival function is approximated by

$$P\left(\bigcap_{k=1}^{K}\{C_t^k = l_k\}\right) = \frac{N_{l_1,\dots,l_k}(t)}{N_{MC}} \tag{16}$$

In a final step, the partial reliabilities for all combinations are multiplied by their probability $\Phi(l_1, \dots, l_k)$, introducing the structural information into the reliability, and then summed yielding the full reliability of the network. This means that no computations must be performed for combinations where the probability in the survival signature is zero, further increasing the efficiency of the simulation. This fact is especially useful in higher dimensions where large parts of the survival signature are negligible. Figure 6 shows the analytically and numerically computed survival function for the network shown in Fig. 5 assuming independent exponential failure distributions for the components with $\lambda_1 = 0.8$ and $\lambda_2 = 1.6$.

MODELLING DEPENDENCIES

The application of different copula families allows for flexible modelling of various kinds of dependencies. This paper is mainly concentrated on the modelling of two types, namely common causes of failure and (inter-)dependencies between nodes inside one or between multiple networks. The investigation of different copula families and construction methods has shown that only vine copulas (see section 3) provide the flexibility necessary to accurately model the dependencies. Restriction the use of only one distinct family of copulas is clearly infeasible, while the dependence structure of hierarchical Archimedean copulas (HAC) lacks versatility. HACs are sufficient for simple problems, but in most cases we require the advanced capabilities of vine copulas as opposed to the dependence clustering structure approach of HACs.

Modelling of dependencies requires some form of data, either through measured failure times for the components that can be used to perform copula inference and determine the underlying dependence structure or through expert knowledge. However, in this paper the methodology is only applied to toy examples in order to show the advantages and appropriate dependence parameters are chosen arbitrarily. Deducing the copula structure by inference is left for future work.

Common Cause of Failure

Common cause of failure is the event that two or more components fail simultaneously due to shared defects (Watson 1981). These weaknesses can include but are not limited to (Hanks 1998):

- Manufacturing defects
- Errors by the maintenance or operator personal
- Shared environmental conditions

In this work, common cause of failures are modelled by applying Clayton copulas. Clayton copulas posses lower *tail dependence* which accurately allows to pull together early stage failure and as such model common cause of failure more accurately than copulas without lower tail dependence. Lower (or upper) tail dependences is a concept expressing higher dependence between random variables in the lower-left (or upper-right) quadrant of $[0, 1]^2$. Figure 7 shows samples drawn from a bivariate Gaussian copula and a bivariate Clayton copula, highlighting the practicality of Clayton copulas.

Consider a very simple system of two parallel components. The component failure times are assumed to be exponentially distributed with $\lambda_1 = 0.8$ and $\lambda_2 = 1.5$ and are sampled from a bivariate Clayton copula with θ chosen such that Kendall's tau equals 0.3. Figure 8 shows a plot of the resulting reliability against the reliability in the independent case. The lower tail dependence of the Clayton copula is clearly visible in the plot, as the reliability of the system including dependence is initially lower than if both component failures are considered to be independent. At later points in time, where the dependence in the Clayton copulas is lower, both survival functions are identical.

As an extension, a copula family exhibiting both lower tail and upper tail dependence could be applied in order to include failures due to old age.

Interdependencies

The treatment of interdependencies is not as simple as for common cause of failures in the previous section. To understand the difficulties it is important to understand the two meanings dependence has in this case. When working with copulas, dependence is a measure of correlation or concordance and as is the nature of copulas, dependence is modelled independently of the marginals. As such, dependence in a statistical sense does not imply causality. However, this is exactly what interdependencies represent. If one component fails there is a chance that a dependent component will fail as well.

Consider two dependent components whose failure times are distributed with marginal distributions F_1 and F_2 and copula C, where $F_1 \neq F_2$. If failure times are sampled for both components from a fully dependent copula and apply the marginals using the inverse transformation method, the failure times for the first component will still be distributed according to F_1 and the failures times for the second component will be distributed with F_2. Even though perfect dependence is assumed, the components will not fail together. Since the copula approach separates the modelling of the dependence structure from modelling of the marginals, this causality can be included in the latter. In this case, a simple aggregation of the marginals is performed using the resulting strength of dependence (Kendall's tau) as a factor as shown in Eq. 17

$$U_1 = (1 - \tau) \cdot F_1^{-1}(u_1) + \tau \cdot F_2^{-1}(u_1) \tag{17}$$

DEALING WITH UNCERTAINTY

Two types of uncertainties must be taken care of during the reliability analysis, namely, aleatory and epistemic uncertainties. Aleatory uncertainty describes the natural randomness inherent in a process such as component degradation and external forces affecting the system (natural hazards, earthquakes, etc.), while epistemic uncertainty represents the uncertainty due to vagueness in information or a lack thereof. The latter is usually regarded as reducible through acquiring of additional data and information.

Aleatory uncertainty can automatically be handled by the reliability analysis technique. Through assuming failure time distributions for the component failures and sampling these during Monte Carlo simulation, the randomness that the model is subject to is fully included. However, the selection appropriate failure time distributions is typically based on either data or expert knowledge, neither of which yield perfect results, in turn introducing epistemic uncertainty into the model. This uncertainty can be reduced by using *probability-boxes* (p-boxes) (Feng et al. 2016).

