# A Computational Framework for Efficient Reliability Analysis of Complex Networks

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## Zusammenfassung

Mit der zunehmenden Größe und Komplexität moderner Infrastrukturnetze stellt sich die Herausforderung, effiziente und zuverlässige Methoden zur Analyse ihrer Zuverlässigkeit zu entwickeln. Besonderes Augenmerk muss dabei auf potenzielle Abhängigkeiten zwischen den Netzen gelegt werden, da deren Vernachlässigung zu katastrophalen Ausfällen führen kann. Darüber hinaus ist es von größter Wichtigkeit, alle Unsicherheiten angemessen zu behandeln. Die Überlebenssignatur ist eine jüngere Entwicklung zur effektiven Analyse komplexer Netze, die entscheidende Vorteile gegenüber traditionelleren Methoden bietet. Ihr wichtigstes Merkmal ist die vollständige Trennung der Systemstruktur von probabilistischen Informationen. Dadurch können verschiedene Phänomene wie Abhängigkeiten von Komponenten, Ausfälle aufgrund gemeinsamer Ursache und ungenaue Wahrscheinlichkeiten berücksichtigt werden, ohne dass die Netzstruktur neu ausgewertet werden muss.

In dieser kumulativen Dissertation werden mehrere wichtige Neuerungen für die Überlebenssignatur vorgestellt, die sich auf die strukturelle Auswertung des Systems sowie auf die Modellierung von Komponentenausfällen konzentrieren.

Es wird eine neue Methode vorgestellt, bei der Abhängigkeiten zwischen Komponenten und Netzwerken mit Hilfe von Vine-Copulas modelliert werden. Darüber hinaus werden aleatorische und epistemische Unsicherheiten durch die Anwendung von Wahrscheinlichkeitsboxen und unscharfen Copulas berücksichtigt. Durch die Nutzung der großen Anzahl verfügbarer Copula-Familien ist es möglich, unterschiedliche Effekte von Abhängigkeiten zu berücksichtigen. Das graphenbasierte Design der Vine-Copulas ergänzt sich gut mit den typischen Beschreibungen von Netzwerktopologien. Die vorgeschlagene Methode wird an einem anspruchsvollen Szenario basierend auf dem IEEE-Zuverlässigkeitstestsystem getestet, um ihre Effektivität zu demonstrieren und die Fähigkeit hervorzuheben, komplizierte Szenarien mit einer Vielzahl von abhängigen Fehlermechanismen zu modellieren.

Der numerische Aufwand, der zur analytischen Berechnung der Überlebenssignatur erforderlich ist, ist für große und komplexe Systeme nicht zu bewältigen. Daher werden in dieser Arbeit zwei Methoden zur Approximation der Überlebenssignatur vorgestellt. Im ersten Ansatz werden Systemkonfigurationen von geringem Interesse mit Hilfe der Perkolationstheorie ausgeschlossen, während die verbleibenden Teile der Signatur durch Monte-Carlo-Simulation geschätzt werden. Die Methode ist in der Lage, die Überlebenssignatur mit sehr kleinen Fehlern genau zu approximieren und gleichzeitig den Rechenaufwand drastisch zu reduzieren. Mehrere einfache Testsysteme sowie zwei reale Situationen werden verwendet, um die Genauigkeit und Effizienz zu verdeutlichen. Mit zunehmender Netzgröße und -komplexität stößt jedoch auch dieses Verfahren an seine Grenzen. Daher wird eine zweite Methode vorgestellt, bei der der numerische Bedarf weiter reduziert wird. In dieser wird nicht die gesamte Überlebenssignatur approximiert, sondern nur einige strategisch ausgewählte Werte mit Hilfe der Monte-Carlo-Simulation berechnet und zum Aufbau eines Ersatzmodells auf der Grundlage normalisierter radialer Basisfunktionen verwendet. Die Unsicherheit, die sich aus der Approximation der Datenpunkte ergibt, wird anschließend durch ein Intervallvorhersagemodell propagiert, das Ober- und Untergrenzen für die verbleibenden Überlebenssignaturwerte und dadurch auch für die Zuverlässigkeit des Netzwerks schätzt. Da wenige Datenpunkte ausreichen, um das Intervallvorhersagemodell zu erstellen, können noch größere Systeme analysiert werden.

Mit steigender Komplexität nicht nur des Systems, sondern auch der einzelnen Komponenten selbst ergibt sich die Notwendigkeit, die Komponenten als Subsysteme zu modellieren, wodurch sich komplexe Systeme aus Systemen ergeben. Es wird eine Arbeit vorgestellt, in der eine zuvor entwickelte Methode zur Resilienzentscheidungsfindung für mehrdimensionale Szenarien erweitert wird, in denen die Subsysteme als Überlebenssignaturen dargestellt werden. Die Überlebenssignatur der Teilsysteme kann aufgrund der inhärenten Trennung der Strukturinformationen vor der Resilienzanalyse berechnet werden. Dies ermöglicht eine effiziente Analyse, bei der die Ausfallraten der Subsysteme für verschiedene resilienzsteigernde Ausstattungen direkt aus der Überlebensfunktion berechnet werden, ohne die Systemstruktur neu auszuwerten.

Zusätzlich zu den Fortschritten auf dem Gebiet der Überlebenssignatur wird in dieser Arbeit auch eine neue Bibliothek für die Quantifizierung von Unsicherheiten mit dem Namen UncertaintyQuantification.jl vorgestellt, die als Paket in der Programmiersprache Julia entwickelt wurde. Julia ist eine moderne dynamische High-Level-Programmiersprache, die sich ideal für Aufgaben wie Datenanalyse und wissenschaftliches Rechnen eignet. UncertaintyQuantification.jl wurde von Grund auf so entwickelt, dass es generalisiert, flexibel und gleichzeitig einfach zu benutzen ist. Das Framework wird ständig weiterentwickelt und hat zum Ziel, eine Toolbox zu werden, die state-of-the-art Algorithmen aus allen Bereichen der Unsicherheitsquantifizierung umfasst und als wertvolles Werkzeug sowohl für die Forschung als auch für die Industrie dienen soll. Zum aktuellen Funktionsumfang von UncertaintyQuantification.jl gehören simulationsbasierte Zuverlässigkeitsanalysen unter Verwendung einer Vielzahl von Verfahren zur Erzeugung von Stichproben, lokale und globale Sensitivitätsanalysen sowie Metamodellierungstechniken.

Schlüsselwörter: Netzwerkzuverlässigkeit, Überlebenssignatur, Abhängigkeiten, Copulas, Monte-Carlo-Simulation, radiale Basisfunktionen, Intervallvorhersagemodelle

### Abstract

With the growing scale and complexity of modern infrastructure networks comes the challenge of developing efficient and dependable methods for analysing their reliability. Special attention must be given to potential network interdependencies as disregarding these can lead to catastrophic failures. Furthermore, it is of paramount importance to properly treat all uncertainties. The survival signature is a recent development built to effectively analyse complex networks that far exceeds standard techniques in several important areas. Its most distinguishing feature is the complete separation of system structure from probabilistic information. Because of this, it is possible to take into account a variety of component failure phenomena such as dependencies, common causes of failure, and imprecise probabilities without reevaluating the network structure.

This cumulative dissertation presents several key improvements to the survival signature ecosystem focused on the structural evaluation of the system as well as the modelling of component failures.

A new method is presented in which (inter)-dependencies between components and networks are modelled using vine copulas. Furthermore, aleatory and epistemic uncertainties are included by applying probability boxes and imprecise copulas. By leveraging the large number of available copula families it is possible to account for varying dependent effects. The graph-based design of vine copulas synergizes well with the typical descriptions of network topologies. The proposed method is tested on a challenging scenario using the IEEE reliability test system, demonstrating its usefulness and emphasizing the ability to represent complicated scenarios with a range of dependent failure modes.

The numerical effort required to analytically compute the survival signature is prohibitive for large complex systems. This work presents two methods for the approximation of the survival signature. In the first approach system configurations of low interest are excluded using percolation theory, while the remaining parts of the signature are estimated by Monte Carlo simulation. The method is able to accurately approximate the survival signature with very small errors while drastically reducing computational demand. Several simple test systems, as well as two real-world situations, are used to show the accuracy and performance.

However, with increasing network size and complexity this technique also reaches its limits. A second method is presented where the numerical demand is further reduced. Here, instead of approximating the whole survival signature only a few strategically selected values are computed using Monte Carlo simulation and used to build a surrogate model based on normalized radial basis functions. The uncertainty resulting from the approximation of the data points is then propagated through an interval predictor model which estimates bounds for the remaining survival signature values. This imprecise model provides bounds on the survival signature and therefore the network reliability. Because a few data points are sufficient to build the interval predictor model it allows for even larger systems to be analysed.

With the rising complexity of not just the system but also the individual components themselves comes the need for the components to be modelled as subsystems in a systemof-systems approach. A study is presented, where a previously developed framework for resilience decision-making is adapted to multidimensional scenarios in which the subsystems are represented as survival signatures. The survival signature of the subsystems can be computed ahead of the resilience analysis due to the inherent separation of structural information. This enables efficient analysis in which the failure rates of subsystems for various resilience-enhancing endowments are calculated directly from the survival function without reevaluating the system structure.

In addition to the advancements in the field of survival signature, this work also presents a new framework for uncertainty quantification developed as a package in the Julia programming language called UncertaintyQuantification.jl. Julia is a modern high-level dynamic programming language that is ideal for applications such as data analysis and scientific computing. UncertaintyQuantification.jl was built from the ground up to be generalised and versatile while remaining simple to use. The framework is in constant development and its goal is to become a toolbox encompassing state-of-the-art algorithms from all fields of uncertainty quantification.jl currently includes simulation-based reliability analysis utilising a wide range of sampling schemes, local and global sensitivity analysis, and surrogate modelling methodologies.

**Keywords:** Network reliability, survival signature, dependencies, copulas, Monte Carlo simulation, radial basis function networks, interval predictor models

"If it weren't for the last minute, nothing would get done."

– Rita Mae Brown

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# 1 Introduction

#### 1.1 Motivation

Efficient reliability analysis of complex infrastructure networks such as power grids, gas and water distribution systems or communication networks is of paramount importance for their safety and operation. The 2008 "Directive on European Critical Infrastructures" defines critical infrastructures as

"critical infrastructure" means an asset, system or part thereof [...] which is essential for the maintenance of vital societal functions, health, safety, security, economic or social well-being of people, and the disruption or destruction of which would have a significant impact [...] as a result of the failure to maintain those functions ([1]).

Society's increasing reliance on the availability of these systems [2] highlights the need for adequate reliability analysis.

The study of network reliability has received extensive attention from researchers over the past decades [3–5], since Moore and Shannon [6] introduced the first probabilistic network model in 1956. Traditional methods for network reliability problems can be roughly categorized into different fields [7]. Direct enumeration methods aim to obtain the reliability of the network from its underlying structure through complete state enumeration or enumeration of minimal path/cut sets [8–11]. Instead of computing the reliability of a large network directly, decomposition methods subdivide the network into smaller more manageable subsystems and obtain the reliability of the full network from the reliabilities of the subsystems [12–17]. The application of Monte Carlo simulation to circumvent the difficulty of solving NP-hard problems has a long history [18–22]. Recently, the combination of Monte Carlo simulation with machine learning techniques has seen increasing research focus [23–25]. Others have applied fault tree analysis to the reliability analysis of power networks [26].

Recently, the survival signature [27] has emerged as a competent tool for the reliability analysis of complex networks. Based on its inherent separation of structural from probabilistic information it provides the means for numerically efficient reliability analysis. Since the structure of the system is evaluated separately, a plethora of effects can be included in the probabilistic modelling of the system failures. These include phenomena such as dependent failures, common cause failures, or imprecise probabilities. Traditional techniques often struggle to include these effects or become intractable for larger networks.

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The survival signature is a generalization of the system signature [28] and has seen wide application since its introduction. Coolen et al. [29] used the survival signature to perform nonparametric predictive inference for system reliability. A generalization to unrepairable multistate components was presented in [30]. A continuous-state survival function and corresponding surrogate model were developed by Winnewisser et al. [31]. George-Williams et al. [32] extended the survival signature to complex systems with non-repairable dependent failures. Other applications to dependent failures can be found in [33, 34]. Recently, Zheng and Zhang [35] have investigated Archimedean copulas to model dependent components. Other areas of interest where the survival signature has seen successful application are imprecise reliability analysis [33] and component importance [33, 36]. Efficient simulation methods for the survival signature were introduced by [37]. Ample research has also focussed on efficient computation of the survival signature [38–41].

#### 1.2 Dependencies

Events such as the 2003 blackout in Italy have highlighted the need for adequate consideration of interdependencies between critical infrastructures [42]. In this event, cascading failures because of network interdependencies lead to a large-scale blackout. The failure of power stations directly caused the failure of nodes on the Internet which subsequently caused more power stations to break down. In this case, there are bidirectional dependencies between the power network and the Internet as power stations depend on the Internet for control and the nodes of the Internet depend on the power stations for electricity. This cascading breakdown is illustrated in Figure 1.1 where one failure in the power system in Figure 1.1a removes nodes from the Internet which in turn causes more nodes in the power system to fail so that after only two steps a large portion of the power net has failed in Figure 1.1c.

In general, dependencies are defined as connections between two networks, such as the electricity required to power nodes of the Internet as seen in the previous example. This is usually a unidirectional relationship where infrastructure a depends on infrastructure b but b does not depend on a [43]. On a lower level, dependencies may also be described between components inside an infrastructure.

For multiple infrastructures connected in a system-of-systems, dependencies are no longer unidirectional. Instead, there are bidirectional interdependencies where infrastructure a depends on infrastructure b through some connections and b is dependent on a through different connections. Infrastructures are *interdependent* when both are *dependent* on the other. [43]

Rinaldi et al. [43] classify interdependencies of critical infrastructures into four types. *Physical* dependencies describe the dependence of one system on the output of another. If a system depends on the information flowing through another system, these interdependencies are classified as *cyber*. *Geographic* interdependencies occur when multiple systems share the same location and are subject to the same environmental conditions. Finally, *logical* interdependencies



Figure 1.1: Cascading failures leading to the 2003 blackout in Italy. The figure presents the power grid as on overlay on the map of Italy and the Internet shifted above. In each subfigure, red nodes indicate newly failed nodes and green nodes are nodes that fail in the next step. Adapted from [42].

are any interdependency not covered by the previous three types.

The study of interdependent critical infrastructure networks is the target of increasing research focus, especially in the context of reliability [44–47] and resilience [42, 48, 49].

#### 1.3 Uncertainties

This section defines different classes of uncertainties and provides brief introductions into modelling approaches.

#### 1.3.1 Characterization of uncertainties

In line with Nikolaidis [50], the definition of *uncertainty* follows logically from the absence of *certainty* describing a state of absolute knowledge where everything there is to know about a process is known. This however is a theoretical and unachievable state in which deterministic models would be sufficient for the analysis of engineering systems. In reality, there is always a gap between certainty and the current state of knowledge resulting in *uncertainty*. This concept is further illustrated in Figure 1.2.



Figure 1.2: Characterization of reducible and irreducible uncertainties. Adapted from [51].

Although a topic of ongoing philosophical debate [51], it is largely accepted that uncertainty can be further classified into two types, namely *aleatory* and *epistemic* uncertainty [52]. The first type, *aleatory* uncertainties, are also called *irreducible* uncertainties or *variability* and describe the inherent randomness of a process. This could, for example, be variability in material properties, degradation of components, or varying external forces such as wind loads or earthquakes. Some researchers debate the existence of aleatory uncertainty under the assumption that if a process was fully understood it would no longer be random. Epistemic uncertainty is the uncertainty resulting from a lack of knowledge or vagueness and is also called *reducible* uncertainty as it can be reduced through the collection of additional data and information. If both types of uncertainties occur together this is known as *hybrid* uncertainty, see for example [53].

According to Bi et al. [54] uncertainties can be divided into four categories:

- Category I: Constant parameters without any associated uncertainty
- Category II: Parameters only subject to epistemic uncertainty represented as intervals
- Category III: Parameters with only aleatory uncertainties represented as precise probability distributions fully described by probability distributions.
- Category IV: Parameters subject to both aleatory and epistemic uncertainty represented as imprecise probabilities described by for example probability-boxes

#### 1.3.2 Modelling of uncertainties

Next follows a brief introduction to the modelling of precise (category III) and imprecise probabilities (category IV).

A precise probability model of an experiment or random process is mathematically described by a probability space  $(\Omega, \mathcal{F}, P)$  [55]. Here,  $\Omega$  is the sample space containing all possible outcomes  $\omega$  of the model or experiment expressed as

$$\Omega = \{\omega_1, \omega_2, \dots, \omega_n\}.$$
(1.1)

The  $\sigma$ -algebra (or  $\sigma$ -field)  $\mathcal{F} \subseteq 2^{\Omega}$  is the event space and defined as a set of subsets of  $\Omega$  containing the events under consideration. Events are the outcomes of an experiment that are of interest. To define the subset representing an event, all outcomes in  $\Omega$  are considered. If the outcome leads to the event happening, it is added to the subset. Events containing only a single outcome are called *elementary* events. The empty set  $\emptyset \in \mathcal{F}$  is an impossible event and the event containing all outcomes, i.e.  $\Omega$  is a certain event. In addition, for any event  $A \in \mathcal{F}$  follows  $\overline{A} \in \mathcal{F}$  where  $\overline{A}$  is the complement of A, i.e. the event that A does not happen. Finally, the set-function P is a probability measure assigning a probability to each event in  $\mathcal{F}$  such that  $P: \mathcal{F} \to [0, 1]$ .

The definition of the probability measure is grounded in Kolmogorov's axioms [56]. For an elementary event  $A \in \Omega$  the first axiom is

$$P(A) \ge 0,\tag{1.2}$$

which states that the probability assigned to an elementary event is non-negative. The second axiom

$$P(\Omega) = 1 \tag{1.3}$$

defines that the probability for the certain event is 1 while the third axiom states that for two mutually exclusive events A and B in  $\Omega$  the probability that either one or both of the events will happen is the sum of the probabilities of the events. As such it allows defining probabilities

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for complex events such as

$$P(A \cup B) = P(A) + P(B),$$
 (1.4)

if  $A \cap B = \emptyset$ . These three axioms in combination with set theory are sufficient to develop probability theory. For a thorough introduction to probability theory, refer to [55].

As a discrete example consider the throw of a six-sided dice. Here  $\Omega = \{1, 2, 3, 4, 5, 6\}$  and  $\mathcal{F}$  contains all possible subsets of  $\Omega$ . This includes elementary events such as the dice landing on a specific number  $\{1\}$  or  $\{6\}$  as well as complex events, for example the dice landing on an even  $\{2, 4, 6\}$  or odd  $\{1, 3, 5\}$  number. The probability assigned to each event is the cardinality of the event, i.e. the size of the set, divided by 6 (the number of possible outcomes  $\omega$ ). For example  $P(\{1\}) = \frac{1}{6}$  and  $P(\{2, 4, 6\}) = \frac{3}{6} = \frac{1}{2}$ . The latter follows directly from a generalization of the third axiom since all the elementary events are mutually exclusive.

A random variable X is uniquely defined by its cumulative density function (CDF)  $F : \mathbb{R} \to [0, 1]$ . By definition, it returns the probability that the random variable will take a value less than or equal to x

$$F_X(x) = P_X(X < x).$$
 (1.5)

A CDF is a right continuous and monotonically non-decreasing function which satisfies

$$\lim_{x \to -\infty} F_X(x) = 0 \tag{1.6}$$

and

$$\lim_{x \to \infty} F_X(x) = 1. \tag{1.7}$$

Consider a small interval of width  $\Delta x$  on the real line  $\mathbb{R}$  and the probability that the value of a random variable X falls in this interval

$$P(x < X \le (x + \Delta x)). \tag{1.8}$$

This probability varies with the magnitude of  $\Delta x$  with a larger interval leading to a higher probability. Normalizing the probability as

$$\frac{1}{\Delta x}P(x < X \le (x + \Delta x)) \tag{1.9}$$

gives the *density* of the probability over the interval. The limit of this density when the interval approaches 0 gives the so-called probability density function (PDF) of X. The PDF of a random variable can be obtained as the derivative of the CDF

$$f_X(x) = \frac{dF_X(x)}{dx} \tag{1.10}$$



Figure 1.3: Example of an exponential p-box with  $\lambda \in [1.2, 2.2]$ .

if it exists. Conversely, the CDF can be defined as the integral of the PDF as

$$F_X(x) = \int_{-\infty}^x f_X(\lambda) d\lambda.$$
(1.11)

Using the PDF and CDF random variables subject to aleatory uncertainty can be described using well established probability theory.

Ferson et al. [57] introduced the notion of a probability box (p-box) for the modelling of imprecise probabilities. Consider two CDFs  $\underline{F}$  and  $\overline{F}$  with  $\underline{F}(x) \leq \overline{F}(x)$  for all  $x \in \mathbb{R}$ . Then,  $[\underline{F}(x), \overline{F}(x)]$  is the set of CDFs F such that  $\underline{F}(x) \leq F(x) \leq \overline{F}(x)$ . This set is called the p-box for an imprecisely known random variable X, where  $\underline{F}(x)$  is the lower bound for the probability that X is smaller than or equal to x, and  $\overline{F}(x)$  is the upper bound of this probability. For an example of a p-box described by two CDFs of the exponential distribution with parameter  $\lambda \in [1.2, 2.2]$  refer to Figure 1.3. Here, only two CDFs are required to fully define the p-box. However, for distribution families described by multiple parameters four or more CDFs are needed to define the p-box. If only the outer CDFs are known and no further information about the CDFs between is available this is known as a distribution-free p-box where every possible CDF between the bounds is a valid CDF for the imprecise random variable X [57].

The epistemic uncertainty is propagated into the result by feeding the bounds of one or more p-boxes into a reliability analysis. As a result, the analysis returns an upper and lower bound on the reliability.

#### 1.4 Signatures

Signatures are condensed representations of a system's topology. Their inherent separation of structural information from the probabilistic component failure times allows for efficient evaluation of the system reliability. Both the system signature [28] and its generalization the survival signature [27] are defined for *coherent* systems.

To begin, consider a system with m components. The state vector  $\mathbf{x} = (x_1, x_2, \ldots, x_m) \in \{0, 1\}^m$  represents the binary states of all components  $x_i$  in the system with  $x_i = 1$  if a component is working and  $x_i = 0$  if it is in a failed state. The components are arbitrarily labelled inside the state vector. However, it is important that this labelling is kept consistent throughout the analysis. The overall state of a system given a state vector is evaluated through the so-called structure function. This function  $\varphi(\mathbf{x}) : \{0, 1\}^m \to \{0, 1\}$  maps each state vector  $\mathbf{x}$  for which the system is working to 1 and the state vectors of failed systems to 0.

A system is *coherent* under two conditions: The structure function is monotone and all n components are relevant to the system's functionality. In this case, the monotonicity of the structure function ensures that a system can not degrade (or fail) by restoring a failed component to working condition. Mathematically, this is defined as  $\varphi(\mathbf{x}) \leq \varphi(\mathbf{y})$  for any two state vectors  $\mathbf{x}$  and  $\mathbf{y}$  if  $\mathbf{x} \leq \mathbf{y}$ . The comparison of state vectors is applied component-wise as  $x_i \leq y_i$  for all  $i \in \{1, 2, ..., m\}$ . This condition also implies  $\varphi(\mathbf{0}) = 0$  and  $\varphi(\mathbf{1}) = 1$ .

A component is considered relevant if it contributes to the structure function. In the opposite case, component i is irrelevant if

$$\varphi(x_1, \dots, x_{i-1}, 0, x_{i+1}, \dots, x_m) = \varphi(x_1, \dots, x_{i-1}, 1, x_{i+1}, \dots, x_m)$$
(1.12)

for all possible combinations of  $(x_1, \ldots, x_{i-1}, x_{i+1}, \ldots, x_m)$ . Any component that is not relevant to the system can be removed to simplify the system while retaining the same functionality.

#### 1.4.1 System signature

The system signature for coherent systems with binary state components was introduced by Samaniego [28]. Assuming i.i.d component failure times the system signature **s** is a vector with m elements where the *i*th entry is the probability that the failure of *i* components results in the failure of the system. If  $T_S > 0$  is the failure time of the system and  $T_i$  is the *i*th component failure then the signature is

$$\mathbf{s}_i = P(T_S = T_i). \tag{1.13}$$

Computation of the system signature is a combinatorial problem. The probability  $\mathbf{s}_i$  is obtained by generating all m! permutations of component failures and calculating the fraction of permutations where the *i*th failure results in the failure of the system. From the assumptions about coherent systems follow that  $\sum_{i=1}^{m} \mathbf{s}_i = 1$ . This task is computationally demanding



Figure 1.4: Simple system with three components.

for large systems. Even for a relatively small system with ten components, 10! = 39916800 permutations of failure times must be evaluated.

As an example, consider a simple system of three components as shown in Figure 1.4. To obtain the signature of this system 3! = 6 permutations of the component failure times have to be evaluated. Two permutations  $X_1 < X_2 < X_3$  and  $X_1 < X_3 < X_2$  lead to a system failure after one component fails, resulting in  $\mathbf{s}_1 = \frac{1}{3}$ . The remaining four permutations  $X_2 < X_1 < X_3$ ,  $X_2 < X_3 < X_1$ ,  $X_3 < X_1 < X_2$ , and  $X_3 < X_2 < X_1$  all lead to system failure after the second component failure, which in turn means that  $\mathbf{s}_2 = \frac{2}{3}$ . A maximum of two component failures are required for this system to fail which implies  $\mathbf{s}_3 = 0$ . The full signature is therefore  $\mathbf{s} = (\frac{1}{3}, \frac{2}{3}, 0)$ .

The reliability of the system given by the survival function is then defined as

$$P(T_S > t) = \sum_{i}^{m} \mathbf{s}_i P(T_i > t).$$
(1.14)

If the failure times of the components follow a known distribution with CDF F(t), the survival function can be analytically computed as

$$P(T_i > t) = \sum_{i=1}^{m} \mathbf{s}_i \sum_{j=0}^{i-1} \binom{m}{j} [F(t)]^j \left[1 - F(t)^{n-j}\right].$$
 (1.15)

#### 1.4.2 Survival signature

Real world systems are often built from multiple different component types. Therefore, Coolen and Coolen-Maturi [27] generalized the system signature to systems with multiple types of components. This new signature is called the survival signature.

Consider a system of K component types. The survival signature is defined as the probability that the system is working while precisely  $l_k$  out of  $m_k$  components of each type  $k \in \{1, 2, ..., K\}$  are working as

$$\Phi(l_1,\ldots,l_K) = \left[\prod_{k=1}^K \binom{m_k}{l_k}^{-1}\right] \times \sum_{\mathbf{x}\in S_{l_1,\ldots,l_K}} \varphi(\mathbf{x}),$$
(1.16)

where the set  $S_{l_1,\ldots,l_K}$  contains all possible state vectors for  $l_1,\ldots,l_K$  working components. This set includes the states where no components of a certain type are functioning with  $l_k = 0$ . This

makes the survival signature a K-dimensional array with dimensionality  $(m_1+1) \times \cdots \times (m_K+1)$ . The individual values in this array will be referred to as *entries* throughout this dissertation.

As an example, consider a simple system of six components equally divided into two component types as shown in Figure 1.5. The survival signature of this system has  $(k_1 + 1) \cdot (k_2 + 1) = 16$ entries. A closer look will be taken at the computation of  $\Phi(1, 2)$ . Since there are  $\binom{m_1}{l_1} = \binom{3}{1} = 3$ possible configurations for one component of type 1 to work and  $\binom{m_2}{l_2} = \binom{3}{2} = 3$  configurations for two components of type 2 to work, set  $S_{1,2}$  contains nine state vectors. Of these nine, only the state vector where components 1, 3, and 6 are working will lead to a functioning system with  $\varphi(1,0,1,0,0,1) = 1$ . As a result, the survival signature entry is calculated as  $\Phi(1,2) = \frac{1}{9}$ . The full survival signature of the system is presented in Tab. 1.1.  $2^6 = 64$  structure function evaluations are necessary to fully calculate it.



Figure 1.5: Simple system with six components divided into two types. The different node shapes refer to the component types.

$l_1$	$l_2$	$\Phi(l_1, l_2)$	$ l_1 $	$l_2$	$\Phi(l_1, l_2)$
0	0	0	2	0	0
0	1	0	2	1	0
0	2	0	2	2	4/9
0	3	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 1.1: Survival signature of the network presented in Fig. 1.5.

The reliability of the system, which is the probability that it survives up to a point in time t, is given by the survival function as

$$P(T_s > t) = \sum_{l_1=0}^{m_1} \dots \sum_{l_K=0}^{m_K} \Phi(l_1, \dots, l_K) P\left(\bigcap_{k=1}^K \left\{C_t^k = l_k\right\}.\right),$$
(1.17)

with  $C_t^k$  representing the number of components of type k functioning at time t. The separation of structural information (given by the survival signature) from the probabilistic information about the component failures can be clearly seen in the equation. As with the system signature,

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there exists an analytical expression for the probabilistic part of the survival function in cases where the CDFs  $F(t)_k$  of the failure time distributions of each component type are known as

$$P\left(\bigcap_{k=1}^{K} \left\{ C_{t}^{k} = l_{k} \right\} \right) = \prod_{k=1}^{K} \left( \binom{m_{k}}{l_{k}} [F_{k}(t)]^{m_{k}-l_{k}} [1 - F_{k}(t)]^{l_{k}} \right).$$
(1.18)

Several simulation based algorithms have been introduced for cases where the CDFs are unknown [37].

The separation of probabilistic information enables the inclusion of various effects such as dependent component failures or imprecise failure time distributions. Feng et al. [58] have shown that when the failure times of the components are described as independent single-parameter p-box the upper and lower bounds of the system reliability  $[\overline{P}, \underline{P}]$  in Eq. 1.18 can be directly obtained from the upper and lower bounds of the CDFs  $[\overline{F}_k, \underline{F}_k]$ 

$$\overline{P}\left(\bigcap_{k=1}^{K}\left\{C_{t}^{k}=l_{k}\right\}\right)=\prod_{k=1}^{K}\left(\binom{m_{k}}{l_{k}}\left[\overline{F}_{k}(t)\right]^{m_{k}-l_{k}}\left[1-\overline{F}_{k}(t)\right]^{l_{k}}\right)$$
(1.19a)

$$\underline{P}\left(\bigcap_{k=1}^{K}\left\{C_{t}^{k}=l_{k}\right\}\right)=\prod_{k=1}^{K}\left(\binom{m_{k}}{l_{k}}[\underline{F}_{k}(t)]^{m_{k}-l_{k}}[1-\underline{F}_{k}(t)]^{l_{k}}\right).$$
(1.19b)

Returning to the example system given in Figure 1.5, assume the failure time distributions of both component types are defined as exponential p-boxes with the failure rates  $\lambda_1 \in [0.8, 1.2]$  for component type 1 and  $\lambda_2 \in [0.7, 0.9]$  for component type 2. The lower and upper bounds of the resulting reliability are presented in Figure 1.6.



Figure 1.6: Upper and lower bounds for the reliability of the system shown in Figure 1.5.

#### 1.5 Copulas

Copulas, from the Latin word for *bond* or *tie*, are multivariate distribution functions with the univariate marginal distributions all being U(0, 1). Because these uniform marginals can be transformed to any marginal distribution through the inverse probability integral transform (using the inverse CDF) the copula essentially enables the coupling of different marginals into new multivariate distributions. Any multivariate distribution in dimension  $d \ge 2$  can therefore be described by univariate marginals and a copula. This is known as Sklar's theorem [59].