P-boxes are defined as bounds on the cumulative distribution function of a random variable. The left and right bounds can be found by for example selecting an appropriate distribution and giving the parameters as intervals. As such, a p-box comprises both the aleatory and the epistemic uncertainty. An example of an exponential p-box with parameters $\lambda \in [1.2, 2.2]$ is shown in Fig. 9.

By feeding the bounds of the p-box into the reliability analysis, the epistemic uncertainty propagates into the result. Thus, instead of one survival function, we obtain an upper and lower bound. Figure 10a shows an example of the upper and lower bounds obtained by performing a reliability analysis of a simple system of two parallel components of the same type, assuming the p-box of Fig. 9 for the failure time distributions.

Similarly to the application of p-boxes to handle epistemic uncertainty in the marginals, we can define the copula parameters as intervals and obtain *imprecise copulas* for the dependencies (Montes et al. 2015). This works especially well since all copula families, including the bivariate Gaussian copula, that are grouped in the vine copula are defined by a single parameter.

Similar to the p-box, the imprecise copula imposes bounds on the system reliability by feeding the parameter interval bounds into the reliability analysis. Consider again a simple system of two parallel components, in this case interlinked by an imprecise Gaussian copula with $\rho \in [0.3, 0.6]$. The upper and lower bounds for the reliability are presented in Fig. 10b.

NUMERICAL EXAMPLE

The network structures for the following numerical example are taken from the IEEE Reliability Test System (RTS) (Grigg et al. 1999). The system is effectively split into two sub-systems (see Fig. 11 and Fig. 12) by removing the the transformers that link the low power to the high power grid. Components in the networks are classified into five types. Component types 1 and 5 are the non-generating nodes in networks 1 and 2 respectively. The generating nodes are divided into three component types 2, 3 and 4. These represent different types of generators such as nuclear, oil or coal power plants. Note that this is no attempt at solving the IEEE RTS. The system is merely providing the network topology.

In a first step to obtain the reliability, the required survival signatures for both networks are calculated using the approach presented in (Behrensdorf et al. 2018). Next, the vine copula that is used for sampling the individual component failure times is assembled from bivariate copulas. A common cause of failure is set among the groups of nodes of types 2, 3, and 4 through imprecise bivariate Clayton copulas. Next, the transformers that were removed to split the network in two, are reintroduced as interdependencies between the nodes 3 and 11, 9 and 24 as well as 10 and 12 using imprecise bivariate Gaussian copulas. All one-dimensional marginal distributions are assumed to be exponentially distributed. The parameters for the marginals and the copulas are presented in Tab. 3.

Finally, the reliability analysis is performed using the previously introduced Monte Carlo simulation method. The upper and lower bounds of the reliability for network 1 is presented in Fig.13. For comparison, the plot also contains a deterministic reliability analysis (all mean values) of network 1.

CONCLUSION

This paper presented a novel approach to the modelling of complex dependencies in interdependent networks by leveraging multivariate copulas. Over the course of this work the necessary theory on copulas, dependence measures and pair copula construction techniques was discussed. Of the investigated structures vine copulas have shown to be ideally suited to model higher dimensional dependencies with sufficient flexibility. The capabilities of the proposed approach were highlighted using a complex scenario based on the network topology of the IEEE Reliability Test System. The application of a vine copula has proven to be able to represent a complicated model with multiple competing failure modes. It was shown that imprecision can easily be included in the reliability analysis. Nonetheless, the modelling flexibility of this method comes at a price. Finding a suitable vine copula structure is not a trivial task and greatly suffers from the curse of dimensionality.

While the numerical example employed in this paper serves well to prove the usefulness of the proposed technique, the next logical step is to apply the methodology to a real world example. This includes deriving the vine copula model from data or expert knowledge. At the same time the inclusion of additional failure mechanisms such as external events (e.g. earthquakes, tsunamis, terrorist attacks) must be investigated.

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TABLE 1. Most popular Archimedean copulas with generators, generator inverses, and parameter domains.

Name	**Generator** $\varphi_\theta(\mathbf{t})$	**Generator Inverse** $\varphi_\theta^{-\mathbf{1}}(\mathbf{t})$	**Parameter** θ
Ali-Mikhall-Haq	$\log\left(\frac{1-\theta(1-t)}{t}\right)$	$\frac{1-\theta}{\exp(t)-\theta}$	$\theta \in [-1, 1)$
Clayton	$\frac{1}{\theta}(t^{-\theta} - 1)$	$(1 + \theta t)^{-1/\theta}$	$\theta \in [-1, \infty)\backslash\{0\}$
Frank	$-\log(\frac{\exp(-\theta t)-1}{\exp(-\theta)-1})$	$-\frac{1}{\theta}\log(1 + \exp(-t)(\exp(-\theta) - 1))$	$\theta \in \mathbb{R}\backslash\{0\}$
Gumbel	$(-\log(t))^\theta$	$\exp(-t^{1/\theta})$	$\theta \in [1, \infty)$
Independence	$-\log(t)$	$\exp(-t)$	
Joe	$-\log(1 - (1 - t)^\theta)$	$1 - (1 - \exp(-t))^{1/\theta}$	$\theta \in [1, \infty)$

TABLE 2. Survival signature of the network shown in Fig. 5.

l_1	l_2	$\Phi(l_1, l_2)$	l_1	l_2	$\Phi(l_1, l_2)$
0	0	0	2	0	0
0	0	0	2	1	0
0	0	0	2	2	4/9
0	0	0	2	3	6/9
1	0	0	3	0	1
1	1	0	3	1	1
1	2	1/9	3	2	1
1	3	3/9	3	3	1

TABLE 3. Failure rate ranges of the exponential marginal distributions and copula parameters used in the numerical example.

Parameter	Definition	Parameter range
λ_1	Failure rate of component type 1	$\lambda_1 \in [0.8, 1.2]$
λ_2	Failure rate of component type 2	$\lambda_2 \in [1.4, 1.5]$
λ_3	Failure rate of component type 3	$\lambda_3 \in [1.6, 1.9]$
λ_4	Failure rate of component type 4	$\lambda_4 \in [2.0, 2.3]$
λ_5	Failure rate of component type 5	$\lambda_5 \in [1.8, 2.2]$
τ_1	Clayton copula parameters on component type 2	$\tau_1 \in [0.1, 0.3]$
τ_2	Clayton copula parameters on component type 3	$\tau_2 \in [0.2, 0.4]$
τ_3	Clayton copula parameters on component type 4	$\tau_3 \in [0.1, 0.3]$
τ_4	Gaussian copula parameters between network 1 and 2	$\tau_4 \in [0.4, 0.8]$

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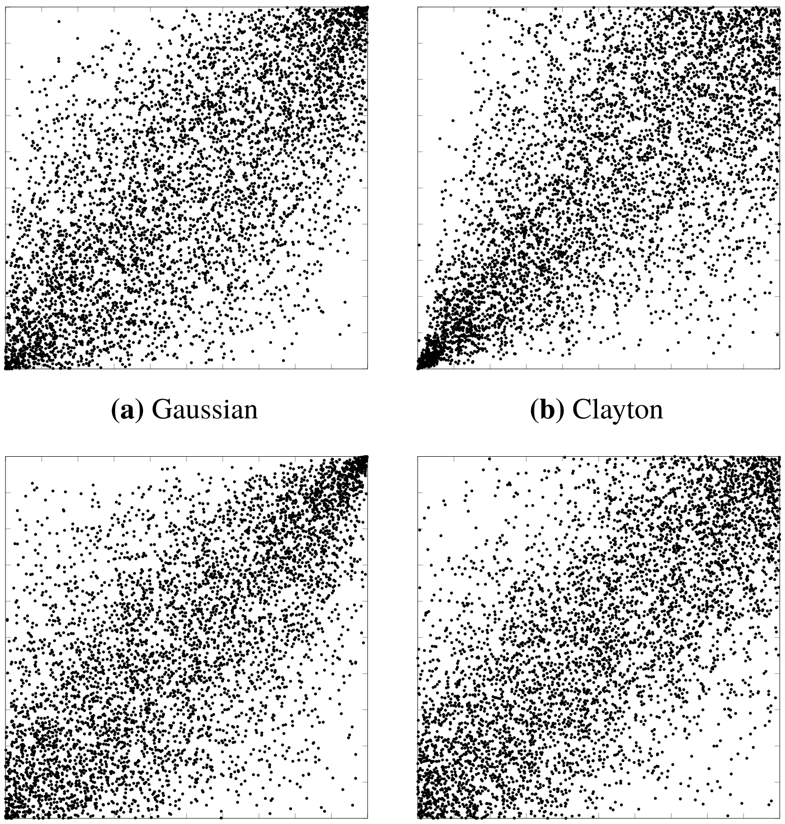


(a) Gaussian **(b)** Clayton

(c) Gumbel **(d)** Frank

Fig. 1. Samples drawn from different bivariate copulas where the parameters have been chosen so that Kendall's tau equals 0.5.