**Theorem 1.5.1** (Sklar's theorem). Let H be a d-dimensional distribution function with marginals  $F_1, \ldots, F_d$ . There exists a d-dimensional copula C such that

$$H(\mathbf{x}) = C(F_1(x_1), \dots, F_d(x_d)), \forall \mathbf{x} \in \mathbb{R}^d$$
(1.20)

If the marginals  $F_1, \ldots, F_d$  are continuous the copula is unique. Otherwise, it is only unique on  $Range(F_1) \times \cdots \times Range(F_d)$ . If C is a d-dimensional copula and  $F_1, \ldots, F_d$  are distribution functions, then the H is a d-dimensional distribution function with marginals  $F_1, \ldots, F_d$ .

This separation of the copula from the marginal distribution functions provides great modelling flexibility and synergizes well with the separation of structural from probabilistic information in the survival signature presented in Eq. 1.17. For a thorough discussion of copulas, refer to [60, 61].

Copulas are invariant under strictly increasing transformation. As such, dependence among random variables can be studied by examining the underlying copula. This requires a dependence measure that is also invariant under strictly increasing transformations. Classically, *correlation* measured as the linear correlation coefficient  $\rho$  is used to measure dependence. Where the linear correlation coefficient  $\rho$  for two random variables is defined as

$$\rho(X,Y) = \frac{\operatorname{Cov}(X,Y)}{\sqrt{\operatorname{Var}(X)}\sqrt{\operatorname{Var}(Y)}},\tag{1.21}$$

with Var and Cov representing the variance and covariance.

However,  $\rho$  is not scale-invariant and may change when transforming from the copula to the marginal distributions. To illustrate this fact, consider the following example adapted from [62]. Figure 1.7 shows two scatter plots. On the left, 100 dependent samples have been drawn with  $x_1 \sim U(0,1)$  and  $y_1 \sim U(0,x_1)$ . On the right, these 100 samples are transformed from [0,1] to marginal distributions with  $x_2 \sim \text{Exp}(1)$  and  $y_2 \sim N(0,1)$ . Visually, these plots look quite different and computing the linear correlation coefficients  $\rho(x_1,y_1) \approx 0.66776$  and  $\rho(x_2,y_2) \approx 0.50486$  tells the same story. However, the underlying dependence structure has not changed at all. This makes  $\rho$  a poor measure of global dependence.

Two better suited scale-invariant dependence measures are Kendall's  $\tau$  [63] and Spearman's  $\rho$  [64] both based on rank correlation instead of linear correlation. Kendall's  $\tau$  will be used



Figure 1.7: Comparison of dependent samples before and after transformation to marginal distributions.

throughout this dissertation.

Kendall's  $\tau$  is defined based on *concordance*. Consider  $(x_1, y_1), \ldots, (x_n, y_n)$  to be a set of n observations of two random variables X and Y. Pairs of  $(x_i, y_i)$  and  $(x_j, y_j)$  are said to be *concordant* when  $(x_i - x_j)(y_i - y_j) > 0$  and *discordant* if the reverse holds true. This means, that "large" values of one random variable are associated with "large" values of the other and the same for "small" values.

Let c be the number of concordant pairs and d be the number of discordant pairs, then Kendall's  $\tau$  for the n observations is defined as

$$\tau = \frac{c-d}{c+d} = \frac{c-d}{\binom{n}{2}}.$$
(1.22)

Going back to the example presented in Figure 1.7 Kendall's  $\tau$  for both plots is  $\tau(x_1, y_1) = \tau(x_2, y_2) \approx 0.49818$ . This proves, that it is better suited to measure dependence in a copula setting than the linear correlation coefficient.

The population version of Kendall's  $\tau$  for X and Y is defined as the probability that a pair is concordant minus the probability that it is discordant for a random pair of observations

$$\tau = P[(X - X')(Y - Y') > 0] - P[(X - X')(Y - Y') < 0],$$
(1.23)

where (X', Y') is an independent copy of (X, Y). To further underline the suitability of Kendall's  $\tau$  one can show that it can be expressed solely based on the copula function (see, [61]) as

$$\tau = 4 \int_0^1 \int_0^1 C \, dC - 1. \tag{1.24}$$

#### 1.5.1 Copula families

There are multiple families of copulas all exhibiting different dependence structures. Two of the most popular classes of copulas are presented here. Elliptical copulas, mainly the Gaussian copula, and Archimedean copulas.



Figure 1.8: Samples drawn from different bivariate copulas families. The parameters have been chosen so that Kendall's  $\tau = 0.5$ .

#### **Elliptical copulas**

The family of elliptical copulas describes copulas underlying multivariate elliptical distributions. The most prominent elliptical distribution is the multivariate normal, providing the Gaussian copula. The d-dimensional Gaussian copula is defined as

$$C_R(u_1, \dots, u_d) = \Phi_R(\Phi^{-1}(u_1), \dots, \Phi^{-1}(u_d)),$$
(1.25)



Figure 1.9: Samples drawn from the copulas presented in Figure 1.8 transformed to standard normal marginals.

where  $R \in [-1, 1]^{d \times d}$  is a positive definite correlation matrix. Here,  $\Phi_R$  is the joint CDF of the multivariate normal distribution with correlation matrix R and  $\Phi^{-1}$  is the quantile function of the standard normal distribution [61]. A Gaussian copula with normal marginal distributions is the multivariate normal distribution.

#### Archimedean copulas

Archimedean copulas are another important family of copulas. Archimedean copulas are constructed from strictly monotone functions called *generators*. A generator  $\varphi : [0, \infty] \rightarrow [0, 1]$  must be strictly decreasing with  $\varphi(0) = 1$  and  $\varphi(\infty) = 0$  [65]. Then, a *d*-dimensional Archimedean copula  $C_{\varphi}$  is defined as

$$C_{\varphi}(u_1, \dots, u_d) := \varphi(\varphi^{-1}(u_1) + \dots + \varphi^{-1}(u_d)), \qquad (1.26)$$

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where  $\varphi^{-1}$  is the inverse of the generator. Note that in some literature the order of  $\varphi$  and  $\varphi^{-1}$  is inverted. Some of the most popular parametric Archimedean copula families with their generators, inverses, and parameter domains are presented in Tab. 1.2. This family of copulas where the parameters control the strength of dependence through the generator provides a large spectrum of dependence structures.

 Table 1.2: Generators, inverse generators, and parameter domains for some of the most popular Archimedean copulas.

Name	Generator $\varphi_{\theta}(t)$	Generator Inverse $\varphi_{\theta}^{-1}(t)$	Parameter $\theta$
$AMH^1$	$\log\left(\frac{1-\theta(1-t)}{t}\right)$	$rac{1- heta}{\exp(t)- heta}$	$\theta \in [-1,1)$
Clayton	$\frac{1}{\theta}(t^{-\theta}-1)$	$(1+\theta t)^{-1/\theta}$	$\theta \in [-1,\infty) \backslash \{0\}$
Frank	$-\log(\frac{\exp(-\theta t)-1}{\exp(-\theta)-1})$	$-\tfrac{1}{\theta}\log(1+\exp(-t)(\exp(-\theta)-1))$	$\theta \in \mathbb{R} \backslash \{0\}$
Gumbel	$(-\log(t))^{\theta}$	$\exp(-t^{1/\theta})$	$\theta \in [1,\infty)$
Independence	$e - \log(t)$	$\exp(-t)$	
Joe	$-\log(1-(1-t)^{\theta})$	$1 - (1 - \exp(-t))^{1/\theta}$	$\theta \in [1,\infty)$

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A special copula is the independence copula

$$C(u_1, \dots, u_d) = \prod_{i=1}^d u_i,$$
 (1.27)

which implies independence between all variables. It can be defined either as a Gaussian copula with identity matrix as the correlation matrix R in Eq. 1.25 or alternatively as an Archimedean copula with generator  $\varphi(t) = -\log(t)$  and inverse generator  $\varphi(t)^{-1} = \exp(-t)$ .

Figure 1.8 shows scatter plots for samples drawn from different bivariate copulas. The parameters of each copula have been chosen so that  $\tau = 0.5$ . Note the visible difference in the dependence structure for the same strength of dependence. This shows the flexibility of copulas when it comes to modelling various types of dependencies by applying different families. The samples obtained from the copulas transformed to standard normal marginal distributions are presented in Figure 1.9. The dependence in the underlying copula is still evident after the transformation to the marginals.

#### 1.5.2 Pair Copula Construction

Constructing multivariate distribution functions is a difficult task. Various approaches have been introduced to build multivariate copulas from combinations of bivariate copulas because the application of simple families such as Archimedean copulas lacks flexibility to model complex dependency structures [61]. This is known as pair copula construction and has the additional benefit that the available theory on bivariate copulas is significantly more extensive in comparison to multivariate copulas [65].

Let  $f_{1:d}(x_1, \ldots, x_d)$  be the joint density function of *d*-dimensional vector of random variables  $\mathbf{X} = (X_1, \ldots, X_d)$ . Here the subscript  $f_{1:d}$  is a shorthand for  $f_{1,2,\ldots,d}$ . This density can be expressed by a combination of conditional densities functions as

$$f_{1:d}(x_1,\ldots,x_d) = f_1(x_1) \cdot f_{2|1}(x_2|x_1) \cdot f_{3|2,1}(x_3|x_2,x_1) \cdot \cdots \cdot f_{d|1:(d-1)}(x_d|x_1,\ldots,x_{d-1}).$$
(1.28)

By applying Sklar's theorem the conditional densities can be deconstructed into bivariate copula densities and densities of univariate margins. Differentiating Eq. 1.20 with respect to a distribution with joint density  $f(x_1, \ldots, x_d)$ , marginals  $f_j$  and marginal CDFs  $F_j$ ,  $j \in \{1, \ldots, d\}$  leads to

$$f_{1:d}(x_1,\ldots,x_d) = c_{1:d}(F_1(x_1),\ldots,F_d(x_d)) \cdot f_1(x_1) \cdot \cdots \cdot f_d(x_d),$$
(1.29)

where  $c_{1:d}(\cdot)$  is the *d*-variate copula density. For the bivariate case this simplifies to

$$f_{1,2}(x_1, x_2) = f_1(x_1) \cdot f_{2|1}(x_2|x_1), \tag{1.30}$$

which will provide the basic building block for the multivariate density functions. It also yields

$$f_{2|1}(x_2|x_1) = \frac{f(x_1, x_2)}{f(x_1)} = c_{12}(F_1(x_1), F_2(x_2)) \cdot f_2(x_2)$$
(1.31)

as the conditional density of a random variable  $X_2$  given  $X_1$  which can be generalized to

$$f_{j|i}(x_j|x_i) = \frac{f(x_i, x_j)}{f(x_i)} = c_{ij}(F_i(x_i), F_j(x_j)) \cdot f_j(x_j).$$
(1.32)

As an example of how to decompose higher dimensional densities, consider a three-dimensional density function expressed through Eq. 1.28 as

$$f_{1,2,3}(x_1, x_2, x_3) = f_1(x_1) \cdot f_{2|1}(x_2|x_1) \cdot f_{3|1,2}(x_3|x_1, x_2).$$
(1.33)

Through Eq. 1.31 the second term of the three-dimensional density function can be expressed as a pair-copula and a marginal distribution. The third term can be further split by selecting either of the conditioning variables  $x_1$  or  $x_2$  where choosing  $x_2$  leads to

$$f_{1,2,3}(x_1, x_2, x_3) = f_1(x_1) \cdot c_{12}(F_1(x_1), F_2(x_2)) \cdot f_2(x_2) \cdot c_{13|2}(F_{1|2}(x_1|x_2), F_{3|2}(x_3|x_2)) \cdot f_{3|2}(x_3|x_2).$$

$$(1.34)$$

The final term can again be deconstructed into another pair-copula and marginal distribution using Eq. 1.31 leading to the final and complete decomposition of the three-dimensional density as

$$f_{1,2,3}(x_1, x_2, x_3) = f_1(x_1) \cdot c_{12}(F_1(x_1), F_2(x_2)) \cdot f_2(x_2)$$

$$c_{13|2}(F_{1|2}(x_1|x_2), F_{3|2}(x_3|x_2)) \cdot c_{23}(F_2(x_2), F_3(x_3)) \cdot f_3(x_3).$$
(1.35)

The conditional densities that are arguments of the copulas can be obtained from the copula CDFs. This recursive methodology can be applied to decompose any multivariate density into combinations of bivariate copulas and univariate marginal. However, not all multivariate copulas can be modelled with this pair copula construction method. To allow for inference and model selection, the assumption is usually made that the pair-copulas only depend on the conditioning variables through the conditional distribution functions as their arguments. Hobæk Haff et al. [66] present which pair-copula decompositions satisfy this condition.

#### Vine copulas

During the decomposition of a multivariate density  $f_{1:d}(x_1, \ldots, x_d)$  into bivariate copulas and marginal densities many choices on conditioning variables have to be made, resulting in numerous possible pair-copula constructions. Bedford and Cooke [67] pioneered the vine copula approach as a graph-theory based tool to organize these decompositions.

Since vine copulas are defined as a set of *trees* the basic notion of a tree is quickly introduced. Let the tuple G = (N, E) be an undirected graph composed of nodes N and edges E which are 2-element subsets of N as

$$E \subseteq [N]^2. \tag{1.36}$$

A path is a sequence of nodes  $n_1, \ldots, n_k$  where for each node  $n_i$  there is an edge connecting it to the next and all nodes in the path are unique, i.e. not visited repeatedly. A special type of path where  $n_1 = n_k$  is called a *cycle*. A *tree* is then defined as an acyclic undirected graph where all pairs of two nodes are connected by exactly one distinct path [68].

A regular vine (R-vine) of d elements is defined as a sequence of d-1 trees  $\mathcal{V} = (T_1, \ldots, T_{d-1})$ with the following conditions: (1)  $T_1$  is a tree of nodes  $N_1 = 1, \ldots, d$  and edges  $E_1$ . (2) Each subsequent tree  $T_j$  for  $j \ge 2$  is a tree with nodes  $N_j = E_{j-1}$  and edges  $E_j$ . Meaning the nodes of tree  $T_j$  are the edges of  $T_{j-1}$ . And (3), each tree  $T_j$  for  $j \in \{1, \ldots, d-1\}$  fulfils the proximity condition stating if  $\{a, b\} \in E_j$  then  $|a \cap b| = 1$ . This condition ensures that any nodes connected in tree  $T_j$  for  $j \ge 2$  share a common ancestor in tree  $T_{j-1}$ . Figure 1.10 shows a five-dimensional regular vine. Note how an edge in  $T_2$  between 1, 2 and 3, 4 is forbidden by the proximity condition.

Starting from d nodes and d-1 pair-copulas in  $T_1$  followed by d-1 nodes and d-1 edges in  $T_2$  until only two nodes and one edge exist in the final tree  $T_4$  one can see that the number of pair-copulas in a d-dimensional vine is



Figure 1.10: Graphical representation of the four trees constructing a five-dimensional regular vine.

$$(d-1) + (d-2) + \dots + 2 + 1 = \frac{(d-1)d}{2} = \binom{d}{2}.$$
 (1.37)

As such, a 5-dimensional vine already requires the evaluation of 10 bivariate copulas of which most involve conditional distribution functions. Assuming conditional independence for some pair-copulas allows to significantly reduce the complexity for higher dimensional vines. Going back to the example in Eq. 1.35, assuming that  $x_2$  and  $x_3$  are independent conditional on  $x_1$ simplifies the final decomposition to

$$f_{1,2,3}(x_1, x_2, x_3) = f_1(x_1) \cdot c_{12}(F_1(x_1), F_2(x_2)) \cdot f_2(x_2)$$

$$c_{23}(F_2(x_2), F_3(x_3)) \cdot f_3(x_3),$$
(1.38)

because the conditional independence implies  $c_{3|12}(F_{1|2}(x_1|x_2), F_{3|2}(x_3|x_2)) = 1$ .

Regular vines are very general. In fact, Morales-Nápoles [69] have shown that there are  $d!/2 \cdot 2^{\binom{d-2}{2}}$  possible R-vines in d dimensions. A smaller subset of R-vines with only d!/2 possible structures known as C-vines (canonical vines) and D-vines provide specific ways to perform the density decomposition. In a C-vine there is a node  $n \in N_i$  in each tree  $T_i$  for which  $|\{e \in E_i | n \in e\}| = d - 1$ , meaning there is one central node that is connected to all other nodes. In a D-vine for each node  $n \in N_i$  the number of edges is  $|\{e \in E_i | n \in e\}| \leq 2$ . The resulting structures for C- and D-vines in five dimensions are presented in Figure 1.11.

There is a straightforward sampling algorithm for sampling d dependent uniform variables in  $[0,1]^d$  from a vine copula. Start by sampling d independent uniform random numbers



Figure 1.11: Graphical representations of C- and D Vines.

 $u_i \sim U(0,1)$  for  $i \in \{1,\ldots,d\}$  and compute

$$x_{1} = u_{1},$$

$$x_{2} = F_{2|1}^{-1}(u_{2}|x_{1}),$$

$$x_{3} = F_{3|1,2}^{-1}(u_{3}|x_{1}, x_{2}),$$

$$\vdots$$

$$x_{n} = F_{n|1,\dots,d-1}^{-1}(u_{d}|x_{1},\dots, x_{d-1}).$$
(1.39)

Implementing this algorithm involves evaluation of the conditional distributions of the form  $F(x|\mathbf{x})$  where  $\mathbf{x}$  is a vector of random variables. Joe [70] has shown that

$$F(x|\mathbf{x}) = \frac{\partial C_{x,x_j|\mathbf{x}_{-j}(F(x|\mathbf{x}_{-j}),F(x_j|\mathbf{x}_{-j}))}}{\partial F(x_j|\mathbf{x}_{-j})},$$
(1.40)

where  $\mathbf{x}_{-j}$  refers to the vector  $\mathbf{x}$  without element j. In the bivariate case and for uniform random variables  $u_1$  and  $u_2$ , i.e.  $f(u_1) = f(u_2) = 1$ ,  $F(u_1) = u_1$ , and  $F(u_2) = u_2$ , this simplifies to

$$h(u_1, u_2; \Theta) = F(u_1 | u_2) = \frac{\partial C_{u_1, u_2}(u_1, u_2, \Theta)}{\partial u_2}.$$
(1.41)

Here, the second parameter  $u_2$  always refers to the conditioning variable and  $\Theta$  is the set of parameters for the copula  $C_{u_1,u_2}$  [71]. The inverse of this function  $h^{-1}(u_1, u_2; \Theta)$  with respect to  $u_1$  is also required.

For a realization  $U_1, \ldots, U_d$  of the vine copula, the samples of the copula distribution are obtained through the quantile functions of the marginals as

$$X_1 = F_1^{-1}(U_1), \dots, X_d = F_d^{-1}(U_d).$$
(1.42)

For a complete discussion on sampling copulas and the definitions of the h and  $h^{-1}$  functions of several bivariate copulas, see [65].

#### 1.6 Resilience

This section provides a quick introduction to the concept of resilience and briefly presents the resilience decision-making methodology of Salomon et al. [72] which is extended and merged with the survival signature in Chapter 6.

Resilience, from the Latin "resilire" meaning "to bounce back" is a concept in which not only the robustness and reliability of a system is analysed but its ability to recover is also taken into account. A failure in a system results in an abrupt loss in system performance followed by a gradual recovery of the system through implemented measures [73]. The loss of performance after a disruptive event at time  $t_0$  and the time it takes to recover, reaching normal levels at  $t_1$ can be visualized in the *resilience triangle* as introduced by Bruneau et al. [73], see Figure 1.12.



Figure 1.12: Resilience triangle. Adapted from [73].

#### 1.6.1 Resilience metrics

The application of resilience relies on the availability of comprehensive quantitative resilience metrics to measure it. For a discussion of several available metrics refer to [74, 75].

#### 1 Introduction

In this dissertation the resilience metric by Ouyang et al. [76] is applied. It is a measure based on the ratio of the time-dependent system performance Q(t) and target system performance  $\mathcal{T}Q(t)$  integrated over the same time domain [0, T]. The metric is defined as the expected value R = E[Y], where

$$Y = \frac{\int_{0}^{T} Q(t)dt}{\int_{0}^{T} \mathcal{T}Q(t)dt}.$$
 (1.43)

A value of R = 1 indicates a system operating at target performance over the whole time period while for R = 0 the system is not working at all. The system performance Q(t) is a stochastic process. Although the target performance  $\mathcal{T}Q(t)$  can also be treated as a stochastic process, for convenience, it is assumed to be a non-random constant number in this work.

#### 1.6.2 Adapted systemic risk measure

In Salomon et al. [72] the resilience metric is combined with an adapted systemic risk measure for complex systems. The original risk measure proposed by Feinstein et al. [77] is based on an input-output model and an acceptance criterion that represents safety standards and regulations. If  $(\Omega, \mathcal{F}, P)$  is a probability space,  $l \in \mathcal{N}$  is the number of entities in the system, and  $k \in \mathbb{R}^l$  is a vector of controls. The random variable  $Y_k(\omega)$  is the outcome of the system for each  $\omega \in \Omega$  and control vector k. The controls k also called "endowments" are capital allocations to the entities in the system whose goal is to improve functionality. The input-output model  $Y = (Y_k)_{k \in \mathbb{R}^l}$  is a non-decreasing random field in a vector space  $\mathcal{X}$ . For all  $k_i \leq m_i$  and  $i \in \{1, \ldots, l\}$  monotonicity requires that  $Y_k \leq Y_m$ . This means, that allocating more resources will always improve the system. The set  $\mathcal{A} \subseteq \mathcal{X}$  describes the acceptance criterion where the requirements of decision-makers are met.

Finally, the systemic risk measure is assembled from the input-output model and the acceptance criterion as the set of endowments resulting in model outputs satisfying the acceptance criterion as

$$R(Y;k) = \left\{ m \in \mathbb{R}^l | Y_{k+m} \in \mathcal{A} \right\}.$$
(1.44)

This systemic risk measure is now applied and adapted to systems with multiple component types and several endowment properties. Consider a system of l components divided into b different types each with n performance-enhancing properties. Any component  $a_i$  for  $i \in \{1, \ldots, l\}$ with properties  $(\eta_{i1}, \eta_{i2}, \ldots, \eta_{in})$  and component type  $z_i \in \{1, 2, \ldots, b\}$  can be described by the row vector

$$(a_i; z_i) = (\eta_{i1}, \eta_{i2}, \dots, \eta_{in}; z_i) \in \mathbb{R}^{1 \times n} \times \mathbb{N}.$$
(1.45)

Based on this vector notation, the system can be described by a matrix  $A \in \mathbb{R}^{l \times n}$  and column

vector  $z \in \mathbb{N}^l$  containing the component types as

$$(A;z) = \begin{pmatrix} \eta_{11} & \eta_{12} & \cdots & \eta_{1n}; & z_1 \\ \eta_{21} & \eta_{22} & \cdots & \eta_{2n}; & z_1 \\ \vdots & \vdots & & \vdots & \vdots \\ \eta_{l1} & \eta_{l2} & \cdots & \eta_{ln}; & z_1 \end{pmatrix}.$$
 (1.46)

Different realizations of A and z are fed into the input-output model as  $Y_{(A;z)}$ . Here it is assumed that the component types z are fixed and only the enhancing properties in A are varied. The corresponding risk measure is defined using the acceptance set

$$\mathcal{A} = \{ X \in \mathcal{X} | E[X] \le \alpha \}, \tag{1.47}$$

with  $\alpha \in [0,1]$  as

$$R(Y;K) = R(Y;(K;z)) = A \in \mathbb{R}^{l \times n} | Y_{(K+A;z)} \in \mathcal{A}.$$
(1.48)

As a result the resilience of the system described by (K + A; z) is greater or equal to  $\alpha$ . For simplicity, K = 0 is assumed and R(Y; 0) is written as R(Y). It may often be required to impose restrictions on A as well such as using the same property configurations for all components of the same type.

#### 1.6.3 Grid search algorithm

A grid search algorithm [77] is used to calculate the set-valued systemic risk measure. To do so, the endowments that are under investigation are divided into a uniform grid. The search starts at the origin of this box which is assumed to be outside R(Y), i.e. is not an acceptable configuration. From there, the acceptance criterion is evaluated for increasing grid points on the line identified by the direction (1, 1, ..., 1) until the first endowment configuration satisfying the acceptance criterion is found. The system will typically be analysed through stochastic simulation methods such as Monte Carlo simulation. Every time an acceptable point is found during the grid search all points with better endowment configurations can also be accepted. At the same time, all endowments below the first accepted points can be rejected. This results directly from the monotonicity condition.

Starting from the first accepted point a sub-box is defined using the points diagonally below (rejected) and above (accepted) of the accepted point. The other corners of this sub-box are then checked for acceptance. Based on the results, new sub-boxes will be defined from one accepted and one rejected point and subsequently evaluated. The algorithm terminates once all points have either been accepted or rejected defining a discrete grid-approximation of R(Y). For illustrative purposes, Figure 1.13 shows what the results for an arbitrary system with two endowment properties  $\eta_1 \in \{1, 2, ..., 8\}$  and  $\eta_2 \in \{1, 2, ..., 8\}$  might look like.



Figure 1.13: Results of the grid search algorithm for an arbitrary system with two endowment properties.

#### 1.6.4 Resilience decision-making

A crucial part of the decision-making process is taking into account monetary restrictions. An increase in endowment properties can mean an exponential increase in the associated cost [78]. This can for example mean using higher quality materials or hiring extra maintenance personal. An increase in the reliability of components in a complex network can be associated with exponentially increasing costs.

For decision-making, a quantity of interest are the cheapest yet acceptable combinations of endowments. To evaluate the cost one must provide a cost function which takes the endowment configuration as arguments and returns the sum of all associated costs. The cheapest acceptable configurations will always be located right on the border of accepted endowment configurations seen in Figure 1.13.

#### 1.7 Software for Uncertainty Quantification

With the increasing complexity of modern engineering structures and systems comes the need for efficient software to ensure their reliability and safety. For this, adequate propagation of uncertainties is of paramount importance. New advancements in simulation methods and analyses for uncertainty propagation are constantly made. Academia as well as industry can
benefit greatly from freely available and generalized frameworks that provide methods to analyse arbitrary systems.

Over the years, many such toolboxes have been developed for a large array of programming languages. Some examples follow in now particular order. *Dakota* [79] is a state-of-the-art software for optimization and uncertainty quantification developed at the Sandia National Laboratories. *OpenTURNS* [80] is an industrial software for uncertainty quantification in simulation developed jointly by EDF R&D, Airbus Group, Phimeca Engineering and IMACS. The Cossan Working Group develops *OpenCossan* [81], a general purpose software to quantify, mitigate and manage uncertainty for risk, reliability and resilient analyses. *UQLab* a general purpose uncertainty quantification framework is developed at ETH Zürich [82], and *UQpy* [83] a general purpose toolbox for modelling uncertainty in physical and mathematical systems is developed by the Shields Uncertainty Research Group at John Hopkins University.

A new framework called *UncertaintyQuantification.jl* is presented in this dissertation. An overview of the different frameworks with programming languages used, licences and latest release is presented in Tab. 1.3.

Table 1.3: List of some available software libraries for uncertainty quantification.					
Name	Language	Licence	Latest $Release^2$		
Dakota	C++	LGPL	6.1.8(18.06.2023)		
OpenCossan	MATLAB	$\operatorname{GPL}$	April 2020 (22.04.2020)		
OpenTurns	C++/ Python	LGPL	$1.21\ (20.06.2023)$		
UQlab	MATLAB	BSD-3	v2.0 (01.02.2022)		
UQpy	Python	MIT	$v4.1.2 \ (04.08.2023)$		
Uncertainty Quantification. jl	Julia	MIT	$0.7.2\ (05.09.2023)$		

 Table 1.3: List of some available software libraries for uncertainty quantification.

<sup>2</sup> As of 06.09.2023

The new framework UncertaintyQuantification.jl [84] is developed as a modern "spiritual successor" to OpenCossan [81] based on the experience gained during the development of the former toolbox. The base of this toolbox was built by the group of Prof. Schuëller at the Institute for Engineering Mechanics of the University of Innsbruck originally only designed to perform stochastic structural analysis and written in Fortran as COSSAN (COmputation Stochastic Structural ANalysis) [85]. The software was completely rewritten in MATLAB and generalized to include a much larger set of algorithms as OpenCOSSAN at the Institute for Risk and Uncertainty at University of Liverpool [81] first released in 2011. The Institute for Risk and Reliability of the Leibniz University Hannover, Germany joined the development in 2015 followed by the Shanghai Institute of Disaster Prevention and Relief, Tongji University, China in 2017. In 2019 the host organization switched from the University of Liverpool to Strathclyde University.

With a long-standing history such as this, it is only expected that a software has accrued a large amount of technical debt. For this reason and issues with MATLAB being an expensive commercial programming language instead the decision was made to build an entirely new framework as an upgrade and replacement using the modern Julia [86] programming language.

Julia is a new language, having been published in version 1.0 in 2018. It is a modern dynamic programming language that is incredibly fast while remaining simple to use due to careful language design. Although the programmer has access to a sophisticated type system, the user is never forced to declare types, and type annotations are not required for performance. Julia is designed for high-performance computing, and the numerical demand of algorithms can often be distributed on existing computing clusters with only a few lines of code.

At the heart of Julia lies its *multiple dispatch* system. In multiple dispatch implemented functions are selected based on the argument types. Types are annotated in the function definitions using the :: syntax. As an example, consider a function designed to square its input. For a scalar number this can be written as

square(x::Number) = x<sup>2</sup>

This function can now be called as, for example, square(4) and it will correctly return  $4^2 = 16$ . However, if instead of a scalar number one would pass a vector to the function Julia would throw an error as no square function is defined for vector arguments. To define a function that squares the elements of a vector element-wise write

square(x::Vector) = x.^2

Now, executing square([1,2,3,4]) would return [1,4,9,16] as expected. Julia is able to select the appropriate function for the argument through the multiple dispatch system. In the case of *UncertaintyQuantification.jl* multiple dispatch makes it possible to, for example, define sampling functions for various standard and quasi Monte Carlo simulation techniques. By passing the appropriate inputs to high-level algorithms these can be passed down to where the sampling is actually performed and Julia will at runtime select the appropriate sampling algorithm. As a result, complex algorithms can be defined for different types of input arguments with minimal code duplication.

# 1.8 Aims and objectives

The main objective of this dissertation is to improve upon the survival signature methodology in order to enable modelling of complex dependent behaviours and allow for the analysis of larger systems than previously possible. Based on the separation of system structure from probabilistic information, a key feature of the survival signature shown in Eq. 1.17, the proposed methods focus on different parts of the survival function.

#### 1 Introduction

On the probabilistic side, the focus lies on new methods for the modelling of complex dependent failure behaviours. Events such as the 2003 blackout in Italy [42] have highlighted the need for inclusion of interdependencies between networks in the analysis which can lead to catastrophic failures if disregarded. Additionally, competing failure modes such as common causes of failure or cascading failures must be included. While applications of the survival signature often assume full independence of component failures some studies have, for example, developed techniques based on Monte Carlo simulation to model common cause failures and cascading failures [32]. The goal in this thesis is to provide a generalized modelling framework for dependent failure based on copulas. Copulas have long been a proven method for complex dependency modelling in many fields such as finance [87, 88], insurance [89, 90] or enterprise risk management [91] and are becoming increasingly popular for engineering applications [92]. Multivariate copulas posses great modelling flexibility through separation of the dependency structure from the marginal distributions. Various bivariate copula families exist, providing different dependency structures for the modelling of entirely different causes of dependent failures. Through pair copula construction these bivariate copulas can be assembled to a single dependency structure for the whole system. Which in turn allows for efficient reliability analysis.