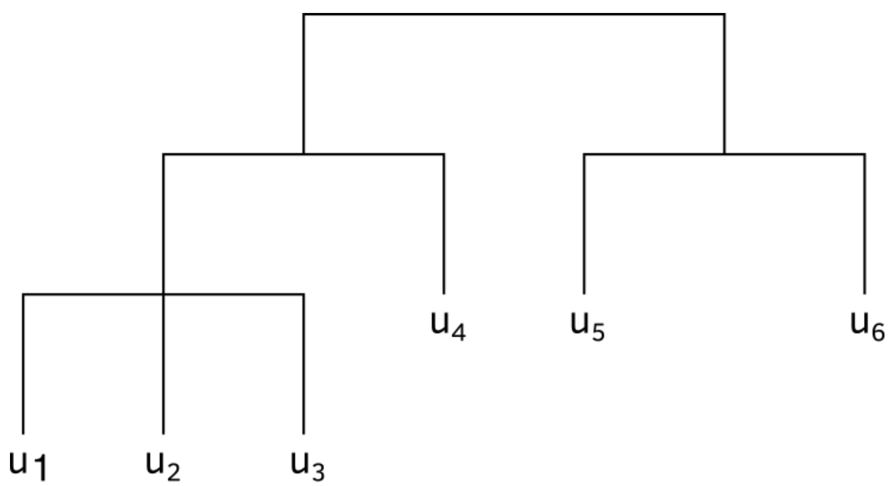


Fig. 2. Structure of a 6-dimensional hierarchical Archimedean copula

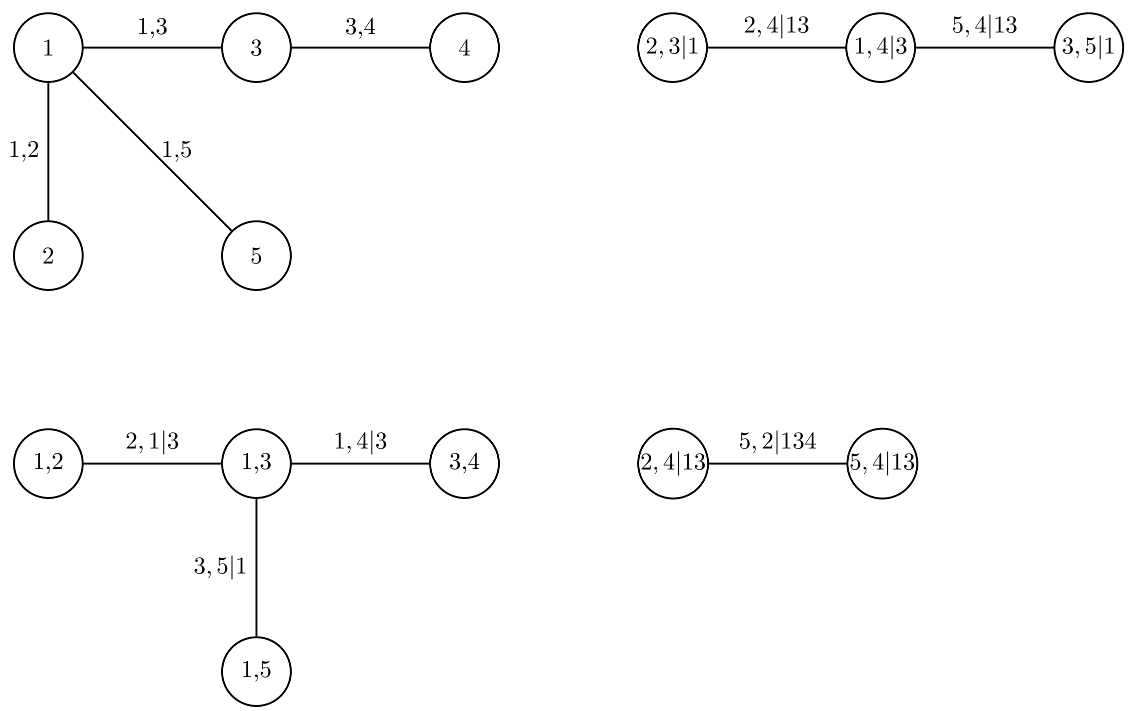


Fig. 3. Graphical illustration of a four-dimensional copula as a regular vine.

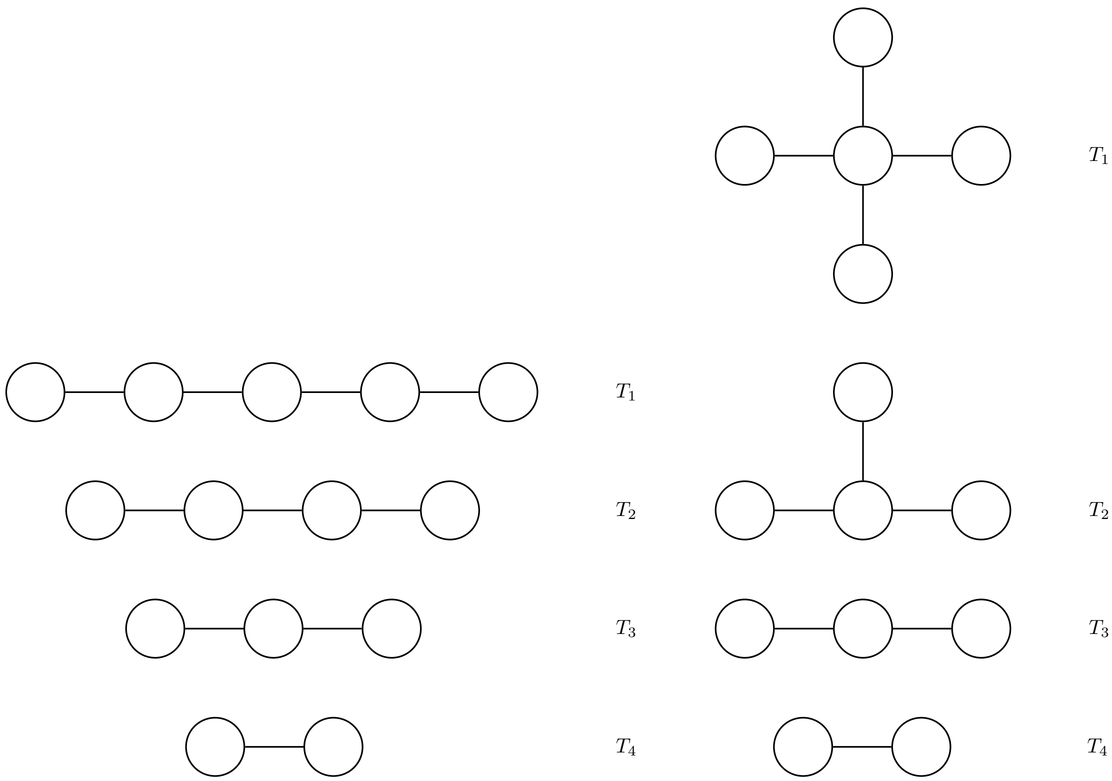


Fig. 4. C-Vine (left) and D-Vine (right) in five dimensions.

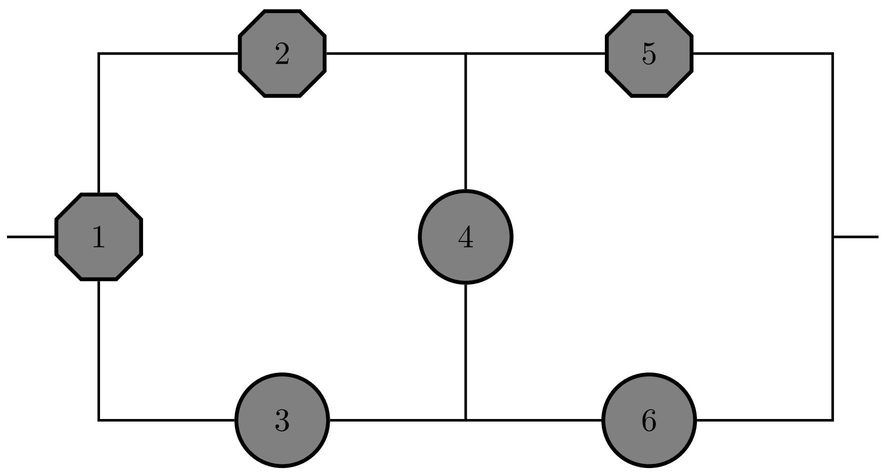


Fig. 5. Network with six components equally divided into two component types.

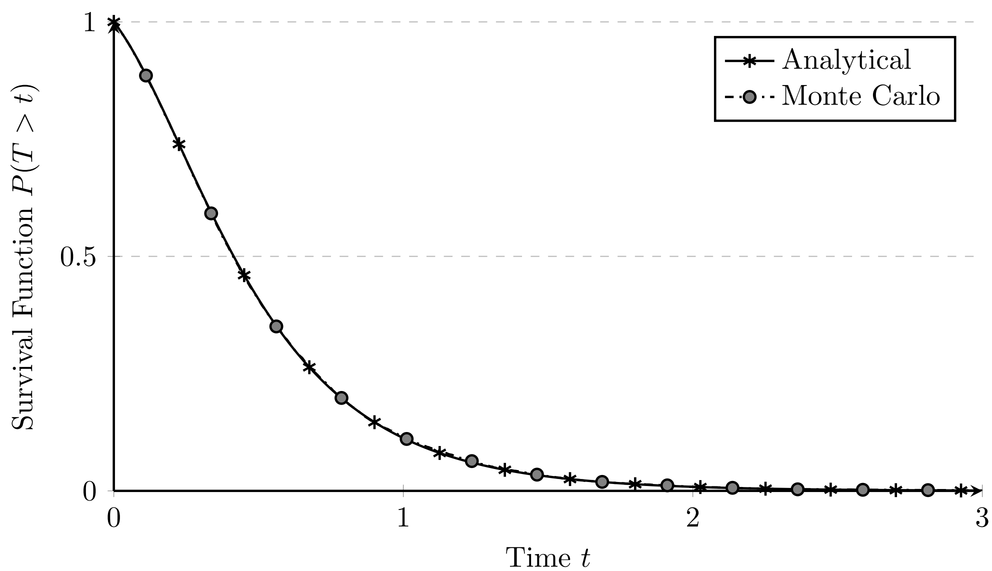
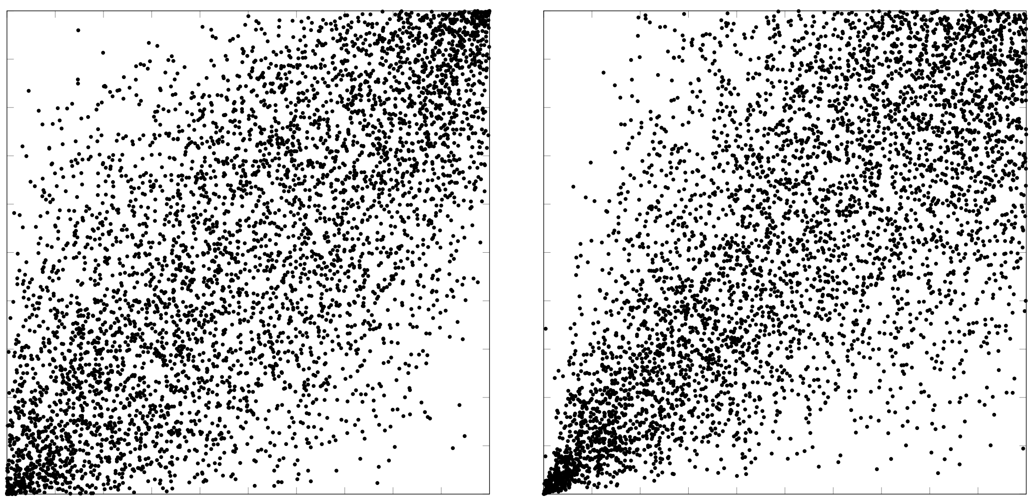