In regard to the structural part of the survival function, i.e. the survival signature, the methods presented in this thesis are focused on approximation techniques for large systems. Computation of the survival signature through Eq. 1.16 involves evaluation of every possible system state for each survival signature entry. With increasing size and complexity of the networks under analysis this analytical computation becomes impossible. Various studies trying to work around this issue have been published. Reed [38] and Reed et al. [39] proposed algorithms based on binary decision diagrams for exact computation of the survival signature. Another approach uses reliability block diagrams and the extended universal generating function [40]. However, these methods are both limited by memory requirements and unsuitable for large systems. This dissertation presents two alternatives to the exact computation of the survival signature to significantly reduce the required numerical effort. The first method applies percolation theory to exclude negligible parts of the survival signature and then uses Monte Carlo simulation to approximate the remaining entries based on a subset of all possible state vectors. The second technique builds a surrogate model of the survival signature instead. An interval predictor model is constructed from a few strategically selected data points which is then used to predict intervals for the remaining entries.

Branching out from the network reliability analysis to the study of resilience, an extension of a resilience decision-making technique [72] is presented where the application of survival signature allows for the efficient resilience analysis of complex substructured systems. The separation of the system structure from component failures presents an opportunity to simplify the analysis of modern systems where the components are also modelled as systems. The survival signature of these subsystems is computed ahead of the resilience analysis during which the component failure rates can be derived from the survival function. In addition to the developments concerning the survival signature, this dissertation also presents a new framework for uncertainty quantification. The goal of this framework is to provide a complete and generalized toolbox where newly developed methods in all fields of uncertainty quantification can be efficiently implemented and shared with the wider community. The new framework is developed as a package in the Julia programming language and is freely available to everyone.

# 1.9 Original contributions

This dissertation consists of four journal papers and two conference contributions. At the core of the original contributions are several enhancements to the survival signature ecosystem.

The first journal publication presents a new method for the reliability analysis of complex dependent networks [93]. Various competing failure modes are modelled through different parametric copula families. Pair copula construction is used to build high-dimensional copulas from combinations of bivariate copulas allowing for high modelling flexibility. Epistemic uncertainty is included in the component failure times through p-boxes and imprecise copulas. A new Monte Carlo simulation method is also developed to obtain the upper and lower bounds of the network reliability. The proposed method is applied to a numerical example based on the IEEE reliability test system.

An approximation method for the survival signature is presented in the second journal paper [94]. In a first step, percolation theory is used to identify areas of the survival signature where the probability of a functioning system is close to zero and therefore negligible. Next, the remaining part is approximated by Monte Carlo simulation. Evaluating only a subset of all possible state vectors significantly reduces the numerical demand an allows for the analysis of larger systems. The method is applied to several toy examples in order to quantify the errors resulting from the percolation and Monte Carlo simulation. The new method is than applied to a real world example based on the S- and U-Bahn metro system of Berlin. The approximation of the survival signature for this large network, where the analytical solution is impossible to obtain, highlights the significance of the presented technique.

A method expanding on the Monte Carlo approximation technique is presented next. The new method is established in the first conference paper [95] and then further refined in the third journal article [96]. Instead of approximating each survival signature entry not excluded by application of percolation theory, only a few selected data points are used to build a surrogate model. This metamodel is a NRBF network constructed with additional constraints which ensure monotonicity of the resulting survival signature. The surrogate model is then extended to an IPM to account for the uncertainty of the Monte Carlo approximation of the data points. This imprecise model yields upper and lower bounds on the survival signature and therefore the network reliability. The method is validated against a toy example and then again applied to the Berlin metro example. An extra component type is used in the journal article to increase the dimensionality of the survival signature. The presented method is able to accurately predict bounds on the survival signature and the reliability at a fraction of the computational demand of the full Monte Carlo simulation method and the analytical solution.

These four papers present the core contribution of this dissertation. In the next journal paper [97], the resilience decision-making method presented by Salomon et al. [72] is extended and merged with the survival signature to allow for efficient reliability analysis of large substructured systems. The survival signatures of the subsystems can be computed ahead of the resilience analysis. During the analysis, the component failures in the subsystem can then be efficiently propagated through the survival signature providing the failure rates of the top-level components through the derivative of the hazard functions. The method is applied to three numerical examples of increasing complexity. The largest example is again based on the Berlin metro system where the individual stations are now modelled as subsystems. Through the presented approach, the system is effectively reduced from 2776 components to the 306 top-level components is still included in the analysis through the survival signatures. As a co-author, the author's contributions to this article focused mostly on conception, providing expertise on the survival signature, assisting with the extension of the grid search to multidimensional spaces, and implementing the proposed approach in software.

The second conference paper [98] and final contribution of this dissertation presents a new framework for uncertainty quantification called *UncertaintyQuantification.jl* [84]. The paper outlines the basic functionality of the framework and shows its application to a few numerical examples. In its current state the implemented algorithms include methods for reliability analysis using various simulation schemes, sensitivity analysis and metamodelling.

Two additional Julia packages have been developed as part of this dissertation. The survival signature approximation methods are implemented in the *SurvivalSignature.jl* [99] package while the resilience decision-making is provided in the *ResilienceDecisionMaking.jl* [100] package. All three modules are officially registered in the Julia *General* registry and publicly available for everyone on GitHub under the MIT licence.

#### 1.10 Structure of the thesis

The remainder of the dissertation is structured as follows. Chapter 2 presents the method for the reliability analysis of complex interdependent networks where the dependencies are modelled through copulas. Because this approach is built on the survival signature, its inherent separation of network topology from component failures allows for efficient consideration of different dependent failure scenarios once without reevaluation of the system structure.

Instead of focusing on the probabilistic modelling of the component failures, Chapter 3 is focused on approximation of the survival signature for large systems. Monte Carlo simulation and percolation theory are applied to estimate the signature for systems where analytical computation is impossible because of the prohibitive numerical demand.

Chapters 4 and 5 improve on the earlier method. Where previously all entries of the survival signature not excluded by percolation had to be approximated now only a few values are strategically selected and used to efficiently build a surrogate model of the survival signature, further reducing the numerical effort required.

In addition to the core developments of this thesis, Chapter 6 presents the extension of a resilience decision-making method. The existing method is merged with the survival signature to allow for efficient multidimensional resilience analysis of substructured systems.

A new framework for uncertainty quantification written in the Julia programming language is presented in Chapter 7.

Chapter 8 ends the thesis with some concluding remarks and outlook into possible areas for future research based on the presented methods.

# 2 Reliability Analysis of Networks Interconnected With Copulas

# **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.

Keywords: Survival signature, interdependencies, vine copulas, imprecise probabilities, Monte Carlo simulation.

## 2.1 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 [101]. 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 [42, 102]. 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 [103]. Therefore, it is of paramount importance to include and accurately model these interdependencies when analysing the reliability of networks.

Behrensdorf et al. [104] presented a novel approach to the numerical reliability analysis of interdependent networks based on Monte Carlo simulation and survival signature. The survival signature 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 [27]. 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 [37]). 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, finance, insurance, and environmental studies [62, 87, 105, 106]. Modelling dependencies with copulas is especially powerful as multivariate copulas allow to separate modelling of the marginal distributions from modelling the dependence structure [61]. Though the popularity of copulas for engineering applications has increased in the recent years [92, 107], 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 [108]. 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 a discussion of copula construction methods. Then, the approach to modelling dependencies is presented. Next, the numerical method used to compute the network reliability is introduced. After discussion methods to handle uncertainties in the analysis, the proposed method is applied to a complex numerical example. Finally, the paper closes with some concluding remarks and an outlook into future works.

#### 2.2 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

# 2 Reliability Analysis of Networks Interconnected With Copulas

copulas, see for example [60] or [61].

Copulas (from the Latin for 'bond' or 'tie') are functions that couple multivariate distribution functions to their one-dimensional marginal distributions functions and as such allow to separate modelling of the dependence structure from modelling the univariate marginals [60]. The foundation of the theory of copulas lies in what is known as Sklar's theorem [59]. 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 2.2.1** (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  $\mathbb{R}^d$ 

$$H(\mathbf{x}) = C(F_1(x_1), \dots, F_d(x_d)).$$
(2.1)

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 a d-copula and  $F_1, \ldots, F_d$  are distribution functions, then the function H defined by Eq. 2.1 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 2.2.2 [60].

**Theorem 2.2.2.** For  $d \ge 2$  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 [62]. There exist multiple copula families with different dependence structures of which some of the most popular are presented in the following.

#### 2.2.1 The Gaussian Copula

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

$$C_R(u_1, \dots, u_d) = \Phi_d(\Phi^{-1}(u_1), \dots, \Phi^{-1}(u_d)), \qquad (2.2)$$

where  $\Phi_d(\cdot; \mathbf{R})$  is the *d*-variate cumulative distribution of a  $\mathbb{N}_d(0, \mathbf{R})$  random vector and  $\Phi^{-1}$  denotes the inverse of the univariate standard Gaussian cumulative distribution function [61].

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

Table 2.1: Most popular Archimedean copulas with generators, generator inverses, and parameter domains.

#### 2.2.2 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 [60]. Additionally, the bivariate Archimedean copulas can be used in multivariate construction methods based on pairs of bivariate copulas [61]. A *d*-dimensional copula  $C_{\varphi}$  is classified as *Archimedean* if it admits to the representation

$$C_{\varphi}(u_1, \dots, u_d) := \varphi(\varphi^{-1}(u_1) + \dots + \varphi^{-1}(u_d)),$$
(2.3)

where the function  $\varphi : [0, \infty] \to [0, 1]$  is called the *generator* of  $C_{\varphi}$ ,  $\varphi^{-1}$  denotes its inverse and  $u_1, \ldots, u_d \in [0, 1]$  [65]. Table 2.1 shows some of the most popular one-parameter (governing the strength of dependence) Archimedean copula families with their generators, inverses and parameter domains.

#### 2.2.3 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*  $\rho$  it is not 'scale-invariant' and as such does not remain unchanged under strictly increasing transformation [62]. 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

$$t = \frac{c-d}{c+d} = (c-d) \middle/ \binom{n}{2}.$$
(2.4)

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

$$\tau(X,Y) = P\left[(X-\widetilde{X})(Y-\widetilde{Y}) > 0\right] - P\left[(X-\widetilde{X})(Y-\widetilde{Y}) < 0\right],$$
(2.5)

where  $(\tilde{X}, \tilde{Y})$  is an independent pair with the same distributions as (X, Y) [62]. Figure 2.1 shows four example scatter plots of samples generated from different bivariate copulas with the respective parameters chosen such that Kendall's tau equals 0.5, highlighting the individual dependence structure.



Figure 2.1: Samples drawn from different bivariate copulas where the parameters have been chosen so that Kendall's tau equals 0.5.



Figure 2.2: Structure of a 6-dimensional hierarchical Archimedean copula

# 2.3 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 [61].

#### 2.3.1 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 2.2 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

$$C_{\varphi_0}(C_{\varphi_1}(u_{1,1},\ldots,u_{1,d_1}),\ldots,C_{\varphi_J}(u_{J,1},\ldots,u_{J,d_J}))$$
(2.6)

where further nesting levels are defined recursively [65]. However, not all arbitrary combinations of J + 1 generators lead to Eq. 2.6 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 [61]. This reduces the modelling flexibility substantially. An implementation of hierarchical Archimedean copulas can be found in the package nacopula for the statistical programming language  $\mathbf{R}$  [109].

#### 2.3.2 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 [65].

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:

$$f_{1:d}(x_1,\ldots,x_d) = f_1(x_1) \cdot f_{2|1}(x_2|x_1) \cdot f_{3|2,1}(x_3|x_2,x_1) \cdot \cdots \cdot f_{d|1:(d-1)}(x_d|x_1,\ldots,x_{d-1}) \quad (2.7)$$

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. 2.1 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

$$f_{1:d}(x_1, \dots, x_d) = c_{1:d}(F_1(x_1), \dots, F_d(x_d)) \cdot f_1(x_1) \cdot \dots \cdot f_d(x_d),$$
(2.8)

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

$$f_{1,2}(x_1, x_2) = c_{1,2}(F_1(x_1), F_2(x_2)) \cdot f_1(x_1) \cdot f_2(x_2),$$
(2.9)

which yields

$$f_{1|2}(x_1|x_2) = c_{1,2}(F_1(x_1), F_2(x_2)) \cdot f_1(x_1).$$
(2.10)

Equation 2.10 can be applied stepwise to Eq. 2.7 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.

# 2.3.3 Vine Copulas

Vines are a graphical representation of valid pair copula decompositions as sets of trees. Basic graph theory is used to define vines [65]. 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  $N_1 = \{1, \ldots, d\}$  and edges  $E_1$ .
- (2) For  $j \ge 2$ ,  $T_j$  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  $T_j$ ,  $j \ge 2$  connecting a and b, in turn a and b must share a common node in  $T_{j-1}$ . Figure 2.3 shows a regular



Figure 2.3: Graphical illustration of a four-dimensional copula as a regular vine.

vine representation of a 5-dimensional copula. There exist a multitude of d-dimensional Rvines. 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 2.4 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 [65]. 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 [110].

# 2.4 Modelling Dependencies

Recalling from the introduction, the goal of this paper is to model complex dependencies between components of one system as well as interdependencies between components of different systems using copulas. For that reason, the previous section introduced some of the most popular copula families and different methods of constructing high dimensional copulas. This section deals with selecting appropriate copula families for different kinds of failures and investigating the usefulness of the copula construction methods in regards to the reliability analysis of complex networks.



Figure 2.4: C-Vine (left) and D-Vine (right) in five dimensions.

Ideally, the dependency structures and therefore the copulas should be inferred from the measured component failure times of the dependent networks. However, as this data is rarely available for complex systems and the aim of this work is to prove the suitability of copulas in this framework, this is left for future work. Instead, a qualitative approach to the modelling of different kinds of failures is chosen. Examples of how to model two distinct classes of failures are given in the subsequent sections. These qualitative estimates could potentially serve as a basis for deducing the copula structure by Bayesian inference.

# 2.4.1 Common Cause of Failure

Common cause of failure is the event that two or more components fail simultaneously due to shared defects [111]. These weaknesses can include but are not limited to [112]:

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

This work concentrates on the first weakness, manufacturing defects, especially those manifesting in early component life. The Clayton copula can be used to describe dependence between marginals where there is strong *lower tail* dependence. Lower (or upper) tail dependence is



Figure 2.5: Reliability of a parallel system subject to common cause of failure.

concept expressing higher dependence in the lower-left (upper-right) quadrant of  $[0,1]^2$ . This property of the Clayton copula is clearly evident from Fig. 2.1b where the samples in the lower-left quadrant are grouped closer together.

Consider a very simple system of two parallel components. The component failure times are assumed to be exponentially distributed with  $\lambda = 1.5$  and are sampled from a bivariate Clayton copula with  $\theta$  chosen such that Kendall's tau equals 0.3. Figure 2.5 shows a plot of the resulting reliability against the reliability in the independent case. The plot clearly shows how the lower tail dependence translates to the reliability of the system. Initially, the reliability is significantly reduced compared to the independent case. At later points in time, as the dependence weakens, this difference decreases. Contrarily, a copula exhibiting strong upper tail dependence might be used to model common cause failures at high component age.

#### 2.4.2 Interdependencies

The treatment of interdependencies is not as simple as for common cause of failures. 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. 2.11

$$U_1 = (1 - \tau) \cdot F_1^{-1}(u_1) + \tau \cdot F_2^{-1}(u_1)$$
(2.11)

#### 2.4.3 Construction of the dependence structure

After selecting appropriate copula families to model the desired failure modes, the overall dependence structure for the network has to be selected. Three approaches exist based on the methods introduced in the previous section. The most straightforward approach is the application of multiple independent copulas to define dependence among groups of components. However, this does not allow for components to be connected to multiple other components by different copula families as one random variable can not be part of two independent copulas and as such is only suitable for simple scenarios. The two more advanced techniques for constructing high dimensional copulas presented are hierarchical Archimedean copulas and vine copulas. While HAC's offer more flexibility in terms of modelling the dependencies, they are still far more restrictive than vine copulas. This is largely due to their nested structure as compared to the graph based nature of vine copulas. Additionally, building a graph based dependence structure has obvious synergies with the reliability analysis of networks. For this reason, vine copulas are selected to build the overall dependence structure.

# 2.5 Reliability Analysis

This section recaps the numerical methodology used to compute the network reliability first introduced in [104]. It is based on the survival signature, an extension of the system signature, and Monte Carlo simulation.

#### 2.5.1 Survival Signature

The survival signature is a novel tool for the quantification of system and network reliability based on the system signature [27, 28]. 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.



Figure 2.6: Network with six components equally divided into two 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

$$\Phi(l) = \binom{m}{l}^{-1} \sum_{\underline{x} \in S_l} \varphi(\underline{x})$$
(2.12)

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, ..., K) and  $l_k$  out of  $m_k$ components per type in a working state, the survival signature becomes

$$\Phi(l_1, \dots, l_K) = \left[\prod_{k=1}^K \binom{m_k}{l_k}^{-1}\right] \times \sum_{\underline{x} \in S_{l_1,\dots,l_K}} \varphi(\underline{x})$$
(2.13)

As an example, consider a system with two component types and three components per type as illustrated in Fig. 2.6. 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 2.2.

While algorithms to calculate the survival signature have already been available for a number of years [38, 113], 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 [114].

	$l_1$	$l_2$	$\Phi(l_1, l_2)$	$ l_1 $	$l_2$	$\Phi(l_1, l_2)$
-	0	0	0	2	0	0
	0	1	0	2	1	0
	0	2	0	2	2	4/9
	0	3	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 2.2: Survival signature of the network shown in Fig. 2.6.

#### 2.5.2 Survival Function

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

$$P(T_s > t) = \sum_{l_1=0}^{m_1} \dots \sum_{l_k=0}^{m_k} \Phi(l_1, \dots, l_K) P\left(\bigcap_{k=1}^K \{C_t^k = l_k\}\right)$$
(2.14)

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.

#### 2.5.3 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  $l_1, \ldots, l_K$  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  $N_{l_1,\ldots,l_K}(t)$ . Then, the probabilistic part of the survival function is approximated by

$$P\bigg(\bigcap_{k=1}^{K} \{C_t^k = l_k\}\bigg) = \frac{N_{l_1,\dots,l_K}(t)}{N_{mc}}$$
(2.15)

In a final step, the partial reliabilities for all combinations are multiplied by their probability  $\Phi(l_1, \ldots, l_K)$ , 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. A pseudo-algorithm illustrating how to obtain the survival function of the system based on the survival signature and the failure times sampled from the vine copula is given in Algorithm 1. The analytically and numerically computed survival functions for the network shown in Fig. 2.6 assuming independent exponential failure distributions for the components with  $\lambda_1 = 0.8$  and  $\lambda_2 = 1.6$  are presented in Fig. 2.7.

Pseudocode 1 Monte Carlo simulation for network reliability

Input:  $\Phi$ survival signature  $t_{fail}$  component failure times sampled from the vine copula  $v_{time}$  vector of time steps  $N_{mc}$  number of Monte Carlo samples **Output:** Ρ Reliability of the network function NETWORKRELIABILITY  $(\Phi, t_{fail}, v_{time}, N_{mc})$  $\triangleright$  Loop over all combinations of the survival for each  $l_1, \ldots, l_K$  in  $S_{l_1, \ldots, l_K}$  do: signature if  $\Phi(l_1, ..., l_K) > 0$  then: for each t in  $v_{time}$  do:  $\triangleright$  Find components working at time t $N_{working} \leftarrow sum(t_{fail} > t)$  $N_{l_1,\ldots,l_K} \leftarrow sum(N_{working} = l_1,\ldots,l_K)$   $\triangleright$  Count matching combinations  $P_{partial}(l_1,\ldots,l_K) \leftarrow N_{l_1,\ldots,l_K}/N_{mc} \cdot \Phi(l_1,\ldots,l_K)$ end for end if end for  $P \leftarrow sum(P_{partial})$  $\triangleright$  Sum partial reliabilites yielding the full system reliability end function

## 2.5.4 Imprecise Reliability Analysis

Two types of uncertainties must be considered 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 is naturally 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 included in the analysis. However, the selection appropriate failure time distributions is typically based on either data or expert knowledge, neither of which yields perfect results. In turn, this introduces epistemic



Figure 2.7: Survival function for the network in Fig. 2.6.

uncertainty into the model. These epistemic uncertainties can be tackled by using imprecise probability methods where instead of a single model, a set of plausible models is applied. As a result, the uncertainty propagates through the models and is ultimately reflected in the probability of failure, i.e. the reliability of the network.

Consider two non-decreasing functions  $\underline{F}$  and  $\overline{F}$  mapping the real line  $\mathbb{R}$  into [0,1], with  $\underline{F}(x) \leq \overline{F}(x)$  for all  $x \in \mathbb{R}$ . Let  $[\overline{F}(x), \underline{F}(x)]$  denote the set of non-decreasing functions mapping  $\mathbb{R}$  into [0,1] such that  $\underline{F}(x) \leq F(x) \leq \overline{F}(x)$ . When  $\overline{F}$  and  $\underline{F}$  circumscribe an imprecisely known probability distribution,  $[\overline{F}, \underline{F}]$  is called the *probability box* or *p-box* of said probability distribution. As a result, if  $[\overline{F}, \underline{F}]$  is a p-box for a random variable X whose distribution is known to be within the p-box, then  $\overline{F}(x)$  and  $\underline{F}(x)$  are the upper and lower bounds on F(x), respectively [57]. An example of an exponential p-box with parameters  $\lambda \in [1.2, 2.2]$  is shown in Fig. 2.8. In this case, only two CDFs need to be computed to fully define the p-box. However, for most families of distributions, four or more CDFs must be evaluated [57].

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, the result is an upper and a lower bound [58]. Figure 2.9a 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 shown in Fig. 2.8 for the failure time distributions.

Similarly to a p-box, instead of considering just one precise copula, a set of copulas can be considered to account for uncertainty in the dependencies. Pelessoni et al. [115] generalized p-boxes to the bivariate case. If  $\underline{C}$  and  $\overline{C}$  are two copulas such that  $\underline{C} \leq \overline{C}$ , then  $[\underline{C}, \overline{C}]$  forms an *imprecise copula*. Let  $[\underline{F}_X, \overline{F}_X]$  and  $[\underline{F}_Y, \overline{F}_Y]$  be two univariate p-boxes for the random



Figure 2.8: Example of an exponential p-box with  $\lambda \in [1.2, 2.2]$ .

variables X and Y respectively, then  $[\underline{F}, \overline{F}]$  defined by

$$\underline{F}(x,y) = \underline{C}(\underline{F}_X(x), \underline{F}_Y(y)) \tag{2.16}$$

and

$$\overline{F}(x,y) = \overline{C}(\overline{F}_X(x), \overline{F}_Y(y))$$
(2.17)

is a bivariate p-box [116]. As with the p-box, defining an imprecise copula from an interval on it's parameters imposes bounds on the system reliability. 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. 2.9b.

# 2.6 Numerical Example

The network structures for the following numerical example are taken from the IEEE Reliability Test System (RTS) [117]. The system is effectively split into two sub-systems (see Fig. 2.10 and Fig. 2.11) by removing 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 [114]. Next, the vine copula that is used for sampling the individual component failure times is assembled from bivariate copulas. A common cause



Figure 2.9: 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.



Figure 2.10: Structure of the first network taken from the IEEE  $\operatorname{RTS}$ 



Figure 2.11: Structure of the second network taken from the IEEE RTS  $\,$ 

Parameter	Definition	Parameter range
$\lambda_1$	Failure rate of component type 1	$\lambda_1 \in [0.8, 1.2]$
$\lambda_2$	Failure rate of component type 2	$\lambda_2 \in [1.4, 1.5]$
$\lambda_3$	Failure rate of component type 3	$\lambda_3 \in [1.6, 1.9]$
$\lambda_4$	Failure rate of component type 4	$\lambda_4 \in [2.0, 2.3]$
$\lambda_5$	Failure rate of component type 5	$\lambda_5 \in [1.8, 2.2]$
$ au_1$	Clayton copula parameters on component type 2	$\tau_1 \in [0.1, 0.3]$
$ au_2$	Clayton copula parameters on component type 3	$\tau_2 \in [0.2, 0.4]$
$ au_3$	Clayton copula parameters on component type 4	$\tau_3 \in [0.1, 0.3]$
$ au_4$	Gaussian copula parameters between network 1 and 2 $$	$\tau_4 \in [0.4, 0.8]$

 Table 2.3: Failure rate ranges of the exponential marginal distributions and copula parameters used in the numerical example.



Figure 2.12: Bounds on the reliability of network 1.

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. 2.3.

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.2.12. For comparison, the plot also contains a deterministic reliability analysis (all mean values) of network 1.

# 2.7 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 scenario based on the network topology of the IEEE Reliability Test System. The application of vine copulas 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.

In order to facilitate a transparent illustration of the approach, we have chosen a relatively small system which still carries the key features of a realistic system. The expansion to a large complex system would require a number of additional numerical challenges to be solved. This is beyond the scope of this paper and therefore left for future work. The challenges include deriving the vine copula model from data. Gruber and Czado [118] presented a promising method for Bayesian model selection and inference of vine copulas. The technique is the first to be able to jointly select the vine tree structure and the copula families. Additionally, the modelling aspects of other competing failure events such as external threats (e.g. earthquakes, tsunamis, terrorist attacks) must be closely investigated.

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# Numerically Efficient Computation of the Survival Signature for the Reliability Analysis of Large Networks

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# Abstract

Societal growth thrives on the performance of critical infrastructure systems such as water supply systems, transportation networks or electrical distribution systems. This makes the reliability analysis of these systems a core focus for researchers today. The survival signature is a novel tool for analysing complex networks efficiently and outperforms traditional techniques in several key factors. Its most unique feature being a full separation of the system structure from probabilistic information. This in turn allows for the consideration of diverse component failure descriptions such as dependencies, common causes of failure and imprecise probabilities. However, the numerical effort to compute the survival signature increases with network size and prevents analysis of complex systems. This work presents a new method to approximate the survival signature, where system configurations of low interest are first excluded using percolation theory, while the remaining parts of the signature are approximated by Monte Carlo simulation. The approach is able to accurately approximate the survival signature with very small error at a massive reduction in computational demands. The accuracy and performance are highlighted using several simple test systems as well as two real world problems. **Keywords:** Survival signature, Monte Carlo simulation, percolation, reliability analysis

#### 3.1 Introduction

Critical infrastructure systems such as electrical, gas and water distribution systems, traffic networks and communication networks are cornerstones of modern societies. Our dependence on these systems comes with a demand for accurate reliability analyses to ensure their functionality. However, with increasing size and complexity, the analysis and assessment of reliability of these systems comes with an increase of computational effort. Extensive research on algorithms for the reliability analysis of systems and networks is readily available [21]. Past research has highlighted the importance of considering effects such as dependencies, common causes of failure and imprecision [42, 119, 120] during the analysis. This is where traditional approaches, e.g. fault tree analysis or reliability block diagrams reach their limits. A recent development in system analysis aiming to alleviate these shortcomings is the survival signature [27].

The survival signature was developed as a generalization of the systems signature [121] to allow for multiple component types. Perhaps the greatest advantage of the survival signature to traditional approaches is the full separation of system structure from probabilistic information.

This is a clear advantage over more common tools for system reliability, where the structure of the system needs to be modified or extra failure events need to be modelled to allow for consideration of the aforementioned effects, as for example pointed out by Li et al. [122]. Recent research showed that repairable systems [36], mission-stage-behaviour [123] and the combination of subsystems [29] can easily be implemented into the survival signature ecosystem. Reliability analysis using the survival signature has been widely studied in recent years, including a variety of simulation algorithms [37], dependent failures [32], imprecision [58] and more.

Just like the traditional techniques, the survival signature suffers greatly from the curse of dimensionality. This means, that with increasing network size and number of component types the numerical demand increases as well with non-polynomial growth. At the number of components and types typical of real infrastructures the computational effort required to evaluate the survival signature becomes prohibitive. Several works aimed at working around this limitation have been published in recent years. Reed [38] presented an efficient method of calculating the survival signature based on transforming a fault tree representation of a system to a binary decision diagram. While this method performs very well in cases where the fault tree or binary decision diagram is already known, it becomes increasingly impractical with growing network size/complexity. Another recently developed approach is based on the extended universal generating function (UGF) [40]. However, deriving the UGF is a non-trivial task itself and restricts the application to systems defined as reliability block diagrams.

This paper presents a new approach to the approximation of the survival signature based on percolation theory and Monte Carlo simulation. First, percolation theory is used to find areas of the survival signature that can be safely excluded [124]. Then, the remaining entries are approximated using Monte Carlo simulation [114]. The method is able to efficiently compute the signatures of arbitrary systems and structure functions.

The remainder of the paper is structured as follows. Section 3.2 presents the theory on the survival signature while Section 3.3 introduces percolation theory. The developed simulation algorithm is discussed in Section 3.4 including the application to toy examples and quantification of errors. Section 3.5 applies the proposed approach to more complex real world examples, followed by some concluding remarks in Section 3.6.

# 3.2 Survival Signature

The current state of a system consisting of m components can conveniently be described by a state vector  $\underline{x} \in \{0, 1\}^m$ . An entry  $x_i = 1$  denotes a functional component i, while  $x_i = 0$ indicates a non-functional or failed component. The labeling must be consistent although its initial choice is arbitrary. The global state of the system is defined by a structure function  $\varphi : \{0, 1\}^m \to \{0, 1\}$ . The structure function is defined for every possible state  $\underline{x}$  of the system and evaluates whether the system is operational ( $\varphi(\underline{x}) = 1$ ) or not ( $\varphi(\underline{x}) = 0$ ).

It is safe to assume in most cases that the system analysed is coherent. A system is labeled

as such if the structure function  $\varphi$  is not decreasing if the amount of working components  $|\underline{x}|$  increases (and vice-versa), i.e., the repair of a component will not lead to a less functional system. A related, however not necessary assumption is that the system is always fully operational in the case of all components working ( $\varphi(\underline{1}) = 1$ ) and not operational if all components are broken ( $\varphi(\underline{0}) = 0$ ).

In case of systems consisting of multiple component types, let  $K \ge 2$  be the number of component types, and  $m_k$  the amount of components of one specific type k. It follows that  $\sum_{k=1}^{K} m_k = m$ . As the labeling of the components in the state vector is arbitrary, it can be written in groups ordered by component type:  $\underline{x} = (\underline{x}^1, \underline{x}^2, \dots, \underline{x}^K)$ . Each of these sub-vectors now indicate the states of all components of that specific type, for example  $\underline{x}^k = (x_1^k, x_2^k, \dots, x_{m_k}^k)$ .

For any such kind of system, the survival signature  $\Phi(l_1, l_2, \ldots, l_K)$  is now defined as follows: Given that exactly  $l_k$  out of  $m_k$  components of every type are working, the probability that the system is operational is  $\Phi$ . In other words,  $\Phi$  denotes the percentage of working system configurations when  $l_k$  out of  $m_k$  components are working, without taking into account the reasons (e.g., failure modes) behind the failure of these components. Additionally, it should be pointed out that components of the same type are indistinguishable, i.e., it is possible to know how many components of a specific type are working, but not in which part of the system. Thus, the survival signature is a k-dimensional array of size  $(m_1 + 1) \times (m_2 + 1) \times \cdots \times (m_k + 1)$ (including case  $l_k = 0$  that none of the components of a type are working) [27]. In the remainder of the paper,  $\underline{l}$  is used as a shorthand for  $l_1, l_2, \ldots, l_K$ .

From the coherency assumptions mentioned above, it trivially follows that

$$\Phi(\underline{l} = \underline{0}) = 0,$$
  

$$\Phi(\underline{l} = \underline{1}) = 1,$$
  

$$\Phi(\underline{l}^{a}) \le \Phi(\underline{l}^{b}) \text{ if } l_{k}^{a} \le l_{k}^{b}, \forall k \in (1, 2, \dots, K),$$
(3.1)

where  $\underline{0}$  and  $\underline{1}$  refer to system configurations with all components failed or working respectively. The vectors  $\underline{l}^a$  and  $\underline{l}^b$  represent two arbitrary entries of the survival signature.