Fig. 6. Survival function for the network in Fig. 5.



(a) Gaussian **(b)** Clayton

Fig. 7. Samples drawn from bivariate Gaussian (a) and Clayton (b) copulas where the parameters have been chosen so that Kendall's tau equals 0.5.

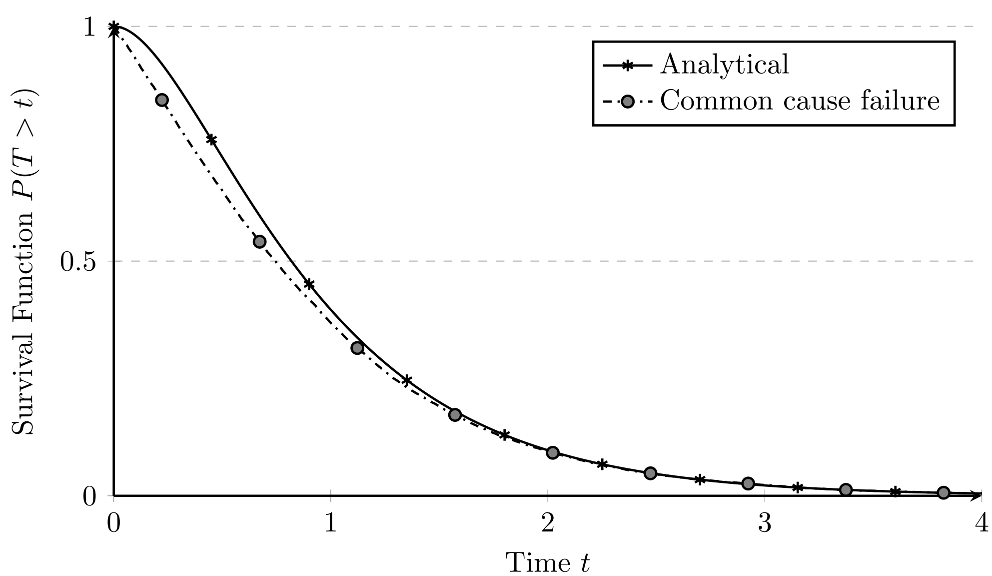


Fig. 8. Reliability of a parallel system subject to common cause of failure.

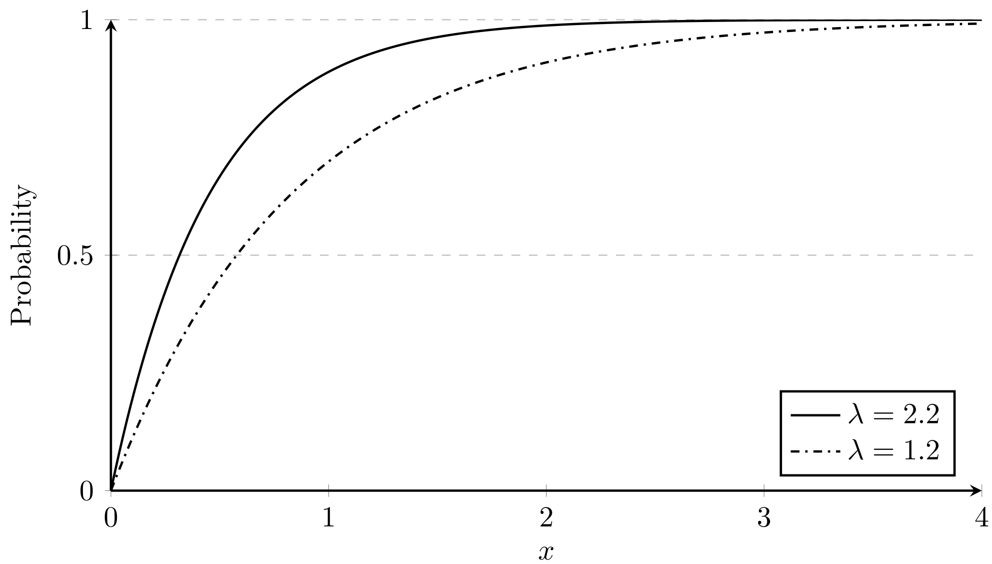
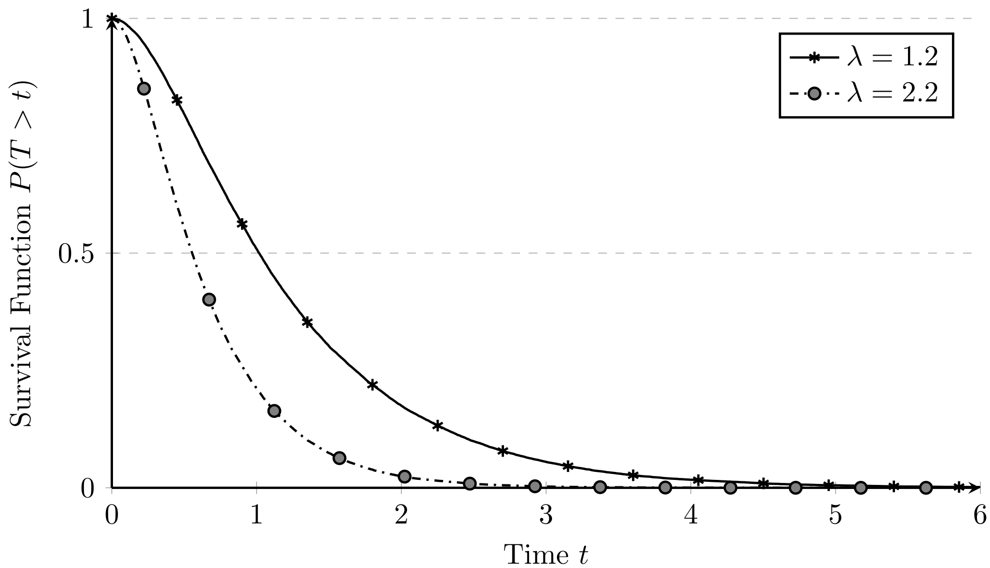
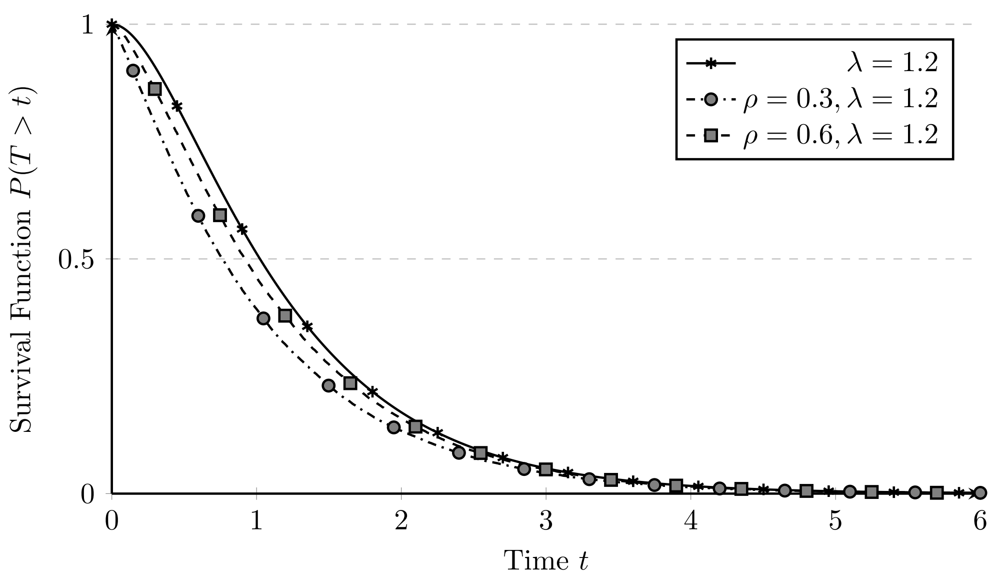


Fig. 9. Example of an exponential p-box with $\lambda \in [1.2, 2.2]$.



(a) Probability-box



(b) Imprecise copula

Fig. 10. Bounds on the reliability resulting from applying a p-box **(a)** or an imprecise Gaussian copula **(b)** to a simple system of two parallel components.