The direct computation of one specific entry  $\Phi(\underline{l})$  of the survival signature is achieved by enumeration of all working states that satisfy the condition that  $l_k$  out of  $m_k$  components are functional for components k = 1, ..., K. The total amount of possible combinations are  $\binom{m_k}{l_k}$ for all k. The set of all these allowed combinations for all components is denoted by  $S_{l_1,...,l_K}$ . Thus the magnitude of this set is  $\prod_{k=1}^{K} \binom{m_k}{l_k}$ . The fraction of functional states over the amount of all possible states now yields the probability of the system being operational:

$$\Phi(\underline{l}) = \left[\prod_{k=1}^{K} \binom{m_k}{l_k}\right]^{-1} \times \sum_{\underline{x} \in S_{l_1,\dots,l_K}} \varphi(\underline{x}),$$
(3.2)

under the condition that the failure times of the individual components of one type are equally likely to occur. The complete survival signature for a simple system of two component types as shown in Fig. 3.1 is presented in Table 3.1.

The structural information of the system functionality is completely separated from the temporal behaviour of the individual components. The component failure times are included as the probability  $P(C_t^k)$  that a specific amount C of component type k is functional at a given point in time t:

$$P(T_s > t) = \sum_{l_1=0}^{m_1} \dots \sum_{l_K=0}^{m_K} \Phi(\underline{l}) P\left(\bigcap_{k=1}^K \{C_t^k = l_k\}\right),$$
(3.3)

providing the probability that the system failure time  $T_s$  is after the current point in time (the system's *survival function*). However, in the case that for any type k the failure times are independently and identically distributed (*iid*) with a known cumulative distribution function  $F_k(t)$ , the probabilistic part of the survival function can be simplified to

$$P\left(\bigcap_{k=1}^{K} \{C_{t}^{k} = l_{k}\}\right) = \prod_{k=1}^{K} P(C_{t}^{k} = l_{k}) = \cdots$$

$$\cdots = \prod_{k=1}^{K} \left(\binom{m_{k}}{l_{k}} F_{k}(t)^{m_{k}-l_{k}} [1 - F_{k}(t)]^{l_{k}}\right).$$
(3.4)

It is in this separation of structural and probabilistic information where the advantages of the survival signature compared to traditional approaches lie. Inclusion of complex effects such as imprecise probabilities or dependent componant failures have no influence on the structural evaluation of the system. Note, that the method presented in this paper is only applicable to the structural (signature) part of the survival function. Simulation techniques for the probabilistic part of the equation and consideration of imprecision and dependencies are already available [37, 93].

In this work, application of the survival signature is restricted to systems consisting of binary components, in accordance with its original definition [27]. Generalization of the survival signature to multi-state systems is still actively being researched [30, 125].



**Figure 3.1:** Example system with K = 2 component types and  $m_1 + m_2 = 3 + 3 = 6$  components. The component types are represented by different shapes.

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

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Table 3.1: Survival signature of the system in Fig. 3.1.

# 3.3 Percolation

If a system's structure function is given as a logical block diagram, it is referred to as a *reliability* block diagram (RBD). The individual components (or subsystems of several components) are represented by blocks connected through edges. Typically two completely reliable nodes are given on both ends of the diagram. The system is operational, if these two *source* (s) and *target* (t) nodes are connected.

Evaluation of the structure function is now equivalent to finding the *s*-*t*-connectivity of an undirected and unweighted graph as the edges of the RBD are exclusively logical connections without any distinction between edges. Additionally, the system can be decomposed into series-and parallel-subsystems to reduce network size.

In the context of survival signature computation the s-t-connectivity needs to be computed for all  $\underline{x} \in S_{l_1,\ldots,l_K}$  for all  $l_k = 0, 1, \ldots, m_k$  considering all K component types. This fact leads to high numerical costs even for medium-sized systems due to the increase in combinations of components to check.

The search of connections between two ends of complex networks or lattices (and the formation of clusters inside a network, which is a related concept) is one of the main aspects of *percolation theory*. Albeit usually introduced as a theory for multidimensional lattice networks [126], the results obtained in percolation theory can easily be applied to graphs and networks. Network robustness is one of the many applications of percolation to graph theory other than the classical use in material sciences. This provides an opportunity to improve the handling of vast state spaces during analysis of structure functions. Percolation theory has been successfully applied to network reliability problems in the past [127].

# 3.3.1 Percolation processes

A percolation process is defined as the random deletion of nodes from the network without any rewiring of the edges connected to the deleted nodes. The amount of deleted nodes can be determined as fraction of removed nodes, denoted by f.

In cases of small fractions f, i.e. where only a small number of nodes is removed from the network, this results in a high probability that a large, system-spanning structure connecting s and t (and all nodes if  $f \to 0$ ) exists. This structure is called a *giant connected cluster* or *giant connected component* [128]. For increasing values of f, more nodes are removed eventually leading to the collapse of the network. The point where the giant connected cluster vanishes is denoted by the critical fraction  $f_c$ .

The connection of two individual nodes has little value when analysing networks/graphs in general, as opposed to reliability block diagrams. Thus, the probability  $P_{\infty}(f)$  that a giant connected cluster exists [129] can be used to evaluate the overall state of the network instead.

One of the main outcomes of percolation theory for graphs is that the behavior of a network depends mainly on three different exponents and the critical value  $f_c$  [130]:

$$\langle s \rangle \sim |f - f_c|^{-\gamma}$$
 (avg. cluster size),  
 $p_{\rm in} \sim (f - f_c)^{\beta}$  (prob. that random node is in cluster),  
 $\xi \sim |f - f_c|^{-\nu}$  (mean distance in cluster). (3.5)

This behaviour resembles phase transitions from statistical mechanics and the exponents are highly dependent on the global structure of the graph. The system tends to maintain its large connected component until  $f_c \cdot \sum_{k=1}^{K} m_k$  are taken away. Then, the system collapses into smaller, isolated clusters. While the exponents are hard to obtain analytically, the critical fraction  $f_c$  (where the giant connected cluster vanishes) can easily be derived directly from the network structure.

#### 3.3.2 Percolation threshold and survival signature

The *Molloy-Reed Criterion* is a simple condition for a giant cluster to exist: For a graph to contain a giant connected component, most nodes need to be connected to at least two other nodes [131]. For any graph, this can be expressed as

$$\kappa = \frac{\langle d^2 \rangle}{\langle d \rangle} > 2, \tag{3.6}$$

with d being the node degree (sum of all connections going into a node), and  $\langle d \rangle$  and  $\langle d^2 \rangle$ being the first and second moment of the degree distribution over the network. The value of  $\kappa$ can be directly computed from any graph representation, e.g. a double loop over the network's adjacency matrix. With the ratio  $\kappa$  the critical threshold for any system is obtained by

$$f_c = 1 - \frac{1}{\kappa - 1},\tag{3.7}$$

without any further computation involving the system structure. From a survival signature point of view, this means that if more than a fraction of components  $f_c$  has failed, there is only

a negligible probability that the system is functional:

$$\sum_{k=1}^{K} l_k < (1 - f_c) \cdot \sum_{k=1}^{K} m_k \Rightarrow \Phi(\underline{l}) \approx 0.$$
(3.8)

This way the computation of all entries in the survival signature below that threshold can be omitted.

Equations (3.6) and (3.8) have also been independently developed by Cohen et al. [132].

# 3.4 Approximation of the survival signature

This section presents the developed method to estimate the survival signature. After application of the percolation theory the remainder of the survival signature is approximated using Monte Carlo simulation. The proposed technique is then applied to simple benchmarking examples in order to quantify the errors resulting from neglecting entries and approximation. A more complex numerical example is presented in the subsequent section.

The method is divided into two steps:

- (1) Identify the area to neglect based on the critical percolation threshold (Eq. 3.8) and set all entries to 0.
- (2) Use Monte Carlo simulation to approximate the remaining entries, effectively replacing the full combinatorial calculation (see Eq. 3.2) with a sampling approach.

The algorithm to approximate a single unknown survival signature entry  $\Phi(\underline{l})$  is as follows. As long as neither a pre-selected maximum number of samples N or a target coefficient of variation C is reached, generate a random network state for the state vector  $\underline{l}$  denoted by s and increase the number of samples  $n_{\underline{l}}$  by one. A simple way of choosing a random network state for a state vector is to randomly shuffle the components of type k and choose the first  $l_k$  for each  $k = 1, \ldots, K$ .

Consider a system with 10 components divided into two types as  $s_1 = [1, 3, 5, 7, 9]$  and  $s_2 = [2, 4, 6, 8, 10]$ . In order to generate a random system for an example state vector  $\underline{l} = [3, 3]$  the component vectors are randomly permutated, e.g.  $s_1 = [3, 7, 5, 9, 1]$  and  $s_2 = [2, 10, 6, 4, 8]$ . Selecting and merging subarrays of lengths  $l_1$  and  $l_2$  from  $s_1$  and  $s_2$  respectively, results in the random network state s = [3, 7, 5, 2, 10, 6].

If the structure function evaluates the random network state as functioning, i.e.  $\varphi(s) = 1$ , increase the counter  $w_l$  by one. Next, update the approximation using

$$\Phi(\underline{l}) \approx \frac{w_{\underline{l}}}{n_{\underline{l}}} \tag{3.9}$$
and the current coefficient of variation by

$$c_{\underline{l}} = \frac{\sqrt{(\Phi(\underline{l}) - \Phi(\underline{l})^2)/n_{\underline{l}}}}{\Phi(\underline{l})}.$$
(3.10)

A pseudo-code implementation of the algorithm is presented in Algorithm 2. Note, that entries where the number of possible network states is smaller than N are calculated analytically through Eq. 3.2.

Eq. 3.10 is based on the coefficient of variation definition for a standard Monte Carlo simulation with continuous random variables. However, since the survival signature approximation involves a very large number of possible combinations, and entries with only a small number of combinations are always calculated exactly, it can be applied here as well.

The complete algorithm has been implemented in the Julia package **SurvivalSignature.jl** and made publicly available on Github [99].

Pseudocode 2 Approximate survival signatu	ire entry
function APPROXIMATE $(\underline{l}, \varphi, N, C)$	
$c, n, w, \Phi \leftarrow 0$	▷ Initialise variables
while $c > C$ and $n \le N$ do	
$n \leftarrow n+1$	
$s \leftarrow \text{random network state for } \underline{l}$	
$\mathbf{if} \ \varphi(s) = 1 \ \mathbf{then}$	
$w \leftarrow w + 1$	
end if	
$\Phi \leftarrow w/n$	
$c \leftarrow rac{\sqrt{(\Phi - \Phi^2)/n}}{\Phi}$	
end while	
return $\Phi$ , $c$	$\triangleright$ Signature entry and coefficient of variation
end function	

To prove the suitability of the method and quantify the error resulting from the approximation, the proposed technique is applied to several example networks of varying sizes. The networks used are simple  $n \times m$  grid networks of the form shown in Fig. 3.2. The nodes distributed among two types in such a way, that any component is only connected to components of the other type. Figure 3.3 shows the convergence of the approximation of  $\Phi(14, 14)$  with increasing sample size for the  $6 \times 6$  network. The associated mean squared errors are presented in Figure 3.4. Next, the algorithm is applied to the full networks in oder to understand the resulting errors and their effect on a reliability analysis using the approximated survival signature.



Figure 3.2: Simple grid network of size  $5 \times 5$  with 25 nodes and 40 edges. The nodes labeled s and t are the source and target nodes.



Figure 3.3: Convergence of the approximated signature entry  $\Phi(14, 14)$  for the 6 × 6 network to the exact value of 0.4741594. The number of state vector evaluations needed for the exact solution is 9 363 600.

#### 3.4.1 Percolation

In a first step, the exact survival signature for all networks is computed using the full combinatorial approach so that the approximation error can be calculated. Next, the critical threshold  $f_c$  of the networks is estimated using Eq. 3.7. For each network, a second survival signature denoted by  $\Phi_{f_c}$  is created by copying all entries from the exact signature in line with Eq. 3.8. Then, the absolute error

$$E_{f_c} = \|\Phi - \Phi_{f_c}\|_F$$
 (3.11)

and relative error

$$\widetilde{E}_{f_c} = \frac{E_{f_c}}{\|\Phi\|_F} \tag{3.12}$$



Figure 3.4: Evolution of the mean squared error when approximating the survival signature entry  $\Phi(14, 14)$  for the 6×6 network with increasing sample size.

made by excluding the entries below the threshold is calculated. The results are presented in Tab. 3.2. It can be seen that the  $f_c$  slowly increases with network size which is also represented in the error. For example, the relative error made by excluding 120 entries from the survival signature of the  $6 \times 6$  network is already less than 0.01 %.

$n \times m$	$f_c$	n	Ν	$E_{f_c}$	$\widetilde{E}_{f_c}$
$5 \times 5$	0.574468	66	182	0.000761789	0.000209180
$5 \times 6$	0.584746	91	256	0.000524625	0.000129065
$6 \times 6$	0.594595	120	361	0.000356815	0.000068137

Table 3.2: Critical thresholds and errors made by percolation of the grid networks. The number of neglected entries based on the critical threshold  $f_c$  is denoted by n. N represents the total number of entries in the survival signature.

Percolation is usually applied to large-scale networks. However, in the context of this work, the application is restricted so smaller networks where the computation of the analytical survival signature is still possible in order to be able to quantify the errors made by the exclusion of low interest system configurations. The effect of applying percolation to the survival signature of large-scale networks should be studied more closely in the future.

## 3.4.2 Monte Carlo Approximation

After applying the percolation based selection criterion, the entries of the survival signature not excluded by the critical percolation threshold are approximated using Monte Carlo simulation (see Section 3.4). The maximum number of samples used for each entry of the survival signature is increased with the network size to reach comparable levels of accuracy. As stated before, the

absolute error

$$E_{mc} = \|\Phi_{f_c} - \Phi_{mc}\|_F \tag{3.13}$$

and relative error

$$\widetilde{E}_{mc} = \frac{E_{mc}}{\|\Phi_{f_c}\|_F} \tag{3.14}$$

introduced by the simulation-based approximation are calculated. Note that  $\Phi_{mc}$  is compared to  $\Phi_{f_c}$  instead of the extact survival signature  $\Phi$  when quantifying the error. This is to ensure that estimated error results only from the Monte Carlo approximation. The results presented in Tab. 3.3 show that good accuracy can be reached with a reasonable amount of samples per entry. For example, using a maximum number of  $10^4$  samples for the  $6 \times 6$  network leads to a relative error of less than 1%.

The number of structure function evaluations for this simulation is  $n_{\varphi} = 2\ 099\ 933$  compared to the  $2^{36}$  needed for the exact computation of the survival signature, a reduction of more than 99%. This great reduction in numerical effort also reflects in the computation time. The simulation takes less than 3 minutes using a single process where the exact computation took 18 hours highly parallelised on 64 processes.

$n \times m$	n	$n_{arphi}$	$E_{mc}$	$\widetilde{E}_{mc}$
$5 \times 5$ $5 \times 6$ $6 \times 6$	$2^{25}$ $2^{30}$ $2^{36}$	$\begin{array}{c} 399256 \\ 862400 \\ 2099933 \end{array}$	$\begin{array}{c} 0.0207 \\ 0.0347 \\ 0.0451 \end{array}$	$\begin{array}{c} 0.0056 \\ 0.0085 \\ 0.0086 \end{array}$

**Table 3.3:** Absolute and relative errors made by approximation of the survival signature. The number of structure function evaluations required for the analytical solution is denoted by n while the number of evaluations required for the approximation is denoted by  $n_{\varphi}$ .

#### 3.4.3 Reliability analysis

Finally, the exact and approximated survival signatures are applied to a network reliability analysis using the analytical solution of the survival function, see Eq. 3.3 and Eq. 3.4.

Let the failure times for components of type 1 have an Exponential distribution with  $\lambda = 1$ and the failure times of components of type 2 have a Weibull distribution with k = 2 and  $\lambda = 1$ . The survival functions of the  $6 \times 6$  network using the exact and approximated signatures are presented in Fig. 3.5. The plot clearly shows how the survival function  $P_{mc}$  using the approximated survival signature  $\Phi_{mc}$  matches the one resulting from the exact signature. The relative error defined by  $\tilde{E}_P = ||P - P_{mc}||_F / ||P||_F$  is approximately 0.13% in this case. The absolute and relative errors for the survival functions of all three test networks are shown in Tab. 3.4.

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$n \times m$	$E_P$	$\widetilde{E}_P$
$5 \times 5$	0.0152	0.0011
$5 \times 6$	0.0235	0.0015
$6 \times 6$	0.0212	0.0013

 Table 3.4: Absolute and relative errors resulting from a reliability analysis using the approximated survival signatures.



Figure 3.5: Survival functions of the  $6 \times 6$  network. The approximated reliability of the network denoted by  $P_{mc}$  closely matches the analytical solution P.

# 3.5 Numerical examples

This section presents the application of the developed methodology to more involved, real world examples in comparison to the simple grid networks used in Section 3.4.

#### 3.5.1 Example 1: Electricity transmission network

The first example used is a representative model of the electricity transmission network of Great Britain as presented in [133]. The network consists of 29 nodes that are split into two component types based on their bus type. Load buses are assigned component type 1, while voltage controled buses are grouped in component type 2. The network's slack bus (node 27) has not been separated into its own type to reduce the complexity of the problem and allow for relatively fast computation of the exact signature for comparison with the approximations. Note, that this is not an attempt at solving the underlying power flow problem but only a computation of the survival signature of the provided network topology. The network topology is displayed in Fig. 3.6.

A structure function is required in order to calculate the survival signature of the power network. The existance of s-t-connectivity as applicable for reliability block diagrams, shown in



**Figure 3.6:** Topology of the electricity transmission network used in example 1. Components of type 1 are shown in blue. Components of type 2 are shown in orange. The locations of the nodes in the figure are not related to their actual geographical location.

Section 3.4, has little meaning for this network. Instead, the so called network efficiency [134] as defined in Eq. 3.15 is used to measure the state of the network for a given state vector.

$$E(G) = \frac{1}{n(n-1)} \sum_{i \neq j \in G} \frac{1}{d(i,j)}$$
(3.15)

where G is the network with n nodes and d(i, j) denotes the length of the shortest path between two nodes i and j.

To define the (binary) structure function it is assumed that the network completely collapses once the loss of efficiency due to failing components exceeds 50% as

$$\varphi(\underline{x}) = \frac{E(G(\underline{x}))}{E(G)} < 0.5.$$
(3.16)

This value has been arbitrarily chosen for this example and implies no real world relevance. It should be noted, that this threshold is not related to the percolation threshold imposed in the first step of the algorithm.

Since this requires to compute the shortest paths between all components for every evaluated system configuration it is significantly more numerically demanding than the s-t-connectivity structure function used previously. An efficient algorithm to calculate the shortest paths is the Floyd-Warshall algorithm [135].

Survival signature approximations are performed with increasing sample sizes and compared to the exact solution to prove convergance. Figure 3.7 presents the mean squared errors and associated standard deviations resulting from 1000 repeated evaluations. A target coefficient of variation of 0.001 was used for all simulations. As evident from the plot, using a sample size of



Figure 3.7: Evolution of the mean squared error resulting from approximation of the survival signature for the network shown in Fig. 3.6 with increasing number of samples used.

1e4 per survival signature entry already results in an adequately low error of  $\approx 1.9e-6$ . On a single processor core running at a clock speed of 3600 MHz the Monte Carlo approximation runs 509 s instead of 11069 s for the full combinatorial evaluation.

#### 3.5.2 Example 2: Berlin metro system

In this second example, the developed method is applied to the model of Berlin's metro system taken from [72]. The model represents Berlin's U-Bahn and S-Bahn systems which, due to the large number of interconnections between the systems, will be considered as a single system. The entire network consists of 306 nodes and 350 edges with nodes separated into two types based on their degree. Nodes with a maximum degree of two are grouped in type 1. Nodes with a degree larger than two are separated into type 2. This results in 245 nodes of type 1 and 61 of type 2. The topology of the network is presented in Fig. 3.8. The same structure function as in example 1 is applied to the network, see Eq. 3.16.

The full survival signature of this system has 15252 entries, the most numerically demanding entries being  $\Phi(122, 30)$ ,  $\Phi(122, 31)$ ,  $\Phi(123, 30)$  and  $\Phi(123, 31)$  each with a total number of approximately  $6.69 \times 10^{89}$  possible combinations to be evaluated. To put this into perspective, these are more combinations for a single entry than the estimated number of atoms in the observable universe ( $\approx 10^{80}$ ). Therefore, calculating the analytical survival signature for this network is impossible using the traditional approaches on present day computers. However, it can be approximated using the presented simulation based technique.

The previous example has shown, that using 1e4 samples per signature entry leads to sufficiently accurate results as evident from Fig. 3.7. The approximation of a single survival signature is essentially the same as computing a probability of failure. The minimum number



Figure 3.8: Topology of the Berlin metro system with 306 nodes. Nodes highlighted in blue represent stations with more than two connections. Adapted from [72].

of samples N required to estimate a probability of failure or in this case survival signature entry  $\Phi(\underline{l})$  is defined by

$$N \le \frac{1}{c^2 \cdot \Phi(\underline{l})},\tag{3.17}$$

where c is the desired coefficient of variation [21]. This shows that the per entry accuracy of the survival signature approximation using a certain number of samples is the same regardless of network size. Based on this, 1e4 samples are chosen to compute the survival signature of the metro system.

The approximation of the survival signature is still numerically demanding, running for 27 h 39 min 35 s using 64 threads on an AMD Ryzen Threadripper 3990X 64-Core Processor. Since no analytical solution is available for this system, the final error resulting from the approximation can not be quantified.

While the results show a significant reduction in numerical demand in comparison to the full combinatorial evaluation, it highlights the demand for more efficient sampling strategy. With increasing size and dimensions of the survival signature, brute force Monte Carlo simulation will still not be sufficient. Potentially, advanced Monte Carlo methods such as line sampling [136] or subset simulation [137] could drastically improve efficiency.

# 3.6 Conclusion

This paper presented a new approach to the approximation of the survival signature. The developed technique significantly outperforms traditional (full combinatorial) approaches in the number of required structure function evaluations and therefore in overall computation time. At the same time, the resulting approximation errors are sufficiently low enough for an accurate reliability analysis.

Both the application of percolation theory to reduce the number of computed signature entries and the Monte Carlo simulation require no additional information on the system other than the structure function. This allows the method to be applied to any problem where the numerical demand prohibits the full evaluation of the survival signature.

The viability of the new method is proved by comparing simple toy examples to their exact solutions and quantifying the errors. More complex and demanding numerical examples are used to show application to real world problems.

However, since the number of samples required for an accurate Monte Carlo approximation increases with growing network size and number of component types this approach will also reach its limits at some point. To analyse even larger and more complex systems the method must be extended to apply advanced simulation techniques such as line sampling or subset simulation in order to reduce the number of samples required to compute an entry of the survival signature.

The developed method is implemented in an open source Julia library and made available to fellow researchers.

#### **CRediT** authorship contribution statement

Jasper Behrensdorf: Conceptualization, Methodology, Software, Writing – original draft, Visualization. Tobias-Emanuel Regenhardt: Conceptualization, Methodology, Writing – original draft. Matteo Broggi: Conceptualization, Methodology, Writing – review & editing. Michael Beer: Conceptualization, Supervision, Funding acquisition.

#### Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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# 4 Imprecise Survival Signature Approximation Using Interval Predictor Models

# Imprecise Survival Signature Approximation Using Interval Predictor Models

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#### Abstract

This paper presents a novel technique for the approximation of the survival signature for very large systems. In recent years, the survival signature has seen promising applications for the reliability analysis of critical infrastructures. It outperforms traditional techniques by allowing for complex modelling of dependencies, common causes of failures and imprecision. However, as an inherently combinatorial method, the survival signature suffers greatly from the curse of dimensionality. Computation for very large systems, as needed for critical infrastructures, is mostly infeasible. New advancements have applied Monte Carlo simulation to approximate the signature instead of performing a full evaluation. This allows for significantly larger systems to be considered. Unfortunately, these approaches will also quickly reach their limits with growing network size and complexity. In this work, instead of approximating the full survival signature, we will strategically select key values of the signature to accurately approximate it using a surrogate radial basis function network. This surrogate model is then extended to an interval predictor model (IPM) to account for the uncertainty in the prediction of the remaining unknown values. In contrast to standard models, IPMs return an interval bounding the survival signature entry. The resulting imprecise survival signature is then fed into the reliability analysis, yielding upper and lower bounds on the reliability of the system. This new method provides a significant reduction in numerical effort enabling the analysis of larger systems where the required computational demand was previously prohibitive.

Keywords: Survival signature, interval predictor models, radial basis function networks

#### 4.1 Introduction

The reliability analysis of critical infrastructure systems, such as electrical, gas and water distribution systems, traffic networks and communication networks is of paramount importance to the safety and development of modern societies. Our increasing dependence on the availability of these systems only escalates this fact. The analysis and assessment of reliability comes with increasingly higher computational demand due to the growing size and complexity of the infrastructure systems. In addition, phenomena such as dependencies inside or between these networks can have adverse effects and must not be disregarded [42]. Unfortunately, this is where traditional approaches such as fault tree analysis or reliability block diagrams quickly reach their limits. A modern development in system analysis built to circumvent these drawbacks is the survival signature [27].

The survival signature was introduced as a generalization of the system signature [121] to systems with multiple component types. It excels in particular where diverse effects such as dependencies, common causes of failure or imprecision need to be included in the reliability analysis. Through the separation of the system structure from probabilistic information about component failures it provides a flexible method where a variety of scenarios can be studied without unnecessary reevaluation of the system structure.

However, like the traditional methodologies, the survival signature suffers greatly from the curse of dimensionality. As a result, the numerical demand to compute the survival signature increases with non-polynomial growth with increasing network size and number of component types. As the number of components in critical infrastructure systems can quickly reach upwards of hundreds or thousands this computational demand to obtain the survival signature becomes prohibitive.

A number of promising solutions to this problem have been proposed over the recent years. These involve for example binary decision diagrams (BDD) [38], extended universal generating functions (UFG) [40] or Monte Carlo simulation [41, 94]. However, obtaining alternative system representations such as the BDD or UFG are non-trivial problems themselves, while standard Monte Carlo simulation will also quickly reach the limits of its feasibility for larger systems.

In this paper we propose a new method based on building an accurate surrogate model for the survival signature of large systems. In a first step, an adaptive strategy is employed to select which values of the survival signature to compute as data points for the surrogate model. These values are computed using the existing Monte Carlo method [94]. Then, a normalized radial basis function network is constructed from these data points to approximate the remaining values of the survival signature. Finally, the uncertainty resulting from the Monte Carlo simulation is used to extend the surrogate model to an interval predictor model (IPM). The uncertainty is propagated through the IPM which ultimately yields bounds on the survival signature.

The remainder of the paper is structured as follows. Section 4.2 presents the survival signature while Section 4.3 discusses the radial basis function based surrogate models. The newly proposed methodology is introduced in Section 4.4 followed by an application of the technique to a numerical example in Section 4.5. The paper closes with some concluding remarks in Section 4.6.

### 4.2 Survival Signature

Consider a system with K different component types and  $m_k$  components of each type  $k \in \{1, 2, ..., K\}$ . The survival signature condenses the structural information of the system into a

probability that the system is working for  $l_k$  out of  $m_k$  components working per type as

$$\Phi(l_1,\ldots,l_K) = \left[\prod_{k=1}^K \binom{m_k}{l_k}^{-1}\right] \times \sum_{\mathbf{x}\in S_{l_1,\ldots,l_K}} \varphi(\mathbf{x}),$$
(4.1)

where  $S_{l_1,\ldots,l_K}$  denotes the set of all state vectors of the system with  $l_1 \ldots, l_K$  working components and  $\varphi(\mathbf{x})$  is the structure function which evaluates to 1 if the system is working for a given state vector and 0 if it is not.

A state vector  $\mathbf{x} = (x_1, x_2, \dots, x_n)$  is the representation of a distinct system state where  $x_i = 0$  indicates a component is failed and  $x_i = 1$  indicates a working component for all  $i \in \{1, 2, \dots, n\}$  components of the system and  $n = \sum_{k=1}^{K} m_k$ .

The survival signature is defined for coherent systems, for which it is monotonically nondecreasing. The monotone behavior can be expressed as

$$\Phi(l_1^a, \dots, l_K^a) \le \Phi(l_1^b, \dots, l_K^b), \text{ if}$$

$$l_k^a \le l_k^b, \forall k \in \{1, \dots, K\},$$
(4.2)

where the superscripts a and b refer to any two inputs of the survival signature. This monotonicity property is exploited later to design a monotone radial basis function network as a surrogate model.

The survival function, that is the reliability of the system at time t, is defined as

$$P(T_s > t) = \sum_{l_1=0}^{m_1} \dots \sum_{l_K=0}^{m_K} \Phi(l_1, \dots, l_K) P\left(\bigcap_{k=1}^K \left\{C_t^k = l_k\right\}\right),$$
(4.3)

where  $C_t^k$  denotes the number of components of type k functioning at time t. For known failure time distributions with cumulative distribution functions (CDF)  $F_k(t)$  the probabilistic part of the survival function can be analytically computed as

$$P\left(\bigcap_{k=1}^{K} \left\{ C_{t}^{k} = l_{k} \right\} \right) = \prod_{k=1}^{K} \left( \binom{m_{k}}{l_{k}} [F_{k}(t)]^{m_{k}-l_{k}} [1 - F_{k}(t)]^{l_{k}} \right).$$
(4.4)

#### 4.3 Monotone Radial Basis Function Networks

Radial basis function (RBF) networks [138] are a very simple type of artificial neural network with only one hidden layer, where the activation functions are radial basis functions, and a linear output layer. Radial basis functions in  $\mathbb{R}^d$  are defined with respect to a distance function between the input and a fixed point called a center. This distance is usually the Euclidean



Figure 4.1: Graphical representation of a radial basis function neural network. From left to right: input layer, hidden layer, linear output layer.

distance defined as

$$||x - c|| = \sqrt{\sum_{j=1}^{d} \frac{(x_j - c_j)^2}{2\sigma_j^2}},$$
(4.5)

where  $x \in \mathbb{R}^d$  is the input vector and the  $\sigma_j$  are normalization constants controlling the spread of the radial basis function in each dimension. The most common radial basis function is the Gaussian function

$$\psi(||x-c||) = e^{-||x-c||^2}.$$
(4.6)

Using the basis functions we can define the RBF network as

$$y(x) = \sum_{i=1}^{N} w_i \psi(||x - c_i||), \qquad (4.7)$$

where N is the number of neurons,  $c_i$  is the center point associated with neuron i and  $w_i$  is the weight of that neuron in the linear output layer. Refer to Figure 4.1 for a simple graphical representation of an RBF network.

The output of the radial basis function network can be normalized as

$$y(x) = \frac{\sum_{i=1}^{N} w_i \psi(||x - c_i||)}{\sum_{i=1}^{N} \psi(||x - c_i||)}.$$
(4.8)

Normalized radial basis function (NRBF) networks have shown to improve extrapolation of the network when compared to regular RBF networks [139]. For the remainder of this paper, the basis functions used will be normalized as

$$\hat{\psi}_i(x) = \frac{\psi(||x - c_i||)}{\sum_{i=1}^N \psi(||x - c_i||)}.$$
(4.9)

In this work, we restrict the center locations of the NRBF network to a regular uniform grid over the entire input domain. This allows for easier selection of the  $\sigma_j$  shape parameters as well as greatly simplifying the monotonicity constraints. In the next step, the NRBF network will be used as a surrogate model of the survival signature. Enforcing monotonicity of the surrogate model greatly improves its performance since the survival signature itself is a monotone function.

Monotonicity of an NRBF network can be enforced through simple linear constraints on the weights. For centers located on a grid, only sequences of weights lying on a line in the direction of the d dimensions need to be monotonic for the NRBF network to be monotonic [140].