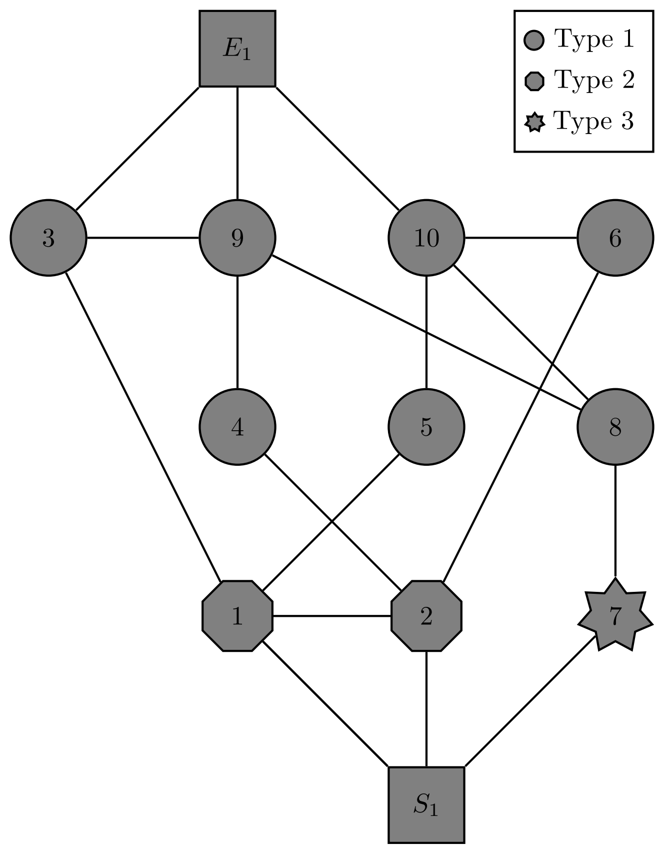


Fig. 11. Structure of the first network taken from the IEEE RTS

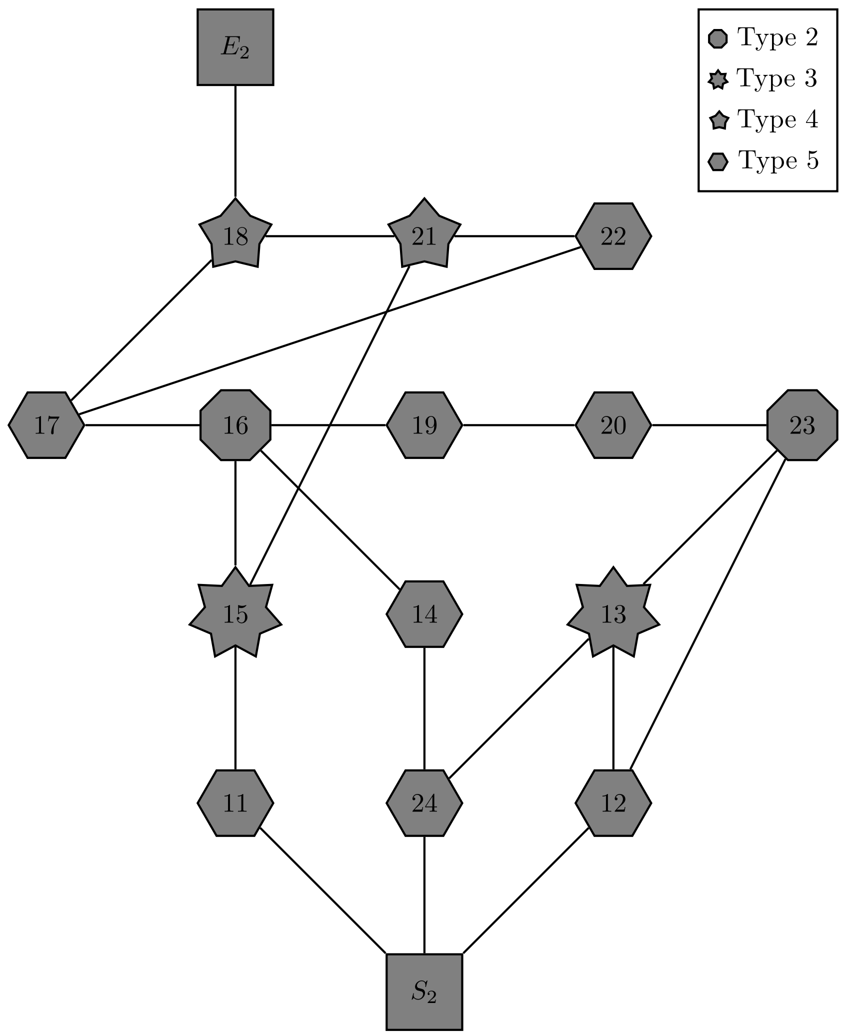


Fig. 12. Structure of the second network taken from the IEEE RTS

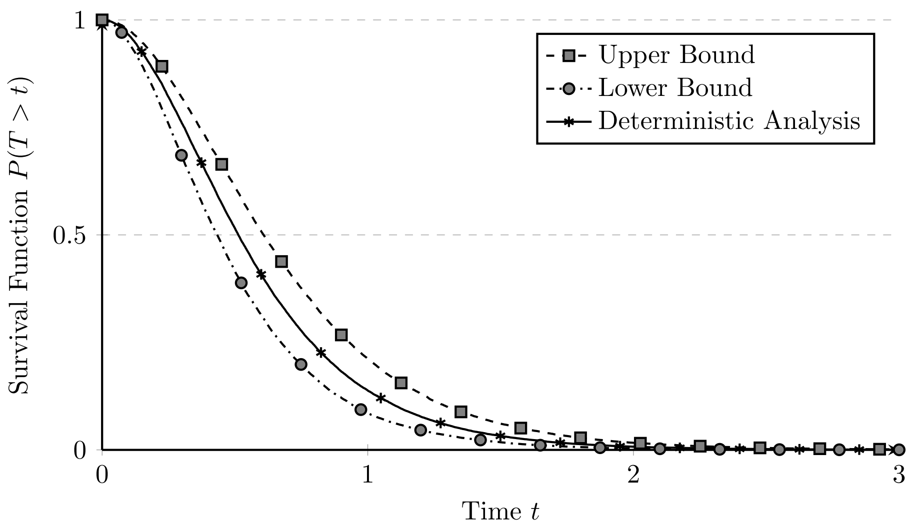


Fig. 13. Bounds on the reliability of network 1.