Assuming M data points  $x_j$  with associated function values  $y_j$  for  $j \in \{1, \ldots, M\}$ , the optimal weights  $w_i$  are determined as the solution to the following constrained least squares optimization problem

$$\begin{array}{ll} \underset{w}{\text{minimize}} & ||\Psi w - y||_2^2 \\ \text{subject to} & w_p \le w_q, \ p, q \in \{1, \dots, N\}, \\ & \text{if } c_p^\alpha < c_q^\alpha, c_p^\beta = c_q^\beta, \alpha \ne \beta, \end{array}$$

$$(4.10)$$

where the superscripts  $\alpha, \beta \in \{1, \ldots, d\}$  refer to the coordinates in dimensions  $\alpha$  and  $\beta$  with  $w = [w_1, \ldots, w_N]^T$  and  $y = [y_1, \ldots, y_M]^T$ . The matrix  $\Psi \in \mathbb{R}^{M \times N}$  is defined as

$$\Psi_{ji} = \hat{\psi}_i(x_j). \tag{4.11}$$

This is a convex optimization problem which can be solved by standard solvers. Here we use the splitting cone solver (SCS) [141] in connection with JuMP [142].

#### 4.4 Approximation of the Survival Signature

This section presents the proposed methodology to the approximation of the survival signature for very large systems. Equation (4.1) clearly shows that the computation of the survival signature is a combinatorial problem which greatly increases in numerical demand with increasing number of components and component types. Therefore, analytical computation of the survival signature is infeasible for very large systems. In [94] we presented an approach to approximating the survival signature using percolation to exclude negligible parts of the signature and approximating the remaining entries with Monte Carlo simulation. While this enabled the analysis of larger systems, this method still requires a significant number of system evaluations and will quickly reach prohibitive computational demand. In this paper, we propose an alternative solution where the survival signature is approximated through a radial basis function network based on a few strategically selected values. In addition, the uncertainty in the survival signature entries resulting from the Monte Carlo approximation is propagated through an interval predictor model and reflected as bounds on the survival signature.

#### 4.4.1 Design of the NRBF network surrogate model

Similarly to the previously developed technique, this new approach starts by applying percolation theory to find the critical threshold  $f_c$  and exclude a significant portion of the survival signature

where the probability that the system functions is negligible, i.e. close to zero [94].

Next, let  $\Omega$  be the set of remaining survival signature entries  $l_1, \ldots, l_K$  for  $l_k \in \{0, 1, \ldots, m_k\}$ and  $k \in \{1, \ldots, K\}$  satisfying the condition

$$\sum_{k=1}^{K} l_k \ge (1 - f_c) \sum_{k=1}^{K} m_k.$$
(4.12)

We start by selecting M initial entries from  $\Omega$  and calculate their survival signature values using Monte Carlo simulation. Note that values that require less than the number of Monte Carlo samples  $N_{MC}$  structure function evaluations are computed exactly. In order to have good coverage of the input space, we generate the M data points by creating a uniform grid between the lower and upper bounds of  $\Omega$  and then select the nearest neighbors in  $\Omega$  as the starting values. In addition, we create a uniform grid of centers  $c_i$  for  $i = 1, \ldots, N$  spread over the entire domain of  $\Omega$ . The spread of the radial basis function  $\sigma_j$  is chosen as half of the distance between two successive centers in the *j*th dimension. These have shown to be a good starting point for NRBF networks [140]. Then, the weights for the initial monotone NRBF approximation of the survival signature are obtained by solving the optimization problem (4.10).

In the next step, new values of the survival signature to be approximated are selected and used to improve the surrogate model. This is performed by means of a Taylor expansion-based adaptive design (TEAD) [143]. The TEAD is a combination of exploration and exploitation based on nearest neighbor distance and Taylor expansion. This allows to both adequately cover the input space as needed as well as concentrate samples where the highest changes in the survival signature are located to provide an accurate surrogate model using a small sample size. At each point a new sample is selected from  $\Omega$  and added to the M data points. Then the weights are updated by again solving the optimization problem (4.10). The search for new points is aborted once the change in weights falls below a defined threshold twice in a row.

#### 4.4.2 Extension to an interval predictor model

Once an adequate surrogate model for the survival signature is obtained, it is extended to an interval predictor model. In difference to regular models, where a single output value is returned for any inputs, interval predictor models return an interval where the value is predicted to fall [144]. The goal here is to propagate the uncertainty of using Monte Carlo simulation to approximate individual entries of the survival signature through the surrogate model. By simply fitting a NRBF network to some estimated values of the survival signature the uncertainty of the Monte Carlo simulation represented by the coefficient of variation of the particular entries would be lost.

The IPM approach is simple. Instead of fitting a single surrogate model to the available data points we fit two models that act as upper and lower bounds. These models are built based on the points identified in the previous step. Both models use the exact same center locations  $c_i$  and their difference in output is only influenced by two different sets of weights  $w_{\min}$  and  $w_{\max}$ . The bounds are defined as

$$\overline{y}(x, w_{\max}) = \Phi(x)^T w_{\max} \tag{4.13}$$

$$y(x, w_{\min}) = \Phi(x)^T w_{\min}, \qquad (4.14)$$

where  $\Psi(x) = [\hat{\psi}_1(x), \dots, \hat{\psi}_N(x)].$ 

The spread of the IPM, i.e. the separation between its limits, is defined as

$$\delta_y(x, w_{\max}, w_{\min}) = \Phi(x)^T (w_{\max} - w_{\min}).$$
 (4.15)

The parameters  $w_{\text{max}}$  and  $w_{\text{min}}$  are given by the following optimization problem

$$\begin{array}{ll} \underset{w_{\max},w_{\min}}{\text{minimize}} & \frac{1}{N} \sum_{j}^{N} \delta_{y}(x_{j}, w_{\max}, w_{\min}) \\ \text{subject to} & \underline{y}(x_{j}, w_{\min}) \leq \underline{y}_{j} \\ & \overline{y}(x_{j}, w_{\max}) \geq \overline{y}_{j} \\ & w_{\min} \leq w_{\max}, \end{array} \tag{4.16}$$

where  $(x_j, \underline{y}_j, \overline{y}_j)$  for  $j \in \{1, \dots, M\}$  are the data points. The bounds  $\underline{y}_j$  and  $\overline{y}_j$  are obtained as

$$\underline{y}_j = y_j - \gamma \cdot y_j \cdot cv_j \tag{4.17}$$

$$\overline{y}_j = y_j + \gamma \cdot y_j \cdot cv_j, \tag{4.18}$$

where  $cv_j$  is the coefficient of variation of the Monte Carlo approximation for  $y_j$ . The parameter  $\gamma \geq 1$  can be adapted to obtain more conservative bounds. In addition to the constraints in (4.16) we also invoke the monotonicity constraints of (4.10) on  $w_{\text{max}}$  and  $w_{\text{min}}$  in order to ensure monotonicity of the IPM bounds.

Once the IPM is obtained by solving the optimization problem (4.16), the bounds on the survival signature can be fed into (4.3) to estimate the bounds of the imprecise survival function. Since bounds of the IPM are strictly monotone functions, it is sufficient to evaluate the survival function for the upper and lower bound. If the CDFs of the component failure times are also imprecise, the bounds on the reliability can be obtained by applying the vertex method [145].

### 4.5 Numerical Example

In this section we apply the proposed technique to a numerical example. The example used is that of the Berlin S- and U-Bahn system as presented in [94], see Fig. 4.2. The entire network consists of 306 nodes and 350 edges. The nodes are separated into two types based on their

degree, with type 1 consisting of nodes with degree of two or less, while type 2 contains all nodes with a degree larger than two. As a result, there are 245 nodes of type 1 and 61 of type 2. The full survival signature of this network has 15252 entries. Let the network efficiency be defined as

$$E(G) = \frac{1}{n(n-1)} \sum_{u \neq v \in G} \frac{1}{d_{uv}},$$
(4.19)

where G is the network consisting of n nodes and  $d_{uv}$  measures the length of the shortest path between nodes u and v [134]. Then, a structure function for the network analysis can be defined by the loss of efficiency for a given network state. Here we assume that the network fails to function once the loss of efficiency exceeds 50 % as given by

$$\varphi(\mathbf{x}) = \frac{E(G(\mathbf{x}))}{E(G)} < 0.5.$$
(4.20)

Computing the full analytical survival signature given this structure function is impossible and even the Monte Carlo simulation requires more than 27 hours using 10 000 samples per entry distributed among 64 cores [94].



Figure 4.2: Topology of the Berlin metro system with 306 nodes. Nodes highlighted in blue represent stations with more than two connections. Adapted from [72].

The approximation of the survival signature starts by applying percolation to find the set of candidate points  $\Omega$ . The critical threshold  $f_c \approx 0.39550$  reduces  $\Omega$  from 15252 points down to 5673. 400 center points  $c_i$  are generated uniformly over the domain of  $\Omega$ , of which 109 are excluded using (4.12), leaving 291 centers. Then, 25 initial points are selected from  $\Omega$ . New points are chosen using the TEAD until the change in weights is less than 1e-3 for two consecutive points. The procedure aborts after 110 new points have been selected. The survival signature entries for all points are approximated using 10 000 Monte Carlo samples. Figure 4.3 shows the initial points as well as the new points chosen by the TEAD. The plot clearly presents how the new points selected by the adaptive technique are concentrated in the area of the survival signature with high relevance whereas only a few points are chosen where the survival signature is negligible. This ability to identify the important region of the signature allows to approximate it accurately using only a low number of evaluated entries.



Figure 4.3: Initial data points and adaptive points selected by the TEAD.

In the final step, the coefficient of variation resulting from the approximation is used to define the upper and lower bounds of the evaluated survival signature entries and the weights for the IPM are obtained from the optimization (4.16).

We assume the failure times for component types 1 are exponentially distributed with  $\lambda = 0.25$ while the failures of type 2 components are exponentially distributed with  $\lambda = 0.5$ . These values are arbitrarily chosen for illustrative purposes and have no real world relevance. The bounds on the resulting survival function are compared to the reliability of the full Monte Carlo approximation in Figure 4.4. For a closer look at the reliability bounds between t = 0.25 and t = 0.5 refer to Figure 4.5. As evident from the plots, the IPM is able to accurately predict upper and lower bounds on the reliability. This accuracy is especially remarkable due to the fact that it only requires the evaluation of 135 out of the 5673 survival signature values necessary for the full Monte Carlo approach. This is a significant reduction in numerical effort and enables the analysis of even larger networks than using the Monte Carlo method alone.



Figure 4.4: Bounds of the IPM surrogate model compared to the NRBF approximation.

### 4.6 Conclusions

This paper presents a novel approach to the approximation of the survival signature using normalized radial basis function networks and interval predictor models as surrogate models. The NRBF networks are able to accurately predict the entire survival signature given only a small fraction of the evaluated signature entries. The uncertainty resulting from using Monte Carlo simulation to approximate individual entries is efficiently propagated through the IPM to yield bounds on the survival signature. An adaptive procedure to select the data points for the surrogate model ensures high accuracy while keeping the numerical demand low. The effectivity of the developed method was proven by applying it to the analysis of a large system and comparing the results with a previously presented technique. The code developed as part of this work will be added to the open source Julia package *SurvivalSignature.jl* [99].

Future effort will be focused on improving the NRBF fit. While the number of centers and parameters controlling the spread of the basis functions chosen in this work serve as a good basis, optimizing these parameters to the specific problem could proof beneficial. Furthermore, the method should be applied to even larger systems with more than two component types to investigate the scalability.

By extending this method to include imprecise probabilities for the failure time distributions of the components such as probability boxes, a fully imprecise survival function can be devised.



Figure 4.5: Bounds of the IPM surrogate model compared to the NRBF approximation between t = 0.25 and t = 0.5.

# 5 Interval Predictor Model for the Survival Signature Using Monotone Radial Basis Functions

# Interval Predictor Model for the Survival Signature Using Monotone Radial Basis Functions

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#### Abstract

This research describes a novel method for approximating the survival signature for very large systems. Over the recent years, the survival signature has emerged as a capable tool for the reliability analysis of critical infrastructure systems. In comparison to traditional approaches it allows for complex modelling of dependencies, common causes of failures as well as imprecision. However, while it enables the consideration of these effects, as an inherently combinatorial method, the survival signature suffers greatly from the curse of dimensionality. Critical infrastructures typically involve upwards of hundreds of nodes. At this scale analytical computation of the survival signature is impossible using current computing capabilities. Instead of performing the full analytical computation of the survival signature some studies have focused on approximating it using Monte Carlo simulation. While this reduces the numerical demand and allows for larger systems to be analyzed, these approaches will also quickly reach their limits with growing network size and complexity. Here, instead of approximating the full survival signature, we build a surrogate model based on normalized radial basis functions where the data points required to fit the model are approximated by Monte Carlo simulation. The resulting uncertainty from the simulation is then used to build an interval predictor model (IPM) which estimates intervals where the remaining survival signature values are expected to fall. By applying this imprecise survival signature we can obtain bounds on the reliability. Because a low number of data points is sufficient to build the IPM this presents a significant reduction in numerical demand and allows for very large systems to be considered. Keywords: Survival signature, Monte Carlo simulation, radial basis function network, interval predictor models, imprecise probabilities

#### 5.1 Introduction

The reliability analysis of critical infrastructure systems, such as electricity, gas, and water distribution systems, transportation networks, and communication networks, is critical to modern society's safety and progress. Our growing reliance on the availability of these systems exacerbates this problem. The analysis of network reliability for these systems comes with increasingly higher computational demand due to their growing size and complexity. Additionally, complex phenomena such as dependencies inside or between these networks can lead to catastrophic failures and must be considered during the analysis [42]. Unfortunately, traditionally applied methodologies such as fault tree analysis or reliability block diagrams are limited in their abilities to include these effects. The survival signature was developed to alleviate these shortcomings and enable a comprehensive reliability analysis [27].

The survival signature was introduced as a generalization of the system signature [121] to systems with multiple component types. A signature is a condensed representation of the system topology that allows efficient computation of the system reliability. Because of its separation of the system's structural information from the component failure times it allows for the consideration of a plethora of complex effects such as imprecision, common cause failures or dependencies. This provides a versatile method for studying a range of scenarios without having to reevaluate the system structure.

However, the survival signature, like traditional techniques, suffers heavily from the curse of dimensionality. The computational demand grows non-linearly with network size and number of component types and the computing burden to obtain the survival signature becomes prohibitive as the number of components in critical infrastructure systems rapidly approaches hundreds or thousands.

Research into solutions to this problem has seen considerable attention in recent years. Reed [38] and Reed et al. [39] proposed algorithms for the exact computation of the survival signature through binary decision diagrams (BDD). However, memory demand (RAM) limits these algorithms for larger systems or those with many component types. Another approach using reliability block diagrams and extended universal generating functions is similarly limited by memory requirements [40]. Estimation methods based on standard Monte Carlo simulation [94] and entropy-driven Monte Carlo simulation [41] have also been presented. While more efficient than the full evaluation of the survival signature these approaches also reach their limits with increasing network size. A recent development uses optimization and Monte Carlo simulation to efficiently estimate the two-terminal survival signature of networks with two component types [146].

In this paper we propose a new method where instead of using Monte Carlo simulation to estimate each entry of the survival signature, only a few strategically selected data points are computed using the existing Monte Carlo method [94] which are then used to construct a monotone normalized radial basis function network as a surrogate model of the full survival signature. In a second step, the surrogate model is extended to an interval predictor model (IPM) which effectively propagates the uncertainty associated with the Monte Carlo approximation of the data points through the model. In the end, we obtain upper and lower bounds of the survival signature and therefore the system reliability.

The remainder of the paper is structured as follows. We first present the survival signature followed by a discussion of (normalized) radial basis function based surrogate models and the theory of interval predictor models. The proposed methodology is then introduced and applied to a toy example followed by a larger numerical example to prove scalability of the method. The paper closes with concluding remarks and outlook into future research.

## 5.2 Survival Signature

The survival signature [27] was introduced as a generalization of the system signature [121] to multiple component types. It condenses the structural information of a system with K different component types into a probability that the system is functioning while  $l_k$  out of  $m_k$  components are in a functioning state for each type  $k \in \{1, 2, ..., K\}$ . More precisely, it is defined as the percentage of all possible system states for  $l_k$  out of  $m_k$  working components that lead to a functioning system.

Let  $\mathbf{x} \in \{0, 1\}$  be a state vector representing the state of all m components in the system with  $m = \sum_{k=1}^{K} m_k$ . An entry  $x_i = 1$  denotes a functional component i while for  $x_i = 0$ the component is non-functional or failed for all  $i \in \{1, \ldots, m\}$ . Note that the labeling of components in the state vector is arbitrary but must be kept consistent. The global system state for any state vector can be evaluated through the structure function  $\varphi : \{0, 1\}^m \to \{0, 1\}$ , which evaluates to 1 if the system is working for a given state vector and 0 if it is not. The survival signature is then defined as

$$\Phi(l_1,\ldots,l_K) = \left[\prod_{k=1}^K \binom{m_k}{l_k}^{-1}\right] \times \sum_{\mathbf{x}\in S_{l_1,\ldots,l_K}} \varphi(\mathbf{x}),$$
(5.1)

where  $S_{l_1,\ldots,l_K}$  denotes the set of all state vectors of the system with  $l_1 \ldots, l_K$  working components. The survival signature can therefore be represented as a K-dimensional array of size  $(m_1 + 1) \times \cdots \times (m_K + 1)$ . This includes the cases with  $l_k = 0$ , where no components of type k are working. For the remainder of the paper we will refer to individual values in this K-dimensional array as survival signature *entries*.

The structure function depends on the system that is being analyzed. It can for example be defined as the *s*-*t*-connectivity of two source (s) and target (t) nodes in a system as used for the toy example to validate the proposed method. This is well known as the two-terminal reliability problem. For the real world numerical example in the penultimate section we define an alternative structure function based on the loss of network efficiency.

The survival signature is defined for coherent systems. In a coherent system, functionality does not decrease with growing number of working components. As such the survival signature is monotonically nondecreasing which can be expressed as

$$\Phi(l_1^a, \dots, l_K^a) \le \Phi(l_1^b, \dots, l_K^b), \text{ if}$$

$$l_k^a \le l_k^b, \forall k \in \{1, \dots, K\},$$
(5.2)

where the superscripts a and b refer to any two inputs of the survival signature. This information will help to obtain a better surrogate model by adding monotonicity constraints to the radial basis function networks in the next section.

Finally, the reliability of the system, that is the probability it survives up to a point in time

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t, is defined as

$$P(T_s > t) = \sum_{l_1=0}^{m_1} \dots \sum_{l_K=0}^{m_K} \Phi(l_1, \dots, l_K) P\left(\bigcap_{k=1}^K \left\{C_t^k = l_k\right\}\right),$$
(5.3)

where  $C_t^k$  represents the number of components of type k functioning at time t. For known failure time distributions with cumulative distribution functions (CDF)  $F_k(t)$  the probabilistic part of the survival function can be analytically computed as

$$P\left(\bigcap_{k=1}^{K}\left\{C_{t}^{k}=l_{k}\right\}\right)=\prod_{k=1}^{K}\left(\binom{m_{k}}{l_{k}}[F_{k}(t)]^{m_{k}-l_{k}}[1-F_{k}(t)]^{l_{k}}\right).$$
(5.4)

For cases where the CDFs are unknown, a number of simulation methods have been developed [37].

The structural information of the system, e.g. the survival signature, is completely separated from the probabilistic information on component failures. It is due to this separation that complex effects such as imprecision or dependent component failures can easily be included as they have no influence on the structural evaluation of the system. In case the failure times of the components are described as independent single parameter probability boxes (p-box) the upper and lower bounds of the system reliability  $[\overline{P}, \underline{P}]$  can be obtained by feeding the upper and lower bounds of the CDFs  $[\overline{F}_k, \underline{F}_k]$  into Eq. 5.4 [58]

$$\overline{P}\left(\bigcap_{k=1}^{K}\left\{C_{t}^{k}=l_{k}\right\}\right)=\prod_{k=1}^{K}\left(\binom{m_{k}}{l_{k}}\left[\overline{F}_{k}(t)\right]^{m_{k}-l_{k}}\left[1-\overline{F}_{k}(t)\right]^{l_{k}}\right)$$
(5.5a)

$$\underline{P}\left(\bigcap_{k=1}^{K}\left\{C_{t}^{k}=l_{k}\right\}\right)=\prod_{k=1}^{K}\left(\binom{m_{k}}{l_{k}}[\underline{F}_{k}(t)]^{m_{k}-l_{k}}[1-\underline{F}_{k}(t)]^{l_{k}}\right).$$
(5.5b)

Evaluation of the complete survival signature is a numerically demanding task. In a previous work we presented an approach where Monte Carlo simulation is used to reduce the number of structure function evaluations in Eq. 5.1 [94]. While this enabled the analysis of larger systems, each individual entry of the survival signature still requires a significant number of structure function evaluations. As the number of entries in the survival signature grows with increasing system size and number of component types this technique also reaches its limits. In the previous study, the numerical example with 306 nodes and 2 component types already required 27 hours of computation time while using 64 cores for parallel computation of survival signature entries and use them to fit a surrogate model. This surrogate model can then be used for the reliability analysis instead of the full survival signature.

## 5.3 Monotone Radial Basis Function Networks

This section presents the monotone radial basis function (RBF) networks which will be utilized as metamodels of the survival signature. RBF networks are a very simple type of artificial neural networks with only one hidden layer, and a linear output layer [138]. The name stems from the fact that radial basis functions are used as activation functions in the hidden layer. A distance function between the input and a fixed point known as a center is used to define these RBFs in  $\mathbb{R}^d$ . This distance is most commonly the Euclidean distance with a normalization constant in each dimension  $j \in \{1, \ldots, d\}$  defined as

$$||x - c|| = \sqrt{\sum_{j=1}^{d} \frac{(x_j - c_j)^2}{2\sigma_j^2}},$$
(5.6)

where  $x \in \mathbb{R}^d$  is the input vector. The spread of the radial basis functions is controlled by the normalization constant  $\sigma_j$ . The most commonly used radial basis function is the Gaussian function

$$\psi(||x-c||) = e^{-||x-c||^2}.$$
(5.7)

In an alternative notation, instead of including the spread in the distance function through the  $\sigma_j$  values, it can be directly included in the radial basis function, usually represented as a shape parameter  $\epsilon$ . For the Gaussian function this would be defined as follows

$$\psi(||x - c||) = e^{-\epsilon ||x - c||^2}.$$
(5.8)

However, this reduction to a single shape parameter reduces modeling flexibility of the radial basis functions when compared to the  $\sigma_j$  as these allow to vary the spread of the basis function in each dimension. For the remainder of this paper, we assume all radial basis functions to be Gaussian of the form defined in Eq. 5.7. Figure 5.1 presents the one dimensional Gaussian radial basis function and how the choice of  $\sigma$  influences the spread of the function. For a thorough discussion of radial basis functions refer to Buhmann [147].

An RBF network is designed based on N neurons each with their own center points  $c_i$  and associated weight  $w_i$  for  $i \in \{1, ..., N\}$  and defined as

$$y(x) = \sum_{i=1}^{N} w_i \psi(||x - c_i||).$$
(5.9)

Estimation of the weights  $w_i$  can be done through linear least squares because y is linear in the weights. Figure 5.2 shows a graphical representation of an RBF network.

Heimes and van Heuveln [139] have shown that normalizing RBF networks improves their extrapolation capabilities in comparison to regular (unnormalized) networks. For the remainder



Figure 5.1: Gaussian radial basis functions centered at c = 0.0 and the influence of different spread values. Note how the functions become less narrow with increasing  $\sigma$ .



Figure 5.2: Graphical representation of a radial basis function neural network. From left to right: input layer, hidden layer, linear output layer.

of this paper, the applied basis functions will always be considered normalized as

$$\hat{\psi}_i(x) = \frac{\psi(||x - c_i||)}{\sum_{i=1}^N \psi(||x - c_i||)}.$$
(5.10)

The output of the normalized radial basis function (NRBF) network is then defined as

$$y(x) = \sum_{i=1}^{N} w_i \hat{\psi}_i(x).$$
 (5.11)

In this study, we limit the NRBF network's center positions to a regular, uniform grid across the whole input domain. This makes it simpler to choose the  $\sigma_j$  shape parameters and considerably reduces the complexity of the monotonicity restrictions in the next step.

The NRBF network will later be utilised as a surrogate model for the survival signature. Since the survival signature is a monotone function, using a monotone surrogate model will in turn lead to a significantly better fit. Simple linear constraints on the weights can be used to enforce the monotonicity of an NRBF network. As shown by Hušek [140], only weights of center points lying on a line pointing in the direction of any of the d dimensions must be monotonic for the entire NRBF network to be monotonic. Note, that this assumption only holds for the Gaussian radial basis functions.

The optimal weights under these monotonic contraints are then found as the solution to the following constrained least squared optimization problem, assuming that there are M data points  $x_j$  with associated function values  $y_j$  for  $j \in \{1, \ldots, M\}$ :

$$\begin{array}{ll} \underset{w}{\text{minimize}} & ||\Psi w - y||_2^2 \\ \text{subject to} & w_p \le w_q, \ p, q \in \{1, \dots, N\}, \\ & \text{if } c_p^\alpha < c_q^\alpha, c_p^\beta = c_q^\beta, \alpha \ne \beta. \end{array}$$

$$(5.12)$$

Here, the superscripts  $\alpha, \beta \in \{1, \ldots, d\}$  refer to the coordinates in dimensions  $\alpha$  and  $\beta$  with  $w = [w_1, \ldots, w_N]^T$  and  $y = [y_1, \ldots, y_M]^T$ . The matrix  $\Psi \in \mathbb{R}^{M \times N}$  is defined as

$$\Psi_{ji} = \hat{\psi}_i(x_j). \tag{5.13}$$

As such, every weight is only bound by up to d constraints (one in each dimension; less at the edges of the domain). For example, a uniform grid of  $20 \times 20 = 400$  center points requires 760 constraints for the entire NRBF network to be monotonic.

This is a convex optimization problem which can be solved with any standard solver. In this work we apply the splitting cone solver (SCS) [141] in connection with Convex.jl [148].

# 5.4 Interval Predictor Models

For larger systems, even individual entries of the survival signature can require prohibitive amounts of structure function evaluations to compute Eq. 5.1 in order to obtain the data required to fit the NRBF network. For this reason, we resort to the previously introduced method [94] and use Monte Carlo simulation to approximate these entries. However, approximating these entries has uncertainty attached to it which must not be disregarded. This section presents the necessary theory on interval predictor models (IPM) [149] which we will later use to propagate the uncertainty of the NRBF approximation into bounds on the survival signature.

Where a regular model such as a NRBF network returns a single value, an IPM returns an interval in which the output is expected to fall. A parametric IPM is obtained as

$$I(x, P) = \{ y = p^T \xi(x), p \in P \},$$
(5.14)

where x is the input vector,  $\xi(x)$  is an arbitrary basis and p is a member of the hyper rectangle

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P defined by

$$P = \{p : p \le p \le \overline{p}\}.$$
(5.15)

Then, the IPM is given as

$$I(x,P) = [\underline{y}(x,\underline{p},\overline{p}), \overline{y}(x,\underline{p},\overline{p})], \qquad (5.16)$$

with y and  $\overline{y}$  being the lower and upper bounds of the IPM defined by

$$\underline{y}(x,\underline{p},\overline{p}) = \overline{p}^T \left(\frac{\xi(x) - |\xi(x)|}{2}\right) + \underline{p}^T \left(\frac{\xi(x) + |\xi(x)|}{2}\right)$$
(5.17a)

$$\overline{y}(x,\underline{p},\overline{p}) = \overline{p}^T \left(\frac{\xi(x) + |\xi(x)|}{2}\right) + \underline{p}^T \left(\frac{\xi(x) - |\xi(x)|}{2}\right).$$
(5.17b)

For the radial basis applied in this work the equations simplify to

$$y(x,p) = p^T \xi(x) \tag{5.18a}$$

$$\overline{y}(x,\overline{p}) = \overline{p}^T \xi(x), \qquad (5.18b)$$

since  $\xi(x) = |\xi(x)|$ .

The parameters p and  $\overline{p}$  are determined by solving the following optimization problem

$$\begin{array}{ll} \underset{\underline{p},\overline{p}}{\text{minimize}} & \frac{1}{M} \sum_{j}^{M} \delta_{y}(x_{j},\underline{p},\overline{p}) \\ \text{subject to} & \underline{y}(x_{j},\underline{p},\overline{p}) \leq y_{j} \\ & \overline{y}(x_{j},\underline{p},\overline{p}) \geq y_{j} \\ & p \leq \overline{p}, \end{array}$$
(5.19)

where  $(x_j, y_j)$  for  $j \in \{1, ..., M\}$  are the data points and  $\delta_y$  is the spread of the IPM, i.e. the separation between its limits defined as

$$\delta_y(x,\underline{p},\overline{p}) = |\xi(x)|^T (\overline{p} - \underline{p}).$$
(5.20)

As an example consider 200 data points generated from the function

$$y(x) = (6x - 2) \cdot \sin(2x) + g \tag{5.21}$$

with  $x \sim U(-3,3)$  and the noise generating term  $g \sim N(0,1)$ . We assume a linear combination of polynomials as the basis  $\xi(x) = [1, x, x^2, x^3, x^4, x^5, x^6, x^7, x^8]$  and solve the optimization problem in Eq. 5.19. Figure 5.3 presents the data points and the resulting IPM envelopes. The bounds contain all the data points and approximate the underlying function well.



Figure 5.3: Interval predictor model envelopes around the noisy data points generated from the true function.

#### 5.5 Imprecise Approximation of the Survival Signature

This section outlines the newly developed method to approximate the survival signature for very large systems. Eq. 5.1 demonstrates unequivocally that computing the survival signature is a combinatorial task, whose numerical demand significantly rises as the number of components and component types increases. As a result, for very large systems, analytical computing of the survival signature is impractical. We described a method for approximating the survival signature by utilizing percolation to remove insignificant portions of the signature and approximating the remaining entries with Monte Carlo simulation [94]. Although this made it possible to analyze larger systems, the method still necessitates a huge number of system assessments and will soon become computationally infeasible. In this article, we suggest a different approach in which the survival signature is approximated using a radial basis function network based on a few carefully chosen values. Additionally, an interval predictor model is used to propagate the uncertainty in the survival signature entries due to the Monte Carlo approximation, which is then reflected as bounds on the survival signature.

#### 5.5.1 Design of the NRBF network surrogate model

Similarly to the previously proposed technique, this new approach begins by using percolation theory to determine the critical threshold  $f_c$  and exclude a major fraction of the survival signature where the chance that the system functions is minimal, i.e. near to zero [94].

Then, the set of remaining survival signature entries  $\Omega$  is defined as all  $l_1, \ldots, l_K$  for  $l_k \in$ 

 $\{0, 1, \ldots, m_k\}$  and  $k \in \{1, \ldots, K\}$  where the following condition holds true

$$\sum_{k=1}^{K} l_k \ge (1 - f_c) \sum_{k=1}^{K} m_k.$$
(5.22)

To start, we calculate the survival signature for M initial data points spread uniformly over  $\Omega$ . Values where the number of required structure function evaluations exceeds the defined maximum number of samples  $N_{MC}$  are approximated using Monte Carlo simulation. The rest are computed exactly using the analytical formulation. This ensures good coverage of the input space for the first approximation. In addition, we create a uniform grid of centers  $c_i$  for  $i \in \{1, \ldots, N\}$  distributed over the entire domain of  $\Omega$ . The spread of the radial basis functions  $\sigma_j$  is chosen as the distance between two successive centers in the *j*th dimension, which has shown to yield good results. In the future optimal strategies for the spread selection should be devised. The solution to the optimization problem Eq. 5.12 yields the weights for the initial monotone NRBF model of the survival signature.

The surrogate model is then improved by selecting new values of the survival signature to be approximated. The Taylor expansion-based adaptive design (TEAD) [143], which is an exploration and exploitation technique based on nearest neighbor distances and Taylor expansion, is used to determine the new points. This allows to sufficiently cover the input space while also concentrating data in areas with the greatest changes in the survival signature in order to generate an accurate surrogate model with a small sample size. Each iteration of the TEAD choses a new point from  $\Omega$  and adds it to the M data points. Then the weights are updated by solving the optimization problem Eq. 5.12. When the change in weights falls below a predefined threshold three times in a row, the search for new points is terminated.

#### 5.5.2 Extension to an interval predictor model

After obtaining an adequate surrogate model for the survival signature, it is expanded to an interval predictor model. In contrast to regular models, which produce a single output value for any input, IPMs return an interval within which the value will likely fall [149]. The reason for the extension to the IPM is that by simply fitting an NRBF network to the approximated values of the survival signature the uncertainty of the Monte Carlo simulation, reflected in the coefficient of variation, would be discarded. Instead, this uncertainty is propagated through the IPM yielding bounds on the survival signature.

The IPM theory defined earlier is slightly adapted to the NRBF basis and the data points evaluated in the previous step. The IPM utilizes the same center locations  $c_i$  for the upper and lower bounds whose difference in output is only influenced by two different sets of weights  $\underline{w}$ 

and  $\overline{w}$ . The bounds are defined as

$$\overline{\Phi}(x,\overline{w}) = \Psi(x)^T \overline{w} \tag{5.23}$$

$$\underline{\Phi}(x,\underline{w}) = \Psi(x)^T \underline{w}, \qquad (5.24)$$

where  $\Psi(x) = [\hat{\psi}_1(x), \dots, \hat{\psi}_N(x)]$ . The parameters  $\underline{w}$  and  $\overline{w}$  are given by the following optimization problem

$$\begin{array}{ll} \underset{\underline{w},\overline{w}}{\text{minimize}} & \frac{1}{N} \sum_{j}^{N} \delta_{y}(x_{j}, \underline{w}, \overline{w}) \\ \text{subject to} & \underline{\Phi}(x_{j}, \underline{w}) \leq \underline{y}_{j} \\ & \overline{\Phi}(x_{j}, \overline{w}) \geq \overline{y}_{j} \\ & w < \overline{w}, \end{array} \tag{5.25}$$

where  $(x_j, [\underline{y}_j, \overline{y}_j])$  for  $j \in \{1, \ldots, M\}$  are the data points obtained in the previous step. The bounds  $\underline{y}_j$  and  $\overline{y}_j$  are computed from the survival signature entry approximations and the associated coefficient of variation  $cv_j$  by

$$y_{i} = \max\{y_{j} - y_{j} \cdot cv_{j}, 0.0\},$$
(5.26)

$$\overline{y}_j = \min\{y_j + y_j \cdot cv_j, 1.0\}.$$
(5.27)

In addition to the constraints in Eq. 5.25 we also invoke the monotonicity constraints of Eq. 5.12 on  $\underline{w}$  and  $\overline{w}$  in order to ensure monotonicity of the IPM envelopes.

After solving the optimization problem Eq. 5.25 to obtain the IPM, the bounds on the imprecise survival function can be computed from Eq. 5.3. Only two evaluations of the survival function are required, because both bounds of the IPM are monotone functions.

#### 5.5.3 Method validation

We validate the proposed method by applying it to an artificial toy problem and comparing the survival signature bounds obtained from the IPM approximation to the full Monte Carlo approximation. Consider a simple grid network as presented in Figure 5.4. We select n = 15and m = 15 and create a network with 225 nodes and 420 edges. The components are divided alternating into two types  $k_1 = [1, 3, 5, \ldots, 223]$  and  $k_2 = [2, 4, 6, \ldots, 225]$ . As structure function  $\varphi(\mathbf{x})$  we define the connectivity between the source node s = 1 and target node t = 225. The survival signature for this network contains 12882 entries of which the most numerically demanding entries have around 1.92e64 different combinations to evaluate. Since analytical evaluation of this survival signature is practically impossible, the newly developed method will be compared to the older full Monte Carlo method [94] with up to 10000 samples per entry and a target coefficient of variation of 1e-3. The TEAD for selecting additional points to compute is aborted once the L2-norm of the difference between the weights before and after adding the new point is less than 1e-3 three iterations in a row. Figure 5.5 shows the initial data points as well as the extra points selected by the TEAD algorithm. The graphic shows how the adaptive technique's new points are focused in areas with high survival signature relevance while choosing only a few points in areas where the survival signature is minimal. This ability to identify the essential section of the signature allows for accurate approximation with a small number of computed entries.



Figure 5.4: Simple grid network of size  $n \times m$  with component types alternating between nodes. The nodes labelled s and t are the source and target nodes.



Figure 5.5: Initial data points and adaptive points selected by the TEAD.

We compute the spread of the IPM signature as defined in Eq. 5.20 in order to assess its quality. Note, that the spread is computed based on all entries in  $\Omega$  not just the data points used to fit the IPM. The quality of the model improves with decreasing spread. The survival signature is approximated using different maximum samples sizes  $N_{MC}$  with the same uniform



Figure 5.6: Upper bounds of the IPM survival signature for the  $15 \times 15$  grid network using different samples sizes for individual entries.

**Table 5.1:** Spread and required data points for different sample sizes of the IPM survival signature for the  $15 \times 15$  grid network. The number of structure function evaluations is denoted as  $n_{\varphi}$ .

$N_{MC}$	M	$n_{\varphi}$	$\delta_y(x)$
100	796	79303	0.29674
1000	296	293003	0.02999
10000	153	1500003	0.00715

grid of 163 center points, 15 in each dimension of which 62 are excluded using the percolation condition in Eq. 5.22. The results in Tab. 5.1 show that the spread reduces with increasing sample size. It can also be seen, that the number of data points M required to accurately fit the model decreases as well. So while the cost of each individual entry rises with larger sample sizes, fewer entries must be computed overall. The table also presents the number of required structure function evaluations  $n_{\varphi}$ . Comparing this to the analytical solution where  $\approx 5.39e67$  evaluations are necessary shows how efficient this new method is. In comparison to the full Monte Carlo approximation with  $N_{MC} = 10000$  where 33 172 770 state vectors must be evaluated, it achieves a further reduction in function evaluations of almost 95%. Figure 5.6 presents the relevant part of the upper bound approximation using  $N_{MC} = 100$  and  $N_{MC} = 10000$  samples. It is clear to see how the approximation using only 100 samples per entry is very rough and estimates large portions of the survival signature to be 1.0 while using more samples per entry leads to a much more precise signature.

Finally, we assume failure time distributions for the two component types to assess the network reliability. Let the failures of component type 1 be distributed exponentially with failure rate  $\lambda = 1.0$ . The failure times for component type 2 follow a Weibull distribution with shape  $\alpha = 2.0$  and scale  $\theta = 1.0$ . Because of the survival signature's monotonicity, we can



Figure 5.7: Bounds on the reliability of the  $15 \times 15$  grid network for the different IPM survival signatures and the Monte Carlo approximation. A closer view from t = 0.0 to t = 0.15 is shown on the right.

simply evaluate Eq. 5.4 for the upper and lower bounds of the signature to obtain the bounds on the reliability. Figure 5.7 presents the reliability using the three different IPM approximations and compares them to the full Monte Carlo approximation. The plots show clearly how the bounds on the reliability shrink around the Monte Carlo solution when increasing the number of samples. Although only a rough estimate, even the approximation just using 100 samples is bounded around the Monte Carlo solution.

# 5.6 Numerical Example

In this section we apply the proposed technique to a numerical example. The Berlin S- and U-Bahn system is used as an example as presented in [94]. The topology of the network is presented in Fig. 5.8. The total network is made up of 306 nodes and 350 edges. The nodes are classified into three categories based on their degree, with type 1 consisting of nodes with degree of two or less, type 2 of nodes with a degree greater than two but lower than five and component type 3 of nodes having a degree of five or higher. As a result, there are 245 nodes of type 1, 53 of type 2 and 8 of type 3. This network's entire survival signature contains 119 556 entries.

We define a structure function based on the loss of network efficiency. In this context, network efficiency for a network G with n nodes is defined as

$$E(G) = \frac{1}{n(n-1)} \sum_{u \neq v \in G} \frac{1}{d_{uv}},$$
(5.28)

where  $d_{uv}$  denotes the length of the shortest path between nodes u and v [134]. The shortest paths between all nodes can be efficiently calculated using the *Floyd-Warshall* algorithm [135].
The network is assumed to fail once the loss of efficiency exceeds 50% as given by

$$\varphi(\mathbf{x}) = \frac{E(G(\mathbf{x}))}{E(G)} < 0.5.$$
(5.29)

Although the *Floyd-Warshall* algorithm is very efficient, this structure function has a much higher numerical demand than the one based on s-t-connectivity in the previous section. Because of this and the large size of the survival signature computing it analytically is impossible and even the Monte Carlo simulation requires vast amounts of computation time.



**Figure 5.8:** Topology of the Berlin metro system with 306 nodes. Nodes marked as • represent stations with two or three connections. Stations with five or more connections are marked with •. Adapted from Salomon et al. [72].

The survival signature approximation begins with percolation to obtain the set of candidate points  $\Omega$ . The critical threshold  $f_c \approx 0.39550$  reduces  $\Omega$  from 119556 to 45441. 2250 center points  $c_i$  are generated uniformly over the domain of  $\Omega$ , of which 603 are excluded using Eq. 5.22, leaving 1647 centers. Then, 125 starting points are uniformly selected from  $\Omega$ . The TEAD is used to choose new points until the weights change is less than 1e-3 for three consecutive points. After selecting 286 new points the algorithm aborts. The survival signature entries are approximated using 10 000 Monte Carlo samples and a target coefficient of variation of 1e-3 for all points.

We assume that component failure times are exponentially distributed with  $\lambda_1 = 0.3$ ,  $\lambda_2 = 0.4$ 



Figure 5.9: Bounds of the IPM surrogate model compared to the Monte Carlo approximation.

and  $\lambda_3 = 0.4$ . These values were arbitrarily chosen for demonstrative purposes and have no real world relevance. In Figure 5.9, the resulting bounds on the survival function are compared to the reliability of the entire Monte Carlo approximation. Only 406 out of the 119556 survival signature values have been computed to build the IPM. This presents a significant reduction in numerical effort. In fact, only 3960256 structure function evaluations are required compared to the 385919420 of the Monte Carlo method, enabling the analysis of even larger networks than previously possible.

Next, rather than assuming precise probabilities for the component failure times, we represent them as p-boxes and create intervals for the distribution parameters as a result. The intervals for the exponential distribution parameters are chosen as  $\lambda_1 \in [0.25, 0.35]$ ,  $\lambda_2 \in [0.35, 0.45]$ and  $\lambda_3 \in [0.45, 0.55]$ . In this example, where only exponential distributions are used, we can obtain the lower and upper bounds of the reliability directly by injecting the upper and lower bounds of the parameters and IPM survival signature into Eq. 5.5. In cases where p-boxes of distributions with multiple parameters such as the Weibull distribution are involved, the reliability bounds can be calculated using a double-loop approach or optimization. Figure 5.10 depicts the bounds on the reliability using the IPM survival signature and the full Monte Carlo approximation. The graphic shows how the upper and lower bounds on the survival signature resulting from only the imprecise distributions are further widened when combined with the imprecise survival signature.

# 5.7 Conclusion

This research proposes a novel way to approximation the survival signature using normalized radial basis function networks and interval predictor models as surrogate models. Given only a small fraction of the evaluated signature entries, NRBF networks can reliably predict the whole



Figure 5.10: Bounds on the reliability of the Berlin metro system with imprecise failure time distributions for the IPM and the Monte Carlo approach.

survival signature. The uncertainty introduced by using Monte Carlo simulation to approximate individual entries is efficiently propagated through the IPM to produce survival signature bounds. An adaptive strategy for selecting data points for the surrogate model ensures excellent accuracy while keeping the numerical demand low. The effectivity of the developed method was demonstrated by applying it to the analysis of a simple designed toy example as well as a larger real world example based on the metro system of Berlin and comparing the results to those of the previously presented full Monte Carlo simulation technique. By combining the imprecise survival signature with imprecise probabilities a fully imprecise survival function is devised. The code developed for this work is added to the open source Julia package *SurvivalSignature.jl* and freely available to everyone [99].

In future work we will focus on improving the NRBF fit. While the number of centers and the spread selected in this study provide a good basis, optimizing these in the future would improve the design. Exploring alternative strategies to the TEAD for adaptively selecting the new points should also be considered. Furthermore, scalability for example with more than three dimensions must be investigated.

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# 6 Multidimensional Resilience Decision-Making for Complex and Substructured Systems

# Multidimensional Resilience Decision-Making for Complex and Substructured Systems

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## Abstract

Complex systems, such as infrastructure networks, industrial plants and jet engines, are of paramount importance to modern societies. However, these systems are subject to a variety of different threats. Novel research focuses not only on monitoring and improving the robustness and reliability of systems, but also on their recoverability from adverse events. The concept of resilience encompasses precisely these aspects. However, efficient resilience analysis for the modern systems of our societies is becoming more and more challenging. Due to their increasing complexity, system components frequently exhibit significant complexity of their own, requiring them to be modeled as systems, i.e., subsystems. Therefore, efficient resilience analysis approaches are needed to address this emerging challenge.

This work presents an efficient resilience decision-making procedure for complex and substructured systems. A novel methodology is derived by bringing together two methods from the fields of reliability analysis and modern resilience assessment. A resilience decision-making framework and the concept of survival signature are extended and merged, providing an efficient approach for quantifying the resilience of complex, large and substructured systems subject to monetary restrictions. The new approach combines both of the advantageous characteristics of its two original components: A direct comparison between various resilience-enhancing options from a multidimensional search space, leading to an optimal trade-off with respect to the system resilience and a significant reduction of the computational effort due to the separation property of the survival signature, once a subsystem structure has been computed, any possible characterization of the probabilistic part can be validated with no need to recompute the structure.

The developed methods are applied to the functional model of a multistage high-speed axial compressor and two substructured systems of increasing complexity, providing accurate results and demonstrating efficiency and general applicability.

**Keywords:** Resilience, Decision-making, Survival signature, Reliability, Complex systems, Substructured systems.

# 6.1 Introduction

In today's highly developed societies, complex systems, such as infrastructure networks, industrial plants and jet engines are both ubiquitous and of paramount importance to the functioning of these modern societies. It is evident that these systems are exposed to a variety of harmful influences of natural, technical and anthropogenic origin. At the same time, as Punzo et al. highlight in [150], "It is an undeniable fact that modern day systems are more integrated, more interdependent, evolve at faster pace and, in a word, are more complex than the systems of the previous century [...]." Considering this high and increasing system complexity, it is impractical to detect and prevent all potential negative impacts. Therefore, it is essential that new developments in engineering focus not only on monitoring and improving the robustness and reliability of systems, but also on their recoverability after adverse events [151]. The concept of resilience encompasses these aspects: analyzing and optimizing robustness, reliability and recovery of systems, from a technical and economic perspective [152–154]. Applying resilience to engineered systems leads to a paradigm shift. Secure systems cannot solely rely on strategies to prevent failures, but must include strategies for efficient recovery in the event of failure as well, see, e.g., [155, 156].

In engineering, the concept of resilience has steadily gained popularity in recent years [74, 150, 157]. The notion of "resilience" appears in various fields such as ecology, economics, and psychology, as well as in the context of mechanical systems, and is derived from the Latin word "resilire," which means "to bounce back." The concept of resilience was first introduced by Holling in the field of ecological systems [158]. Although several other definitions by various scientists followed, most of them have certain key aspects in common that were already captured by Holling's early definition [159–163]. In [164], Ayyub provides a literature review and develops a comprehensive definition of resilience in the context of complex systems based on the content of the Presidential Policy Directive (PPD) on critical infrastructure security and resilience [165]. His definition provides a solid foundation for quantifying resilience.

Numerous options exist for improving the resilience of complex systems. However, resources are not unlimited and resilience cannot be increased at will. Therefore, it is essential not only to be able to distinguish and weigh between a variety of different resilience-enhancing measures, but to also consider their monetary aspects [166, 167]. In [72], Salomon et al. present a method for identifying the most cost-effective allocation of resilience-enhancing investments by merging the resilience metric of [76] and an adaptation of the systemic risk measure of [77]. Their approach allows for a direct comparison of the effects of heterogeneous controls on the resilience of a system over an arbitrary time period in a two-dimensional parameter space.

Additionally, current research in the context of resilience focuses on improved resilience quantification measures, as proposed in [168], and overarching frameworks for stakeholder decision-making, e.g., for transportation networks in the presence of seismic hazards [169]. For a comprehensive literature review on resilience assessment frameworks that balance resources and performance, see [170]. Other researchers recently studied the complexity of realistic infrastructure systems, failure consequences, recovery sequences, and varying external effects. In [171], for example, the authors revealed the vast complexity of modern critical infrastructures and their multi-factorial nature as cyber-human-physical systems and studied appropriate modeling and resilience analysis approaches. Further, the works [172] and [173] are concerned with the effects on decision-making when considering stakeholder preferences or enhancement and recovery strategies. External effects and challenges arising from climate change were studied in the context of resilience, e.g., in [174].

Various technical and infrastructural systems in today's society are large and complex in

nature. In particular, when system components have such complexity that they themselves need to be modeled as systems, so-called systems of systems [175, 176], resulting in a significantly high number of components. This is in accordance to Batty, who highlights "A very simple definition of a complex system is 'a system that is composed of complex systems'" [177]. As each of the subsystems affects the top-level system under consideration, this causes a significant increase in computational effort for system analysis and constitutes a major challenge [178, 179]. Therefore, it is particularly important to have tools capable of efficiently assessing all three resilience phases. Typically the reliability phase involves the most system evaluations, in particular when various different system configurations need to be assessed that have an impact on the probability structure of the subsystems and thus on the overall system. Therefore, a particularly efficient analysis approach is required for this phase.

An efficient approach to modeling the reliability of systems with multiple component types is provided by the concept of survival signature, introduced and discussed in [27, 180] by Coolen and Coolen-Maturi. Its major benefit over conventional approaches is the separation of the system structure from the probabilistic properties of the system components. Once the system structure has been analyzed, any possible probabilistic characterization can be tested without having to reevaluate any system states. Consequently, this approach reduces the computational cost of repeated model evaluations typically required in design and maintenance processes [37]. Current research is focused on multi-state components [37], common cause failures [33], multiple failure modes and dependent failures [32], approximation techniques for large systems [94] and reliability analysis in consideration of imprecision [181].

In this paper, theoretical fundamentals are summarized and the resilience decision-making method introduced in [72] is extended to multidimensional parameter spaces. Next, a novel and encompassing methodology is developed, consisting of its two major ingredients, the extended resilience decision-making method and the survival signature. This allows for an efficient and multidimensional resilience analysis of complex, large and substructured systems. The extension and novel methodology are then applied to a functional model of a multistage high-speed axial compressor, an arbitrary complex system as well as the U-Bahn and S-Bahn system of Berlin, to prove general applicability.

# 6.2 Resilience decision-making

Assessing the resilience of complex systems subject to technical or monetary constraints requires a sophisticated methodology to efficiently derive optimal decisions. In [72], Salomon et al. propose a versatile approach with three key elements, including a metric for resilience quantification, an adapted systemic risk measure, and a grid search algorithm that increases computational efficiency.

# 6.2.1 Resilience quantification

A suitable quantitative measure of resilience is a fundamental prerequisite for assessing resilience in engineering. In [74, 75, 182], the authors provide a comprehensive overview of resilience metrics in a systemic context. While Bergström et al. emphasize the general concept of resilience in the current literature as a critical link between increasing complexity of systems and their risk [74], Sun et al. focus on resilience of infrastructures and highlight the close link between resilience and functionality respectively performance measures [182]. Hosseini et al. proposed a general scheme for categorizing resilience quantification approaches [75]. In summary, performance-based resilience metrics are most widely used. These determine the resilience of a system by comparing its performance before and after a destructive event. Further subcategories relate to time in-/dependence and characterization as deterministic or probabilistic processes.

According to [183] and [75], performance-based and time-dependent metrics are capable of considering the following system and transition states before and after a disruptive event:

- The original stable state, i.e., the duration until a disruptive event occurs, relying on the reliability of the system.
- The system vulnerability, represented by a loss of performance after the occurrence of a disruptive event and the robustness counteracting the vulnerability and mitigating this performance loss. Both are governed by degradation characteristics of the system components.
- The system recoverability, characterized by the disrupted state of the system and its recovery to a new stable state.

An illustration of these phases and transitions is shown in Fig. 6.1. The performance level of the new stable state might differ from the performance level of the original state.

The area of performance loss between original and new stable state in Fig. 6.1 refers to the well-known principle of "resilience triangle" introduced by Bruneau et al. [73], as illustrated in Fig. 6.2. In their work, Bruneau et al. proposed a time-dependent, performance-based, and deterministic metric for resilience loss of a community due to seismic disasters as follows. Let  $t_0$  be the time a disruptive event occurs and  $t_1$  be the time of completed recovery. Further, Q(t) denotes the quality of the community infrastructure at time t, specifying the type of system performance. Then, the metric is defined as:

$$R_{Br} = \int_{t_0}^{t_1} [100 - Q(t)] dt.$$
(6.1)

Note that the system performance is compared with a time-independent ideal performance of 100 in the considered interval of performance loss. The approach forms a strong basis for



Figure 6.1: In the evolution of a system before and after the impact of a disruptive event, different phases can be distinguished: (i) the original stable state, (ii) disruptive impact, vulnerability, robustness, (iii) disrupted state and recovery; adapted from [183].

several, later proposed metrics in various contexts, see [184–186].



Figure 6.2: Resilience triangle; adapted from [73].

In [72], Salomon et al. utilize the probabilistic and time-dependent metric developed by Ouyang et al. [76]. The metric is defined as the expected ratio of the integral over the actual system performance Q(t) from 0 to a given time T and the corresponding integral of a target system performance  $\mathcal{T}Q(t)$  over the same time interval:

$$Res = E[Y], (6.2)$$

where

$$Y = \frac{\int_0^T Q(t)dt}{\int_0^T \mathcal{T}Q(t)dt}.$$
(6.3)

Thereby, the system performance Q(t) is a stochastic process. The target system performance  $\mathcal{T}Q(t)$  can be generally considered as a stochastic process as well, however, for simplicity,  $\mathcal{T}Q(t)$  may be assumed as a non-random and constant quantity  $\mathcal{T}Q$ . Assuming that the actual system performance does not exceed the target performance, the metric takes values between 0 and 1. For Res = 1, the system performance is equal to the target system performance, while Res = 0 indicates that the system is not functioning during the entire period under consideration.

#### 6.2.2 Adapted systemic risk measure

In [77], Feinstein et al. proposed a general approach to measuring systemic risk, e.g., pursued in finance [187]. In [72], this risk measure was adapted and extended for the application to engineering systems as summarized in this section. The adapted systemic risk measure comprises a descriptive input-output model and an acceptance criterion that represents normative resilience standards of a regulatory authority.

Let a system be given with m components  $i \in \{1, \ldots, m\}$  of type  $k_i \in \{1, 2, \ldots, K\} \subseteq \mathbb{N}$  with e properties that influence the system performance Q(t). These properties, hereafter referred to as "endowment properties", affect system resilience and can be improved through capital allocations. Then, the component i is characterized by

$$(\boldsymbol{a}_i; k_i) = (\eta_{i1}, \eta_{i2}, \dots, \eta_{ie}; k_i) \in \mathbb{R}^{(1 \times e)} \times \mathbb{N},$$
(6.4)

where  $(\eta_{i1}, \eta_{i2}, \ldots, \eta_{ie})$  are the numerical values of the *e* relevant endowment properties. Consequently, the entire system can be described by a tuple, consisting of the matrix  $\mathbf{A} \in \mathbb{R}^{(m \times e)}$ and the column vector  $\mathbf{z} \in \mathbb{N}^m$  that captures the component types:

$$(\boldsymbol{A}; \boldsymbol{z}) = \begin{pmatrix} \eta_{11} & \eta_{12} & \cdots & \eta_{1e}; & z_1 \\ \eta_{21} & \eta_{22} & \cdots & \eta_{2e}; & z_2 \\ \vdots & \vdots & & \vdots & \vdots \\ \eta_{m1} & \eta_{m2} & \cdots & \eta_{me}; & z_m \end{pmatrix}.$$
(6.5)

The system under consideration is defined via a descriptive, non-decreasing input-output model  $Y = Y_{(\boldsymbol{A};\boldsymbol{z})}$  that is specified by this tuple and relates endowment properties to system performance. With respect to Eq. 6.2, the model output is specified as  $Y = Y_{(\boldsymbol{A};\boldsymbol{z})}$  dependent on the current endowment allocation  $(\boldsymbol{A};\boldsymbol{z})$ .

Further, consider the following specific acceptance set

$$\mathcal{A} = \{ X \in \mathcal{X} \mid E[X] \ge \alpha \}$$
(6.6)

for a normalized model output X and its expected value E[X] with  $\alpha \in [0,1]$ . Correspondingly,

the risk measure is defined as

$$R(Y) = \left\{ \boldsymbol{A} \in \mathbb{R}^{m \times e} \mid Y_{(\boldsymbol{A};\boldsymbol{z})} \in \mathcal{A} \right\},$$
(6.7)

that is the set of all endowment property allocations A such that the system reaches a resilience value greater or equal to  $\alpha$ .

In practice, it might be necessary to impose structural restrictions on the matrix in Eq. 6.5. For example, consider the case that any component *i* of a specific type should be configured in the same way, i.e., the row vectors  $\mathbf{a}_i$  are claimed to be equal. In [77], Feinstein et al. capture such constraints by monotonously increasing functions  $g_z : \mathbb{R}^p \to \mathbb{R}^{(m \times e)}, a' \mapsto (A; z)$ with  $z \in \mathbb{R}^m$  denoting the component types. Such a function maps a lower-dimensional set of parameters  $a' \in \mathbb{R}^p$  to the system description given in Eq. 6.5.

#### 6.2.3 Grid search algorithm and the curse of dimensionality

According to [77] and [72], the measure of systemic risk might be determined via a combination of a grid search algorithm and stochastic simulations. The grid search algorithm operates in the space of all possible endowments, while stochastic simulations are employed to evaluate system resilience for the endowment allocations according to the grid search algorithm. The probabilistic resilience metric (Eq. 6.2 and Eq. 6.3) is estimated by means of Monte Carlo simulation. The grid search algorithm given in [77] consists of two phases and can be recapitulated as follows:

- (I) Search along the main diagonal of the space of endowment properties until the first acceptable combination is found based on the adapted systemic risk measure.
- (II) Identify the Pareto front between the set of acceptable endowments R(Y) and its complement  $R(Y)^c$  starting at the first accepted allocation.

The algorithm allows to compute the entirety of R(Y) while significantly reducing the computational cost due to the assumed monotonicity property of the input-output model  $Y_{(A;z)}$ given in Sec. 6.2.2. For a detailed description of a grid search algorithm for two dimensional problems, see [77], Ch. 4.

In [72] this algorithm was included in the resilience decision-making method and applied to case studies with two dimensional parameter spaces. In their work [77], Feinstein et al. point out that the grid search algorithm is applicable to higher dimensional problems "[...] at the price of substantially larger computation times and required memory capacity.". However, when analyzing real technical systems, it is often inevitable to consider a large number of influencing factors and thus a higher dimensionality of the parameter space. Therefore, in Sec. 6.5, an extension of the previously proposed resilience decision-making methodology to *n*-dimensional problems is applied to a four-dimensional functional model of an axial compressor and, in Sec. 6.7, as part of the novel methodology proposed in Sec. 6.4, it is applied to the *U-Bahn* and *S-Bahn* system of Berlin, addressing a five-dimensional problem.

# 6.3 Concept of survival signature

Introduced in [27], the concept of survival signature allows to compute the survival function of a system with multiple component types and attracted increasing attention for its advantageous features over the last decade. One of its merits is the high efficiency in repeated model evaluations due to the separation of the topological system reliability and the probability structure of system component failures. At the same time, the survival signature radically condenses information on topology. System components are of one type if their failure times are independent and identically distributed (*iid*) or exchangeable. This differentiation is important when it comes to modeling dependent component failure times [180]. A brief recap of the concept is provided in the following subsections. Detailed information about both the derivation of the concept and further applications can be found in [27, 58, 180].

#### 6.3.1 Structure function

Let a system be given consisting of m components of a single type. Further, let  $\boldsymbol{x} = (x_1, x_2, \ldots, x_m) \in \{0, 1\}^m$  define the corresponding state vector of the m components, where  $x_i = 1$  indicates a functioning state of the *i*-th component and  $x_i = 0$  indicates a non-functioning state. Then, the structure function  $\phi$  is a function of the state vector  $\boldsymbol{x}$  defining the operating status of the considered system:  $\phi = \phi(\boldsymbol{x}) : \{0, 1\}^m \to \{0, 1\}$ . Accordingly,  $\phi(\boldsymbol{x}) = 1$  denotes a functioning system and  $\phi(\boldsymbol{x}) = 0$  specifies a non-functioning system.

Suppose that a system consists of components of more than one type, i.e.,  $K \ge 2$ . Then, the quantity of system components is denoted by  $m = \sum_{k=1}^{K} m_k$ , where  $m_k$  is the number of components of type  $k \in \{1, 2, ..., K\}$ . Correspondingly, the state vector for each type is given by  $\boldsymbol{x}^k = (x_1^k, x_2^k, ..., x_{m_k}^k)$ .

# 6.3.2 Survival signature

The survival signature summarizes the probability that a system is functioning as a function solely depending on the number of functioning components  $l_k$  per component type  $k \in \{1, 2, ..., K\}$ . Assuming the failure times within a component type to be *iid* or exchangeable, the survival signature is defined as:

$$\Phi(l_1, l_2, \dots, l_K) = \left[\prod_{k=1}^K \binom{m_k}{l_k}^{-1}\right] \times \sum_{\boldsymbol{x} \in S_{l_1, l_2, \dots, l_K}} \phi(\boldsymbol{x}),$$
(6.8)

where  $\binom{m_k}{l_k}$  corresponds to the total number of state vectors  $\boldsymbol{x}^k$  of type k and  $S_{l_1,l_2,...,l_K}$  denotes the set of all state vectors of the entire system for which  $l_k = \sum_{i=1}^{m_k} x_i^k$ . Consequently, the survival signature depends only on the topological reliability of the system, independent of the time-dependent failure behavior of its components that is described in Sec. 6.3.3. For more information on claimed exchangeability in practice, see [180, 181].

#### 6.3.3 Probability structure

The probability structure of system components specifies the probability that a certain number of components of type k is functioning at time t. Accordingly,  $C_k(t) \in \{0, 1, ..., m_k\}$  represents the number of components of type k in a functioning state at time t. Further, assume the probability distribution for the failure times of type k to be known with  $F_k(t)$ , denoting the corresponding cumulative distribution function. Then,

$$P\left(\bigcap_{k=1}^{K} \{C_{k}(t) = l_{k}\}\right) = \prod_{k=1}^{K} P\left(C_{k}(t) = l_{k}\right)$$

$$= \prod_{k=1}^{K} \binom{m_{k}}{l_{k}} [F_{k}(t)]^{m_{k}-l_{k}} [1 - F_{k}(t)]^{l_{k}}$$
(6.9)

describes the probability structure of the system, regardless of its topology.

# 6.3.4 Survival function

The survival function describes the probability of a system being in a functioning state at time t and results from Sec. 6.3.2 and 6.3.3 as:

$$P(T_s > t) = \sum_{l_1=0}^{m_1} \dots \sum_{l_K=0}^{m_K} \Phi(l_1, l_2, \dots, l_K) \times P\left(\bigcap_{k=1}^K \{C_k(t) = l_k\}\right),$$
(6.10)

where  $T_s$  denotes the random system failure time. Clearly, the concept of survival signature separates the time-independent topological reliability and the time-dependent probability structure. Thus, the survival signature, calculated once in a pre-processing step, can be reused for further evaluations of the survival function, which are necessary, for example, when analyzing a variety of different system configurations that affect the probability structure given a constant system topology. The survival signature can be stored in a matrix, thereby summarizing the topological reliability. The utilization of this matrix circumvents the repeated evaluation of the often computationally expensive structure function. Note that it is precisely these properties of the survival signature concept that provide an important advantage over conventional methods when system simulations need to be performed repeatedly [37]. In terms of computational demand, Monte Carlo simulation may be used to approximate the survival signature of large systems [94].

# 6.4 Proposed methodology

In this section, the proposed methodology for computationally efficient resilience analysis in the context of complex substructured systems is illustrated. The approach integrates the concept of survival signature described in Sec. 6.3 into the resilience decision-making framework recapped in Sec. 6.2. First, the preparation of the complex system by means of a formalized substructuring approach is presented. Second, the novel methodology is proposed.

### 6.4.1 Definition of substructured systems

Assume a substructured system S that is composed of a set of subsystems and a set of components. The subsystems can again be comprised of further subsystems and components. This substructuring approach can be conducted for  $L \ge 1$  levels of subsystems, where only components exist at level L + 1. Components are directly associated with probability distributions describing their time-dependent probabilistic behavior. Note that the level 1 relates to the overall system level. Figure 6.3 illustrates the substructuring concept.



Figure 6.3: Illustration of the proposed substructuring concept.

Let there be  $n^v$  subsystems  $\mathcal{S}_1^v, \mathcal{S}_2^v, \ldots, \mathcal{S}_{n^v}^v$  and  $m^v$  components  $\mathcal{C}_1^v, \mathcal{C}_2^v, \ldots, \mathcal{C}_{m^v}^v$  at level  $v = 1, 2, \ldots, L$ . During the analysis, the information on component behavior is propagated from level L+1 to level 1 before determining the state  $s^0$  of the overall system  $\mathcal{S}$  in dependence on various topological (sub)system structures. In the context of the resilience framework in Sec. 6.2, the state  $s^0 \in S \subseteq \mathbb{R}^+$  with state space S of the overall system S corresponds to the system performance Q(t) that is basis for the resilience measure Res, see Eq. 6.2. Note that multiple resilience analyses might be conducted for various Q(t). The quantity  $s^0$  indicates system functionality from an ordered perspective and depends on the functionality of its directly subordinate subsystems and components. Given level  $v = 1, \ldots, L$ , the dependency of the (sub)system state  $s_i^v$  on the state vector  $\boldsymbol{x}_j^v$  is modeled via the mapping  $s_j^v = \phi_j^v(\boldsymbol{x}_j^v) \in \{0,1\}$ , where  $\phi_j^v$  is a structure function, i.e., a topological rule for system functioning as presented in Sec. 6.3.1. The state vector is introduced as  $\boldsymbol{x}_j^v = (s_1^w, s_2^w, \ldots, s_{n_j^w}^w, c_1^w, c_2^w, \ldots, c_{m_j^w}^w)$  for the *j*-th subsystem at level v with  $j = 1, 2, ..., n^v$  and w = v + 1. Thereby,  $s_p^w, c_q^w \in \{0, 1\}$  denote the functionality of the p-th subsystem and q-th component, respectively. Further,  $n_i^w$  is the number of subsystems at level w contained in subsystem j at level v and  $\sum_{i}^{n^{v}} n_{i}^{w} = n^{w}$ . Analogously,  $m_i^w$  has the equivalent interpretation for components. At level v = 1, the notation reduces to  $s^0 = \phi^0(\boldsymbol{x}^0)$ . The state vectors at level L comprises only component states as  $\boldsymbol{x}_{j}^{L} = (c_{1}^{w}, c_{2}^{w}, \dots, c_{m_{i}^{w}}^{w})$  with  $j = 1, 2, \dots, n^{L}, c_{i}^{w} \in \{0, 1\}$  and w = L + 1.

The probability distributions governing the component states  $c_i^v$  are assumed to be known as CDF  $F_k(t)$  for given component type k according to Sec. 6.3.3. Note that different subsystems might rely on the same component types. The assumption  $s_j^v, c_i^v \in \{0, 1\}$  is due to the fact that the concept of survival signature is based on a binary-state consideration. However, multiple researchers work on extensions of the concept to a discrete or continuous multi-state consideration, see e.g. [30, 188–190].

#### 6.4.2 Extension of the adapted systemic risk measure

In the resilience analysis of complex, substructured systems, it may be important that endowments can be formally assigned not only to system components but to other system structures, such as subsystems. To enable the incorporation of such endowment assignments in the novel methodology, the adapted systemic risk measure, cf. Sec. 6.2.2, is extended as follows.

Let a system, in addition to its m components, be given with a total of n subsystems  $j \in \{1, \ldots, n\}$  of  $b_j \in \{1, 2, \ldots, B\} \subseteq \mathbb{N}$  types over all system levels L with d endowment properties that influence the system performance Q(t). Then, the subsystem j is characterized by

$$(\mathcal{S}_j; b_j) = (\xi_{j1}, \xi_{j2}, \dots, \xi_{jd}; b_j) \in \mathbb{R}^{(1 \times d)} \times \mathbb{N},$$

$$(6.11)$$

where  $(\xi_{j1}, \xi_{j2}, \ldots, \xi_{jd}; b_j)$  are the numerical values of the *d* relevant endowment properties. The entire system is then, in addition to the description by the tuple consisting of the matrix  $\mathbf{A} \in \mathbb{R}^{(m \times e)}$  and the column vector  $\mathbf{z} \in \mathbb{N}^m$ , capturing the components, described by the tuple composed of the matrix  $\mathbf{D} \in \mathbb{R}^{(n \times d)}$  and the column vector  $\mathbf{h} \in \mathbb{N}^n$ , capturing the subsystems:

$$(\boldsymbol{D};\boldsymbol{h}) = \begin{pmatrix} \xi_{11} & \xi_{12} & \cdots & \xi_{1d}; & h_1 \\ \xi_{21} & \xi_{22} & \cdots & \xi_{2d}; & h_2 \\ \vdots & \vdots & & \vdots & \vdots \\ \xi_{n1} & \xi_{n2} & \cdots & \xi_{nd}; & h_n \end{pmatrix}.$$
(6.12)

The system under consideration is defined via the descriptive, non-decreasing input-output model  $Y = Y_{(\boldsymbol{A};\boldsymbol{z}),(\boldsymbol{D};\boldsymbol{h})}$  that is specified by both tuples and relates endowment properties to system performance. Again, with respect to Eq. 6.2, the model output is specified as  $Y = Y_{(\boldsymbol{A};\boldsymbol{z}),(\boldsymbol{D};\boldsymbol{h})}$  dependent on the current endowment allocation for components  $(\boldsymbol{A};\boldsymbol{z})$  and subsystems  $(\boldsymbol{D};\boldsymbol{h})$ . Then, with the specific acceptance set  $\mathcal{A}$  from Eq. 6.6, the extended adapted systemic risk measure is defined as

$$R(Y) = \left\{ \boldsymbol{A} \in \mathbb{R}^{m \times e}, \boldsymbol{D} \in \mathbb{R}^{(n \times d)} \mid Y_{(\boldsymbol{A};\boldsymbol{z}),(\boldsymbol{D};\boldsymbol{h})} \in \mathcal{A} \right\},$$
(6.13)

that is the set of all endowment property allocations A and D such that the system reaches a resilience value greater or equal to  $\alpha$ . Note that in this manner, equivalently, any performance-

influencing endowments, of any system structures, or even endowments independent of system structures, can be incorporated into the resilience decision-making analysis.

#### 6.4.3 Augmentation of the resilience analysis

The system resilience *Res* is governed by the reliability, robustness and recoverability of a system as illustrated in Fig. 6.1. The magnitude of these quantities is influenced by the endowment allocations that are captured in the tuples (A; z) and (D; h). The assigned resilience-enhancing endowment properties  $(\eta_{i1}, \eta_{i2}, \ldots, \eta_{im})$  and  $(\xi_{j1}, \xi_{j2}, \ldots, \xi_{jd})$  can either relate to a specific quantity or a subset of the three quantities and correspond to different implementations in the overall system performance model, i.e., input-output model  $Y_{(A;z),(D;h)}$ .

The reliability is typically the most computationally challenging quantity when evaluating system resilience *Res.* Thus, this part of the computation is augmented by the concept of survival signature with its advantageous separation and compact storage properties as well as the fundamental substructuring approach proposed in the previous Sec. 6.4.1 in order to enable efficient resilience analyses of large and highly complex systems.

In a pre-processing step, the survival signatures  $\Phi_j^v(l_1, l_2, \ldots, l_K)$  of the  $n = \sum_v^L n^v$  subsystems  $S_j^v$  are computed based on the corresponding structure functions  $\phi_j^v$  as described in Sec. 6.3.2. Subsequently, the survival signatures are utilized to efficiently retrieve the topological subsystem reliability (online) for varying endowment configurations.

In order to identify the set of all acceptable endowments R(Y), repeated evaluations of  $Y_{(A;z),(D;h)}$  are required according to the grid search algorithm – various endowment allocations in the search space spanned over discretized numerical values of  $A \in \mathbb{R}^{m \times e}$  with  $m = \sum_{v}^{L+1} m^{v}$  and  $D \in \mathbb{R}^{(n \times d)}$  with  $n = \sum_{v}^{L+1} n^{v}$  need to be evaluated analogous to Sec. 6.2.3. In each evaluation N stochastic simulations of  $Y_{(A;z),(D;h)}$  have to be performed to obtain E[Y], see Eq. 6.2, and corresponding status assignments according to the acceptance set  $\mathcal{A}$  in Eq. 6.6. Given the number of dimensions that need to be evaluated according to the grid search algorithm as M, the number of evaluations for Q(t) is  $M \cdot N \cdot u$  with u being the total number of time steps per simulation. Consequently, simulating system resilience is a complex, demanding and repeating challenge.

Computing the resilience directly relates to the computation of at least one structure function that can be any function that expresses the relation of interacting elements. The structure function can correspond to simple logical expressions, such as Reliability Block Diagrams (RBD) or fault trees, up to sophisticated simulation models, e.g., when assessing the network efficiency of a graph. In fact, such models often become extremely challenging in the context of real world systems. The evaluation of a global structure function including the entirety of all components at once might even be computationally unfeasible. In contrast, given a system in a substructered form S as proposed in Sec. 6.4.1, the computation of the system functionality splits into the evaluation of multiple hierarchically ordered structure functions. Such a consideration enables a wider range of application in terms of system size and complexity, especially when the computational capacity is limited.

The computational efficiency is further enhanced by application of the survival signature. Given a system, substructered according to Sec. 6.4.1 with  $L \ge 2$ , the computation of subsystem reliabilities can be propagated from level L to level 1 by evaluating the survival functions of subsystems  $S_j^v$  based on the survival functions of  $S_p^w$  instead of computing  $s_j^v = \phi_j^v(\boldsymbol{x}_j^v)$  for each level. Coolen et al. proposed a methodology to merge survival signatures of specifically arranged subsystems in the context of substructured systems [29]. However, note that this approach differs from the one developed in the current paper. The survival function  $P(T_{s_j^v} > t)$  of the *j*-th subsystem at level v is then computed according to Eq. 6.10 w.r.t. the survival signature  $\Phi_j^v(l_1, l_2, \ldots, l_K)$ . At top-level 1, the failure rates of the subsystems  $S_j^1$  with  $j = 1, 2, \ldots, n^1$ , utilized to sample subsystem functionality, can then be obtained via the cumulative hazard function and its derivative:

$$\lambda^{s_j^1}(t) = -\frac{d\ln P(T_{s_j^1} > t)}{dt}.$$
(6.14)

This enables to sample the subsystem state  $s_j^1$  for time step  $(t_h, t_{h+1})$  online with significantly reduced computational effort when evaluating the system resilience *Res*. The computation of *Res* then only involves  $n^1 + m^1$  instead of  $\sum_{v}^{L+1} m^v$  elements. In addition, significantly increased computational efficiency is achieved due to the separation of system topology and probability structure, the latter determined by the current endowment allocation. While the component probability structure varies, the topological reliability, independent of the endowment allocation, is captured in the survival signature in a compact manner and can be retrieved repeatedly with close to no costs. Note that subsystems of the same type share the same survival signature. This can be exploited for increased efficiency as well. In fact, the computational advantage of the proposed approach scales with size and complexity of the considered system S. The developed and employed algorithm is outlined in Alg. 6.4.3 for illustrative purposes.

In order to prove efficiency and general applicability, the novel approach is applied to an arbitrary complex system in Sec. 6.6 and to the *U-Bahn* and *S-Bahn* system of Berlin in Sec. 6.7.

#### Algorithm 6.4.3

- Step A Computation of the survival signatures for all subsystem  $S_j^v$  with v = 1, 2, ..., L and  $j = 1, 2, ..., n^v$ .
- Step B Identification of the Pareto front by executing the grid search algorithm; each endowment allocation is evaluated by performing the following steps:
  - Step B1. Generation of the failure rate matrix with dimensions  $n^1 \times T$  based on Eq. 6.14 for each subsystem and each timestep  $t_h$  with h = 1, 2, ..., u and generation of the failure rate matrix with dimensions  $m^1 \times T$  for each component and

each timestep; if  $L \ge 2$ , the failure rate matrix for v = 1 for each subsystem is generated recursively from bottom to top by computing the survival functions.

Step B2. Perform N samples with time  $t_h = 0$ :

- a) Evaluate the system performance  $Q(t_h)$ .
- b) Sample possible failures of subsystems  $S_j^1$  for  $j = 1, 2, ..., n^1$  and components  $C_i^1$  for  $i = 1, 2, ..., m^1$  based on the failure rate matrices computed in Step B1.
- c) Check if any failed subsystem/component has recovered; if a subsystem/component recovers, set the time counter of its specific failure rate to 0.
- d) Set  $t_h = t_{h+1} = t_h + \Delta t$  and repeat Steps a) d) until  $t_h = T$ , i.e., the maximum time is reached.
- Step B3. Obtain *Res* for the current endowment configuration via Eq. 6.2 and Eq. 6.3 over all time steps u and all samples N.

The complete algorithm has been implemented in the Julia package *ResilienceDecisionMak-ing.jl* and made publicly available on Github [100].

# 6.5 Multistage high-speed axial compressor

Axial compressors are complex, multi-component key elements of gas turbines. Therefore, it is critical in both design and maintenance to consider as many factors affecting system performance as possible to efficiently maximize compressor resilience. To address this challenge, the decision-making analysis proposed in [72] regarding system resilience is extended in order to deal with components, respectively factors, of different types.

#### 6.5.1 Model

In [191], the authors present a functional model of a four-stage high-speed axial compressor from the Institute of Turbomachinery and Fluid Dynamics at Leibniz Universität Hannover, Germany, depicting its functionality as well as reliability characteristics. For detailed information about this particular axial compressor see [192–194].

The model captures the dependence of the overall performance of the compressor, i.e., the total-to-total pressure ratio and the total-to-total isentropic efficiency, on the surface roughness of the individual blades. These are arranged in rotor and stator rows. The model is based on the results of a sensitivity analysis of an aerodynamic model of the compressor and the so-called Relative Important Indices, cf. [58]. A network representation of the functional model is shown in Fig. 6.4. Each component represents either a stator (S1 - S4) or rotor (R1 - R4) row.



Figure 6.4: Functional model of the multistage high-speed axial compressor.

The rows are classified into K = 4 component types  $k_i \in \{1, 2, 3, 4\} \forall i \in \{1, \ldots, 8\}$ . This classification, as well as the arrangement of the components, is based on the resulting effect of their blade roughness on the two performance parameters of the compressor. More precisely, an interruption between start and end implies that a roughness-induced performance variation of at least 25% is exceeded, corresponding to a non-functional compressor. This defines the system performance Q(t) of the functional model for subsequent application of the resilience decision-making method. The system performance is determined at each time point  $t_h$  and is 1 if there is a path from start to end and 0 if this connection is interrupted. More detailed information about the functional model and its derivation can be obtained from [191].

For the resilience analysis, it is assumed that each row, i.e., each component of the functional model, is characterized by two endowment properties, a roughness resistance re and a recovery improvement rec, such that a component is fully described by  $(a_i; k_i) = (re_i, rec_i; k_i)$ . In this context, the roughness resistance can be interpreted as a qualitative coating that counteracts the roughnesing of the blade surfaces. Both the roughness resistance  $re_i$  and the recovery improvement  $rec_i$  of each row i are assumed to be functions of the component type  $k_i$ , i.e.,  $re_i = re_{i'}$ ,  $rec_i = rec_{i'}$  if  $k_i = k_{i'}$ .

Each component of the functional model can fail randomly after system performance is calculated at time  $t_h$ . A failed component is considered as no longer being part of the model and does not contribute to the overall system performance at time  $t_{h+1}$  and at all subsequent times until it is completely recovered. The failure probability of a component *i* in the time interval  $(t_h, t_{h+1})$  is assumed to be constant in time, cf. [191], and is specified by

$$P\{(a_i; k_i) \text{ fails during } (t_h, t_{h+1})\} = \Delta t \cdot \lambda_i$$
(6.15)

with

$$\lambda_i = 0.8 - 0.03 \cdot re_i, \tag{6.16}$$

where  $\lambda_i$  is the time-independent failure rate. Increasing the roughness resistance of a blade

row reduces the degradation of the surface and consequently the corresponding failure rate  $\lambda_i$ .

When a component i fails, its functionality is assumed to be immediately and completely recovered after a certain number of time steps, according to

$$r = r_{max} - rec_i \quad \text{with} \quad rec_i < r_{max}$$

$$(6.17)$$

where  $r_{max}$  is an upper bound on the number of time steps for recovery and  $rec_i$  is the recovery improvement that reduces the recovery duration. Note, that this recovery model corresponds to a one-step recovery profile and various alternative characteristic profiles of recovery are possible as well, cf., [164] and [153].

#### 6.5.2 Costs of endowment properties

Optimal endowment properties are related to the quality of the components, and an increase in their production quality is associated with increasing costs. This should be taken into account in resilience decision-making. As discussed in [78], increasing the reliability of components in complex networks can be associated with an exponential increase in cost.

Increasing the endowment property of roughness resistance reduces the failure rate of blades in a row and thus improves reliability, see Eq. 6.15 and Eq. 6.16. Thus, its total cost is assumed to be

$$cost^{re} = \sum_{i=1}^{8} price_{(re_i;k_i)}^{re} \cdot 1.2^{(re_i-1)},$$
(6.18)

where  $re_i$  is the roughness resistance value of component *i*,  $k_i$  its type and  $price_{(re_i;k_i)}^{re}$  an arbitrary common basic price. Accordingly an exponential relationship is assumed for the cost associated with recovery improvement:

$$cost^{rec} = \sum_{i=1}^{8} price^{rec}_{(rec;k_i)} \cdot 1.2^{(rec_i-1)}.$$
 (6.19)

The total cost  $cost_{(A;z)}$  of an endowment is the sum of these costs:

$$cost_{(A;z)} = cost^{re} + cost^{rec}.$$
(6.20)

#### 6.5.3 Scenario

In order to apply the decision-making method for resilience-enhancing endowments to the multistage high-speed axial compressor, the model parameter values and simulation parameter values shown in Tab. 6.1 are considered.

In a first step, the set of all acceptable endowments corresponding to a resilience value of at least Res = 0.85 over the considered time period is determined. Since any axial compressor blade improvement involves costs, the second step is to identify the most cost-efficient acceptable

Parameter	Scenario
Acceptance threshold $\alpha$	0.85
Number of time steps $u$	200
Length of a time step $\Delta t$	0.05
Maximum time $T$	10
Base failure rate $\lambda$	0.8
Roughness resistance $re$	$re_i \in \{1, \ldots, 20\}$
Roughness resistance price $price_{(re_i:k_i)}^{re}$ :	$800 {\textcircled{\in}} \forall k_i \in \{1, 2, 3\}$
(-6)-6)	$500 \in \forall k_i = 4$
Maximum recovery time $r_{max}$	21
Recovery improvement $rec$	11
Recovery improvement price $price_{(rec:k_i)}^{rec}$ :	600€
Sample size $N$	500

 Table 6.1: Parameter values for the resilience decision-making method for the functional model of the multistage high-speed axial compressor.

endowment, denoted as  $\hat{A}$ . The recovery improvement *rec* is assumed to be fixed for all components, regardless of the type,  $rec_i = 11 \forall i \in \{1, \ldots, m\}$  and the roughness resistance *re* is examined over  $re_i \in \{1, \ldots, 20\} \forall i \in \{1, \ldots, m\}$ . The roughness resistance values may be interpreted in ascending order as increasing quality levels of coatings.

Figure 6.5 illustrates the results of the grid search algorithm. It shows the roughness resistance combinations contained in R(Y), i.e., all combinations that lead to a satisfying system resilience of at least Res = 0.85. It can be clearly seen that the roughness resistance of the blades of the fourth stage (component type 3) has the greatest influence on the system resilience. Combinations with coating qualities of  $re_i \leq 15$  at the fourth stage are generally not sufficient to achieve an acceptable level of resilience, regardless of the endowment property values of the other component types. In addition, the roughness resistance of the four stators (component type 4) has the least influence on system resilience of all types. Here, a minimum coating quality of  $re_i = 1$  as endowment is in various combinations already sufficient to achieve acceptable resilience values. The same applies to the rotors of component type 1 and type 2. However, the components of the other types require significantly higher coating qualities compared to the stators in order to compensate for the small roughness resistance values in these both types.

The design, maintenance and optimization of complex systems, such as an axial compressor, are invariably subject to monetary limitations. It is crucial for decision-making to be able to take these financial constraints into account. Therefore, Fig. 6.6 shows only those roughness resistance combinations included in R(Y) that result in an acceptable system resilience of at least Res = 0.85 and are less expensive than a predefined cost limit for the total roughness resistance, that is arbitrarily assumed to be  $cost^{re} = 40\,000 \in$  in this case study.

The results reveal that only configurations with low coating qualities for stators (component type 4) are below the cost limit. On the one hand, this is due to their aforementioned low



Figure 6.5: Numerical results of the 4D grid search algorithm for the functional model of the axial compressor with explored roughness resistance values.

influence on system resilience, and on the other hand to the high cost of the quality levels for the stators. Although the base price of 500€ is rather low, it is significantly higher in terms of cost for the entire component type than for the other types due to the higher total number of components of this type. In addition, only configurations that provide the highest quality levels of  $re_i \ge 18$  for the type 3 rotor are acceptable and below the price limit. The roughness resistance of this rotor has such a large impact on system resilience that at lower quality levels, compensation by higher quality levels of the remaining stages would exceed the given budget. Although the roughness resistance of the rotor of component type 2 has a lower influence on the system resilience than that of component type 3, minimal quality levels of the coating can not be compensated by high qualities of the other components. Therefore, at least  $re_i = 5$  for  $k_i = 2$  is required to fulfill the acceptance criterion.

The grid search algorithm is able to reduce the numerical effort for the calculation of R(Y) by about 98%. As a result, only 2% of the potential combinations of roughness resistance values need to be evaluated.

Taking into account the base prices in Tab. 6.1, the most cost-efficient endowment is characterized by roughness resistances of  $re_i = 7$  for  $k_i = 1$ ,  $re_i = 13$  for  $k_i = 2$ ,  $re_i = 19$  for  $k_i = 3$  and  $re_i = 1$  for  $k_i = 4$  for the respective components. In Fig. 6.6 the corresponding configuration is highlighted in blue. The final cost results from Eq. 6.20 as  $cost_{(\hat{A};z)} = cost^{re} + cost^{rec} = 35\,209 \mbox{\ensuremath{\in}} + 29\,720 \mbox{\ensuremath{\in}} = 64\,929 \mbox{\ensuremath{\in}}$ .



**Figure 6.6:** Numerical results of the 4D grid search algorithm for the functional model of the axial compressor with explored roughness resistance values and a cost threshold for roughness resistance of  $40\,000 \in$ .

# 6.6 Complex system

In [37] and [181] the authors apply their introduced simulation approaches for reliability analysis on an arbitrary complex system. In order to demonstrate the wide applicability and efficiency of the proposed methodology developed in this paper, this complex system is considered, adapted by means of substructuring, and an efficient resilience decision-making analysis is conducted.

#### 6.6.1 Model

The arbitrary complex system consists of n = 14 subsystems, each assigned to one of B = 6subsystem types. Figure 6.7 illustrates the complex system and the assignment of subsystems to their types. A connection between start node and target node indicates a functioning state and an interruption of this connection indicates a non-functioning state of the overall system. This defines the system performance Q(t) of the functional model for subsequent application of the resilience decision-making method. The system performance is determined at each time point  $t_h$  and is 1 if there is a path from start to end and 0 if this connection is interrupted. Note that the complex system is thus formally an RBD. For illustration and simplicity, it is assumed that there is only one level of subsystems, i.e., l = L = 1, and thus  $\mathbf{x}^s = (s_1, s_2, \ldots, s_{14})$ ,  $S_j^1 = S_j$ , and  $\lambda^{s_j^1}(t) = \lambda^{s_j}(t)$ . Figure 6.8 illustrates the structure of the six subsystem types. These are formally RBDs as well. It is assumed that each subsystem of the same type is represented by the same RBD. A subsystem  $S_j$  is considered to be functional if a connection exists from start to end and non-functional if this connection is interrupted, i.e.,  $s_j \in \{0,1\} \forall j \in \{1,\ldots,14\}$ . Depending on the type, the subsystems consist of seven to ten components. Thus, the overall system is composed of m = 106 individual components.



Figure 6.7: Representation of the arbitrary complex system with 14 components, adapted from [37].

The components are classified into K = 2 types  $k_i \in \{1, 2\} \forall i \in \{1, ..., 106\}$ , i.e., 50 components of type 1 and 56 components of type 2. For the resilience analysis, each component of the model, is assumed to be characterized by an endowment property, that is the reliability improvement *rel*, such that a component is fully described by  $(a_i; k_i) = (rel_i; k_i)$ . Note that the reliability improvement *rel*<sub>i</sub> of each component *i* is assumed to be function of the component type  $k_i$ , i.e.,  $rel_i = rel_{i'}$  if  $k_i = k_{i'}$ . Further, each component type, and thus each component, is characterized by a specific time-dependent failure behavior. In practice, the underlying distribution functions, describing this behavior, need to be derived from existing operational data. However, the consideration of real data is often highly challenging due to the inherent uncertainty caused by, e.g., lack of data, measurement inaccuracies, subjective expert knowledge, small sample sizes, etc. New developments in the context of the survival signature as introduced, e.g., in [181], allow for the efficient consideration and propagation of uncertainties through the entire model. They will be incorporated into the proposed methodology towards an imprecise resilience approach in future work of the authors. However, for the purpose of proof of concept and applicability, exponential distributions are considered for both component types in this



Figure 6.8: Representation of the B = 6 subsystem types of the complex system.

case study as

$$F_i(t;\lambda_i(rel_i)) = 1 - e^{-\lambda_i(rel_i)t} \text{ for } t \ge 0,$$
(6.21)

with

$$\lambda_i(rel_i) = \lambda_{i,\max} - \Delta\lambda_i \cdot rel_i, \tag{6.22}$$

being the failure rate of component *i* of type *k* depending on the corresponding reliability improvement  $rel_i$ .  $\lambda_{i,\max}$  is the maximum failure rate and  $\Delta\lambda_i$  denotes the failure rate reduction per reliability :improvement  $rel_i$  that is assumed to be constant for each component type, leading to equidistant failure rate variations.

The simulation can be summarized as follows: after the system performance has been computed at time  $t_h$ , each subsystem  $S_j$  of the complex system can fail at random based on the extracted and time-dependent failure rate  $\lambda^{s_j}(t_h)$  from corresponding survival function, cf. Eq. 6.14. A failed subsystem is treated as no longer present in the model and does not contribute to the overall system performance Q(t) at time  $t_{h+1}$  and all subsequent time points until it is fully recovered. The failure probability of a subsystem  $S_j$  in the time interval  $(t_h, t_{h+1})$ is

$$P\left\{\mathcal{S}_{j} \text{ fails during } (t_{h}, t_{h+1})\right\} = \Delta t \cdot \lambda^{s_{j}}(t_{h}).$$
(6.23)

If a subsystem  $S_j$  failed, its functionality is assumed to be immediately and fully recovered after r time steps, again corresponding to a one-step recovery profile. It is assumed that a repaired subsystem and thus all components of the subsystem are in as-new original condition after repair. Note that this is an assumption for the sake of demonstration, and in reality deviating states might be obtained after repair, possibly depending on further endowment properties that affect the duration and quality of recovery. After recovery, the survival function of a subsystem is time-zeroed, such that the resulting failure rate per simulation step  $\lambda^{s_j}(t_h)$  evolves over time equivalent to that of a subsystem in new condition.

#### 6.6.2 Costs of endowment properties

The improvement of endowment properties is inevitably associated with costs. Increasing the endowment property "reliability improvement" reduces the failure rate of components and consequently of corresponding subsystems. Again, an exponential relationship between costs and improvements is assumed. Then the total costs can be defined as

$$cost_{(A;z)} = cost^{rel} = \sum_{i=1}^{106} price_{(rel_i;k_i)}^{rel} \cdot 1.2^{(rel_i-1)},$$
(6.24)

where  $(rel_i; k_i)$  is the reliability improvement value of component *i*,  $k_i$  its type and  $price_{(rel_i;k_i)}^{rel}$  is an arbitrary common basic price.

#### 6.6.3 Scenario

The considered model parameters and simulation parameters values for the application of the resilience decision-making method for complex and substructured systems to the arbitrary complex system illustrated in Fig. 6.7, are shown in Tab. 6.2. The recovery is assumed to be fixed with r = 20 time steps for all subsystems, regardless of the type. The reliability improvement  $rel_i$  is explored over  $rel_i \in \{1, ..., 10\} \ \forall i \in \{1, ..., m\}$ .

In a pre-processing step, the survival signatures of all 14 subsystems are determined. As an example, Tab. 6.3 depicts the survival signature values of subsystem type 5 of the complex system. For clarity, only the non-trivial survival signature values are shown, i.e., all values that are neither zero or one. Then the analysis starts as follows: In a first step, the set of all acceptable endowment configurations R(Y), corresponding to a resilience value of at least Res = 0.9 over the considered time period, is determined according to Algorithm 6.4.3. Since any improvement of the system components is associated with costs, the second step is to identify the most cost-efficient acceptable endowment  $\hat{A}$ .

Figure 6.9 illustrates the results of the grid search algorithm. It shows the reliability improvement combinations contained in R(Y), i.e. all combinations that lead to a satisfying system resilience. It can be seen, that the reliability improvement of components of type 1 is

Parameter	Scenario
Acceptance threshold $\alpha$	0.90
Number of time steps $u$	200
Length of time step $\Delta t$	0.05
Maximum time $T$	10
Maximum failure rate $\lambda_{i,\max}$	$\lambda_{i,\max} = 0.15$ for $k_i = 1$
	$\lambda_{i,\max} = 0.20$ for $k_i = 2$
Failure rate reduction $\Delta \lambda_i$	$\Delta \lambda_i = 0.014$ for $k_i = 1$
	$\Delta \lambda_i = 0.019$ for $k_i = 2$
Reliability improvement $rel_i$	$rel_i \in \{1, \dots, 10\}$ for $k_i \in \{1, 2\}$
Reliability improvement price $price_{(rel_i;k_i)}^{rel}$	$price_{(rel_i;1)}^{rel} = 1000 \in$
	$price_{(rel_i;2)}^{rel} = 2000 \in$
Recovery time steps $r$	20
Sample size $N$	500

Table 6.2: Parameter values for the resilience decision-making method on the arbitrary complex system.

more important, i.e., has a higher impact on the overall system resilience than the reliability improvement of components of type 2. For maximum reliability improvement values for type 1, i.e.,  $rel_i = 10$  for  $k_i = 1$ , even low reliability improvement values for type 2, i.e.,  $rel_i = 2$ for  $k_i = 2$ , are sufficient in order to fulfill the acceptance criterion and reach system resilience values of at least Res = 0.90. On the other hand, with maximum reliability improvement for components of type 2, i.e.,  $rel_i = 10$  for  $k_i = 2$ , a moderate reliability improvement for type 1 of at least  $rel_i = 4$  for  $k_i = 1$  is required to meet the acceptance criterion.

These results are plausible, since a detailed examination of the subsystem types and their topology, cf. Fig. 6.8, reveals that components of type 1 hold a total of six so-called bottleneck positions within the subsystems, i.e., positions where the failure of a single component interrupts the functioning of the entire subsystem, while components of type 2 occupy only three of these positions. This results in a higher influence of component type 1 on the functionality of the subsystems and thus ultimately in a higher influence on overall system resilience. Accordingly, the quality of reliability improvement of component type 1 is more relevant than that of component type 2. Looking at the probabilistic structure of the components, it is noticeable that the failure rate reduction for components of type 2 probabilistically generates a higher surplus value compared to improvements of type 1. However, this obviously cannot balance the influence gradient between both types and thus underlines the critical topological importance of type 1 components.

The design, maintenance and optimization of complex systems is typically restricted by economic limitations. It is crucial for decision-making to be able to take these monetary constraints into account. Assuming the arbitrary base prices in Tab. 6.2, the most cost-effective

$l_1$	$l_2$	$\Phi\left(l_{1},l_{2}\right)$
2	4	1/25
3	3	3/50
2	5	3/25
4	3	3/20
3	4	9/50
2	6	1/5
5	3	11/50
6	3	3/10
3	5	3/10
4	4	33/100
3	6	2/5
5	4	23/50
4	5	12/25
6	4	3/5
4	6	3/5
5	5	16/25
6	5	4/5
5	6	4/5

**Table 6.3:** Non-trivial survival signature values of subsystems with  $b_j = 5$  of the complex system, shown in Fig. 6.7 and Fig. 6.8.

acceptable endowment  $\hat{A}$  is specified by a reliability improvement configuration of  $rel_i = 8$  for  $k_i = 1$  and  $rel_i = 4$  for  $k_i = 2$  for the respective components. In Fig. 6.9, the corresponding configuration is highlighted. Note that due to the monotonicity of the input-output model and the monotonically increasing endowment costs, the most cost-efficient endowment can only be located on the dominant vertices of the Pareto front. Therefore, only these configurations need to be examined in terms of cost. The final cost results from Eq. 6.24 as  $cost_{(\hat{A}:z)} = 372.695 \in$ .

Due to the utilization of the grid search algorithm, the numerical effort required to compute R(Y) is reduced. Only 23% of all possible configurations of reliability improvement values need to be evaluated. This reduction effect scales with the size and dimensionality of the endowment search space. By means of the novel resilience decision-making method, the considered complex system could be reduced from its entirety of 106 individual components to 14 components on the top-level with respect to the resilience analysis and the associated identification of all acceptable endowment configurations, which drastically reduces the computational effort. Nevertheless, all 106 components and their influence were considered by incorporating and propagating the subsystems' survival functions. Again, this effect scales with increasing complexity and size of the investigated systems.



Figure 6.9: Numerical results of the 2D grid search algorithm for the complex system with explored reliability improvement values.

# 6.7 U-Bahn and S-Bahn system of Berlin

About two thirds of the total of 1.5 billion passengers per year are transported by Berlin's subway U-Bahn and suburban trains S-Bahn [195, 196], making these two transport services the most used means of public transport in Berlin and thus of utmost importance for the German capital. Key infrastructures that are of such significant social and economic relevance to modern societies obviously and inevitably need to be as resilient as humanly possible. The applicability of the methodology developed in this work to large complex systems is demonstrated on a comprehensive model of the Berlin U-Bahn and S-Bahn system. The objective is to identify suitable resilience-enhancing properties for all stations in the system, taking into account monetary constraints. This allows the characterization of acceptable endowments for the system in terms of reliability, robustness, and recoverability. This approach can be applied not only to any phase during the life cycle of existing systems, but also to systems in the design phase, in order to optimize their resilience.

#### 6.7.1 Model

Berlin's U-Bahn and S-Bahn systems are highly interconnected systems that are linked by numerous stations. According to [197], they may therefore be considered as a unified system, hereafter referred to as "metro system". In [72] the authors apply their introduced approach for resilience decision-making to a model of the Berlin metro system. In order to demonstrate the wide applicability and efficiency of the proposed methodology developed in this work, this model is considered, extended and adapted by means of substructuring, and an efficient and multidimensional resilience decision-making analysis is conducted.

In [198], Zhang et al. proposed how mapping of metro networks into topological graphs can be conducted. Based on this, the Berlin metro system consists of 306 nodes for 306 metro stations and 350 edges for 350 connections between these stations. For simplicity, parallel connections are mapped to single edges in the model, and are assumed to be undirected. These assumptions reduce the complexity of the metro system. Figure 6.10 illustrates the graph representation.



Figure 6.10: Topological network for the Berlin metro system.

The functionality of systems depends on the functionality of its components. However, the functionality of these components often depends again on the functionality of a variety of subcomponents, etc. A major challenge in modeling is therefore determining an appropriate level of detail.

The resilience decision-making methodology proposed in this paper allows for the incorporation of such subsystem structures by live propagation of corresponding reliability characteristics up to the top-level. Therefore, for the resilience analysis of the metro system, each metro station is modeled as a subsystem with own functionality and performance function. Again, for illustrative purposes and sake of convenience, assume that there is only one level of subsystems, i.e., l = L = 1, and thus  $\boldsymbol{x}^s = (s_1, s_2, \ldots, s_{306})$ ,  $\mathcal{S}_j^1 = \mathcal{S}_j$  and  $\lambda^{s_j^1}(t) = \lambda^{s_j}(t)$  with n = 306subsystems respectively metro stations.

In terms of reliability modeling, subcomponents could correspond to structural elements, such as stairs, columns, ceilings, station rails as well as electric facilities, such as railway power supply, elevators, escalators, ventilation plants, information systems and illuminations. These subcomponents can be subdivided in terms of their functionality and relevance to the metro station, such as in rail operations related components and user accessibility related components. For illustrative purpose, the analysis is restricted to reliability modeling of metro stations. Therefore, functional models are defined for the metro station subsystems that are, as in the previous case study, formally RBDs. Again, a subsystem  $S_i$  is considered to be functional if a connection from start to end exists and non-functional if this connection is interrupted, i.e.,  $s_j \in \{0,1\} \ \forall j \in \{1,\ldots,306\}$ . Figure 6.10 illustrates three of these subsystems for three different metro stations as an example. The metro stations are classified into B = 6 types, depending on the number of their connections to direct neighbors, i.e., stations with only one connection form subsystem type 1, stations with two direct neighbors form subsystem type 2, etc. For the analysis, each subsystem is assumed to be characterized by an endowment property, that is the recovery improvement rec, such that a metro station j with type  $b_j$  is described by  $(\mathcal{S}_j; b_j) = (rec_j; b_j)$ . Note, that the recovery improvement  $rec_j$  of each metro station is assumed to be a function of the station type  $b_i$ , i.e.,  $rec_i = rec_{i'}$  if  $b_i = b_{i'}$ . For simplicity, it is assumed that each metro station of a type is represented by the same RBD. Figure 6.11 displays the structure of all six subsystem types and Fig. 6.12 tabulates the number of individual metro stations per type.

Depending on the type and thus with increasing complexity related to the number of direct neighbors, also known as node degree, the subsystems consist of four up to twenty-one components. Taking into account the information from Fig. 6.12, the overall system therefore consists of a total of m = 2776 considered individual components.

The components are classified into K = 4 types  $k_i \in \{1, 2, 3, 4\} \forall i \in \{1, \dots, 2776\}$ . For the analysis, each component is assumed to be characterized by an endowment property, that is the reliability improvement rel, such that a component is fully described by  $(a_i; k_i) = (rel_i; k_i)$ . Note, that the reliability improvement  $rel_i$  of each component is assumed to be a function of the component type  $k_i$ , i.e.,  $rel_i = rel_{i'}$  if  $k_i = k_{i'}$ . Further, each component is characterized by a specific time-dependent failure behavior. For the purpose of proof of concept and applicability, for component type 1 and 3, i.e.,  $k_i = 1$  and  $k_i = 3$ , exponential distributions are considered according to Eq. 6.21 and Eq. 6.22. For component type 2 and 4, i.e.,  $k_i = 2$  and  $k_i = 4$ , two



Figure 6.11: Representation of the B = 6 station types of the Berlin metro system.

parametric gamma distributions are considered. The cumulative distribution function of the gamma distribution can be derived based on its probability density function that is given in terms of the rate parameter  $\lambda_i(rel_i)$  depending on the current reliability endowment value  $rel_i$ 

6 Multidimensional Resilience Decision-Making for Complex and Substructured Systems



Figure 6.12: Number of individual metro stations per type.

of component *i* of type  $k_i$  as

$$f(t;\alpha_i,\lambda_i(rel_i)) = \frac{t^{\alpha_i - 1}e^{-\lambda_i(rel_i)t}\lambda_i(rel_i)^{\alpha_i}}{\Gamma(\alpha_i)},$$
(6.25)

for  $t, \alpha_i, \lambda_i(rel_i) > 0$ , where  $\alpha_i$  is the shape parameter,  $\lambda_i(rel_i)$  is the rate parameter, and  $\Gamma(\alpha_i)$  is the well-known Gamma function. Consequently, the cumulative distribution function can be obtained by integration and with respect to the current endowment of component *i* it can be formulated as

$$F(t;\alpha_i,\lambda_i(rel_i)) = \int_0^t f(u;\alpha_i,\lambda_i(rel_i))du.$$
(6.26)

 $\lambda_i(rel_i)$  is again a function of the component specific reliability improvement and given by Eq. 6.22.

In order to perform a resilience analysis, the definition of an appropriate system performance measure for the metro system is imperative. As in [198] and [72], in this case study, the so-called network efficiency  $E_f$  is adopted as the relevant performance measure, i.e.,  $Q(t) = E_f(t)$ . Zhang et al. justified in [198] their choice by stating that connectivity between individual metro stations is an essential criterion for evaluating metro operations. As described by Latora and Marchiori in [134], network efficiency is a quantitative indicator of network connectivity and is defined as:

$$E_f = \frac{1}{n(n-1)} \sum_{u \neq v} \frac{1}{d_{uv}}$$
(6.27)

with n the number of subsystems, i.e., metro stations in the network and  $d_{uv}$  the path length between metro station u and metro station v, i.e., the shortest distance between these stations. A comprehensive overview of algorithms to efficiently determining the path length  $d_{uv}$  between stations, such as the algorithms of Floyd, Dijkstra's, or Bellman-Ford, is provided in [199] and [200].

The simulation procedure corresponds to that from the previous case study and the failure

probability of a subsystem  $S_j$ , i.e., metro station, in the time interval  $(t_h, t_{h+1})$  is defined by Eq. 6.23. Unlike in the previous case study, a failed metro station is not entirely removed from the system, but remains in the set of metro stations; however, their node degree becomes 0, i.e., all existing connections to direct neighbors are removed. This assumption is essential, as the computation and interpretation of the system performance network efficiency depends on the number of nodes. The case study therefore relies on the fact that the number of nodes is constant.

If a subsystem  $S_j$  failed, its functionality is assumed to be immediately and fully recovered after a certain number of time steps r:

$$r = r_{\max} - 2 \cdot rec_i$$
 with  $rec_i < r_{\max}$ , (6.28)

where  $rec_j$  is the recovery improvement specific to the station  $S_j$  and  $r_{max}$  is an upper bound for number of time-steps for recovery. After recovery, all previous connections to other metro stations are assumed to be restored, unless these are in a state of failure. As each time-step has a specific length of  $\Delta t = (T/u)$ , the duration of the recovery process is  $r \cdot (T/u)$ . Again, this recovery model corresponds to a one-step recovery profile and as mentioned before, various alternative characteristic profiles of recovery are possible as well. A repaired station and thus all components of the station are assumed to be in a as-new original condition after repair. This is an assumption for the sake of demonstration, and deviating states are possible. After recovery, the survival function of a metro station is time-zeroed, such that the resulting failure rate per simulation step  $\lambda^{s_j}(t_h)$  evolves over time equivalent to that of a station in new condition.

#### 6.7.2 Costs of endowment properties

The improvement of both endowment properties, "reliability improvement" and "recovery improvement", is inevitably associated with costs. Again, exponential relationships between total costs and improvements are assumed:

$$cost^{rel} = \sum_{i=1}^{2776} price_{(rel_i;k_i)}^{rel} \cdot 1.2^{(rel_i-1)},$$
(6.29)

where  $rel_i$  is the reliability improvement value of component *i*,  $k_i$  its type and  $price_{(rel_i;k_i)}^{rel}$  an arbitrary common basic price. Accordingly an exponential relationship is assumed for the total cost associated with recovery improvement:

$$cost^{rec} = \sum_{j=1}^{306} price_{(rec_j;b_j)}^{rec} \cdot 1.2^{(rec_j-1)},$$
(6.30)

where  $rec_j$  is the recovery improvement value of station j,  $b_j$  its type and  $price_{(rec_j;b_j)}^{rec}$  an arbitrary common basic price. The total cost  $cost_{(A;z),(D;h)}$  of an endowment is the sum of

these costs:

$$cost_{(A;z),(D;h)} = cost^{rel} + cost^{rec}.$$
(6.31)

In practice, it is crucial to include the economic aspects of failure and recovery processes in detail in the resilience assessment. Mitigating resilience losses through system improvements imposes direct costs on stakeholders, such as improving component properties. Note, however, that for a comprehensive analysis, it is important to also consider indirect costs to the affected population and businesses, when the performance of a key system declines, as stated in [173]. Further, it is reasonable to incorporate the subjective preferences of stakeholders into the resilience assessment, as suggested in [172]. These considerations have the potential to significantly influence the outcome of a resilience decision-making process. Therefore, they should be integrated into the proposed methodology in future work by including additional cost conditions and discount rates for the corresponding deterioration and recovery sequences.

# 6.7.3 Scenario

In order to apply the resilience decision-making method to the Berlin metro system illustrated in Fig. 6.10, the model parameter and simulation parameter values, shown in Tab. 6.4, are considered. The recovery improvement  $rec_j$  is explored over  $rec_j \in \{1, ..., 10\} \forall j \in \{1, ..., 306\}$ , but considered to be equal for each station, regardless of the type  $b_j$ . The reliability improvement  $rel_i$  again is explored over  $rel_i \in \{1, ..., 10\} \forall i \in \{1, ..., 2776\}$  for  $k_i \in \{1, ..., 4\}$ .

In a pre-processing step, the survival signatures of all 306 metro stations are determined. As an example, Tab. 6.5 illustrates the non-trivial survival signature values, i.e.,  $\Phi(l_1, \ldots, l_4) \neq 0$ and  $\Phi(l_1, \ldots, l_4) \neq 1$ , of station type 2 of the metro system. Then, the set of all acceptable endowment configurations R(Y), corresponding to a resilience value of at least Res = 0.99over the considered time period, is determined according to Algorithm 6.4.3. Further, as any improvement of the system components and stations is associated with costs, the most cost-efficient acceptable endowment, denoted by the tuple  $(\hat{A}, \hat{D})$ , is determined.

In Fig. 6.13 the results of the grid search algorithm are illustrated. It shows the accepted endowments contained in R(Y), i.e. all combinations that lead to a satisfying resilience of the metro system. It is clearly visible that type 1 components as well as the recovery improvement of the metro stations have the greatest influence and thus the highest importance for the metro system. Only endowments with a reliability improvement of at least  $rel_i = 8$  for type 1 components and endowments with a recovery improvement for all metro stations of at least  $rec_j = 8$  lead to a system resilience meeting the acceptance criterion. In addition, type 2 components are of considerable relevance. Here, only endowments with a reliability improvement of at least  $rel_i = 6$  are acceptable. The reliability improvements of type 3 and 4 components, on the other hand, are of less significance. For both types of components, there are numerous acceptable configurations that include minimum reliability improvement values for one of these types.

Parameter	Scenario
Acceptance threshold $\alpha$	0.99
Length of time step $\Delta t$	0.05
Number of time steps $u$	200
Maximum time $T$	10
Shape parameter gamma distribution $\alpha_i$	$\alpha_i = 1.2$ for $k_i = 2$
	$\alpha_i = 2.6$ for $k_i = 4$
Maximum failure rate $\lambda_{i,\max}$	$\lambda_{i,\max} = 0.34$ for $k_i = 1$
	$\lambda_{i,\max} = 0.43$ for $k_i = 2$
	$\lambda_{i,\max} = 0.36$ for $k_i = 3$
	$\lambda_{i,\max} = 0.66$ for $k_i = 4$
Failure rate reduction $\Delta \lambda_i$	$\Delta \lambda_i = 0.03$ for $k_i = 1$
	$\Delta \lambda_i = 0.04$ for $k_i = 2$
	$\Delta \lambda_i = 0.034$ for $k_i = 3$
	$\Delta \lambda_i = 0.051$ for $k_i = 4$
Reliability improvement $rel_i$	$rel_i \in \{1, \dots, 10\}$ for $k_i \in \{1, \dots, 4\}$
Reliability improvement price $price_{(rel_i;k_i)}^{rel}$	$price_{(rel_i;1)}^{rel} = 100 \in$
	$price_{(rel_i;2)}^{rel} = 200 \in$
	$price_{(rel:3)}^{rel} = 200 \in$
	$price_{rel}^{(rel, 3)} = 400 \in$
Maximum recovery time $r_{max}$	$\frac{1}{22}$
Recovery improvement $rec_i$	$rec_i \in \{1,, 10\}$
Recovery improvement price price <sup>rec</sup>	$price^{rec}$ $= 100 \in$
$J$ I I I $(rec_j;b_i)$	$mice^{rec}$ = 200€
	$\frac{Price^{rec}}{rec_j;2} = 300 \pounds$
	$\frac{price_{(rec_j;3)}}{price_{rec}} = \frac{5000}{4000}$
	$price_{(rec_j;4)} = 400\varepsilon$
	$price_{(rec_j;5)} = 500 \in$
	$price^{rec}_{(rec_j;6)} = 600 \in$
Sample size $N$	500

Table 6.4: Parameter values for the resilience decision-making method on the metro system of Berlin.

These results again prove to be plausible, as in the previous case study, upon closer examination of the topological structures of the metro system and its subsystems. Several U-Bahn and S-Bahn lines start and end in long chains of directly interconnected type 2 stations, see Fig. 6.10. The resilience analysis of the Berlin metro system published in [72] revealed that especially an interruption of these chains has a major negative impact on the network efficiency and thus on the resilience of the metro system. Accordingly, the importance of type 2 stations is particularly high not only due to their multiplicity in the system, but due to their topological contribution in terms of connectivity as well. Consequently, components of this station type have a significant impact on the resilience of the overall system. An examination of the type 2 subsystem model, see Fig. 6.11, shows that type 1 components take on a predominant position. Once both type 1 components in this subsystem fail, the entire metro station fails. No other components of a single type can cause this in station type 2.

The significant influence of type 2 components can easily be explained by examining the
$l_1$	$l_2$	$l_3$	$l_4$	$\Phi(l_1,\ldots,l_4)$
2	2	1	1	1/4
2	1	1	2	1/4
2	2	2	1	3/8
2	2	1	2	3/8
2	1	2	2	3/8
3	2	1	1	1/2
2	3	1	1	1/2
2	1	3	1	1/2
3	1	1	2	1/2
2	3	1	2	1/2
2	1	1	3	1/2
2	2	1	3	1/2
2	3	1	3	1/2
2	2	2	2	9/16
3	2	2	1	3/4
2	3	2	1	3/4
2	2	3	1	3/4
3	2	1	2	3/4
3	1	2	2	3/4
2	3	2	2	3/4
2	1	3	2	3/4
2	1	2	3	3/4
2	2	2	3	3/4
2	3	2	3	3/4
3	2	2	2	7/8
2	2	3	2	7/8

Table 6.5: Non-trivial survival signature values of stations with  $b_j = 2$  of the metro system, shown in Fig. 6.11.

type 3 and 5 station systems, see again Fig. 6.11. Of all stations, only here bottleneck positions exist, where the failure of a single component interrupts the functioning of the entire station. Both of these positions, in type 3 and type 5 stations, are occupied by type 2 components. Since both station types have three and five direct connections to other stations, they can be considered to be particularly interconnected and thus of high relevance to network efficiency and thus of high relevance to system resilience.

Type 3 and 4 components, on the other hand, do not occupy any particularly significant positions in the stations' systems. This explains their low influence. The enormous influence of the recovery improvement is intuitively explainable. As resilience is established via the integral of the actual system performance, each recovered metro station contributes directly and immediately to the network efficiency and thus to the resilience of the system. Therefore, improvement of this property results in an immediate and intuitive increase in resilience.

Assuming the arbitrary base prices in Tab. 6.4, the most cost-efficient acceptable endowment  $(\hat{A}, \hat{D})$  results from a reliability improvement configuration of  $rel_i = 10$  for  $k_i = 1$ ,  $rel_i = 9$ 



Figure 6.13: The set of all accepted endowments R(Y) evaluated via the 5D grid search algorithm for the Berlin metro system with explored reliability improvement and recovery improvement values.

for  $k_i = 2$ ,  $rel_i = 7$  for  $k_i = 3$ ,  $rel_i = 2$  for  $k_i = 4$  for components of type 1 to 4 and a maximum recovery improvement configuration of  $rec_j = 10$  for  $b_j \in \{1, 2, 3, 4\}$ , i.e., all stations, regardless of their type. In Fig. 6.14, the corresponding configuration is highlighted. Due to the monotonicity of the input-output model and the assumed monotonically increasing endowment costs, only the endowment configurations on the dominant vertices of the Pareto front have to be examined for the identification of the most cost-efficient endowment. Therefore, only these endowment configurations are shown in Fig. 6.14. The resulting costs are given by Eq. (6.29, 6.30, 6.31) with  $cost_{(\hat{A},\hat{D})} = 1\,700\,829 \mbox{ee} + 361\,185 \mbox{ee} = 2\,062\,014 \mbox{ee}.$ 

Due to the utilization of the grid search algorithm, the computational effort could be significantly reduced in this case study as well – only 0.159% of all potential endowment configurations had to be examined in order to assign a distinct state to each configuration in the search space as accepted or not accepted. By means of the novel approach, the metro system could be reduced from its entirety of 2776 individual components to 306 components on the top-level with respect to the resilience analysis, drastically reducing the computational effort. Nevertheless, all 2776 components and their influence were considered. As in the case study of the axial compressor, not only the most cost-efficient endowment configuration can be identified but also investigations on configurations that are below certain budget limits can be conducted.

Note that, in this case study, as well as in the previous ones, various complexity variations



Figure 6.14: Dominant Pareto front endowments of the 5D grid search algorithm for the Berlin metro system with explored reliability improvement and recovery improvement values and the most cost-efficient endowment  $(\hat{A}, \hat{D})$  is highlighted.

such as so-called cascading failures, see [42, 201, 202], are possible to implement due to the timestep-accurate simulation. In the case of infrastructure systems, e.g., the increasingly frequent natural disasters can thus be considered, that typically have an impact as local phenomena and affect stations that are geographically close to each other. It has already been shown in [72] that these can be taken into account in the resilience decision-making analysis of infrastructure systems.

#### 6.8 Conclusion and outlook

This paper addresses the challenge of efficient multidimensional decision-making for complex and substructured systems between resilience-influencing parameters. By merging an extension of the resilience framework proposed in [72] with the survival signature, an efficient and novel methodology is derived. The approach allows for direct comparison of the impact of heterogeneous controls on system resilience, such as failure prevention and recovery improvement arrangements, both during the design phase as well as during any phase in the life cycle of already existing complex systems.

Due to the time-step accurate simulation of the system performance on system level during the resilience analysis, complexity extensions such as cascading failures and other dependency structures can be considered without difficulties. The new methodology has a high numerical efficiency. The majority of the endowment properties examined affect the probability structure of the system components. The numerous changes in the probability structure caused by constantly changing endowment properties during the resilience analysis can be ideally covered with minimal effort due to the separation property of the survival signature.

The novel approach includes a substructuring approach for large, complex systems. This and the integration of the survival signature allow for the propagation of subsystem reliabilities through any number of system levels to the top-level and lead to a significant reduction of the computational load. This way, and with the extension of the adapted systemic risk measure, it is now possible to analyze systems with a large number of components in terms of their resilience.

Monetary restrictions can easily be included in the analysis. More precisely, not only the most cost-efficient, accepted endowment is identified, but subsets of the set of all accepted endowments below defined price levels can be formed. Budget limits can thus be specifically taken into account in the decision-making process.

The methodology is applied to three entirely distinct systems: A functional model of a multistage high-speed axial compressor, an arbitrary system consisting of numerous subsystems and components and a comprehensive substructured model of the metro system of Berlin, proofing wide and general applicability. All results obtained are plausible with the corresponding assumed model parameters. Note, that the approach can be utilized to systems of any kind.

In the development of our proposed methodology, some simplifying assumptions were made that do not accurately reflect reality. However, the authors strongly believe that the presented approach can be considered as a meaningful core development that, for a reality-based application on highly multifactorial systems, such as cyber-human-physical systems, should be combined with future as well as existing developments to ensure an efficient and comprehensive resilience decision-making analysis taking into account all technical and monetary aspects of modern socities.

Future work will address the incorporation of various existing extensions of the concept of survival signature, such as accounting for uncertainty and propagating it toward imprecise system resilience and considering multiple state or continuous component functionality. Further, future work regarding multidimensional parameter spaces must deal with the limitations in computing time and storage capacity in order to enable application to even higher-dimensional problems. Namely, techniques such as advanced sampling methods, e.g. Subset Simulation, see [203], must be investigated to further reduce numerical effort.

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# 7 UncertaintyQuantification.jl: A new Framework for Uncertainty Quantification in Julia

## UncertaintyQuantification.jl: A new Framework for Uncertainty Quantification in Julia

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#### Abstract

This work presents a new framework for uncertainty quantification developed as a package in the Julia programming language called UncertaintyQuantification.jl. Julia is a modern high-level dynamic programming language ideally suited for tasks like data analysis and scientific computing. UncertaintyQuantification.jl was developed from the ground up to be generalized and flexible while at the same time being easy to use. Leveraging the features of a modern language such as Julia allows to write efficient, fast and easy to read code. Especially noteworthy is Julia's core feature multiple dispatch which enables us to, for example, develop methods with a large number of varying simulation schemes such as standard Monte Carlo, Sobol sampling, Halton sampling, etc., yet minimal code duplication. Current features of UncertaintyQuantification.jl include simulation based reliability analysis using a large array of sampling schemes, local and global sensitivity analysis, meta modelling techniques such as response surface methodology or polynomial chaos expansion as well as the connection to external solvers by injecting values into plain text files as inputs. Through Julia's existing distributed computing capabilities all available methods can be easily run on existing clusters with just a few lines of extra code. **Keywords:** 

#### 7.1 Introduction

The increasing complexity of modern engineering systems requires adequate simulation methods to ensure their safety and reliability. At the same time, a reliable analysis can only be performed when taking into consideration the present uncertainties. New analyses and simulation methods for the treatment of these uncertainties are constantly developed. A generic and freely available framework, which includes these methods and can be applied to a large array of engineering problems, can be a valuable tool for researchers, students, and industry alike.

Many such frameworks have been developed for a variety of programming languages. *Dakota* (C++) [79], *OpenTURNS* (C++/Python) [80], *OpenCossan* (MATLAB) [81], *UQLab* (MATLAB) [82], and *UQpy* (Python) [83] to name a few.

This work presents an alternative to these frameworks called *UncertaintyQuantification.jl* [84]. This new framework is developed as a module for the Julia programming language. The Julia language [86] has been developed as a new approach to scientific computing. Julia is designed to be fast yet easy to use at the same time. Its core principal *multiple dispatch* allows to write

simple reusable code, where the appropriate algorithm is automatically selected based on the input arguments to a function. This allows us to efficiently implement a variety of simulation techniques for the same underlying analysis with little extra effort. Julia was designed from the ground up with parallelization and high performance computing in mind. The large numerical demand of modern simulation methods can often be distributed to computing clusters with only a few extra lines. This makes Julia ideally suited for the development of a generic and complete package for uncertainty quantification.

UncertaintyQuantification is registered in the official General registry and can be installed from the Julia REPL by switching to the package manager with a closing square bracket ].

#### julia> ] add UncertaintyQuantification

The goal of UncertaintyQuantification is to build a complete and generalized framework for uncertainty quantification where newly developed methods are constantly implemented and shared with fellow researchers. UncertaintyQuantification is released under the MIT license and publicly available on Github. While development is still in the early stages, the basic features and key analyses have been completed. In its current version UncertaintyQuantification includes simulation based reliability analysis through standard and advanced Monte Carlo simulation, local and global sensitivity analysis, metamodels, and the ability to connect any of these methods to external solvers. This paper only presents the basic usage of the module. For a thorough explanation of all included simulations the reader is refered to the online documentation.

The remainder of the paper is structured as follows. In Section 7.2 we introduce the basics of *UncertaintyQuantification* including how to define input parameters, random variables and models. Section 7.3 and Section 7.4 present how to use the framework to perform reliability and sensitivity analyses, respectively. How to build metamodels as approximations is presented in Section 7.5, followed by a few numerical examples in Section 7.6. The paper closes with conclusions and a brief outlook into future development of the framework.

#### 7.2 Getting Started

In this section we introduce the basic building blocks of *UncertaintyQuantification*. This includes the inputs such as **Parameter** or **RandomVariable** which will feed into any **Model** for a variety of different analyses. We will also present more advanced concepts including how to model dependencies between the inputs through copulas.

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#### 7.2.1 Inputs

#### Parameters

A Parameter is defined as a constant scalar value. In addition to value the constructor also requires a Symbol by which it can later be identified in the Model. A Symbol is a Julia object which is often used as a name or label. Symbols are defined using the : prefix. Parameters represent constant deterministic values. As an example we define a Parameter representing the gravity of Earth.

g = Parameter(9.81, :g)

Parameters are very handy when constants show up in the Model in multiple spaces. Instead of updating every instance in the Model, we can conveniently update the value by changing a single line.

#### **Random Variables**

A RandomVariable is essentially a wrapper around any UnivariateDistribution defined in the *Distributions.jl* package [204]. Similarly to the Parameter, the second argument to the constructor is a Symbol acting as a unique identifier. For example, a standard gaussian random variable is defined by passing Normal() and :x as arguments.

x = RandomVariable(Normal(), :x)

A list of all possible distributions can be generated by executing subtypes(UnivariateDist ] ribution) in the Julia REPL (read-eval-print loop). Note that, *Distributions* is re-exported from *UncertaintyQuantification* and no separate using statement is necessary. In addition, the most important methods of the UnivariateDistribution including pdf, cdf, and quantile, are also defined for the RandomVariable.

Random samples can be drawn from a **RandomVariable** by calling the **sample** method passing the random variable and the desired number of samples.

```
samples = sample(x, 100) # sample(x, MonteCarlo(100))
```

The sample method returns a DataFrame with the samples in a single column. When sampling from a Vector of random variables these invidivual columns are automatically merged into one unified DataFrame. By default, this will use stardard Monte Carlo simulation to obtain the samples. Alternatively, any of the quasi-Monte Carlo methods can be used instead.

```
samples = sample(x, SobolSampling(100))
samples = sample(x, LatinHypercubeSampling(100))
```

Many of the advanced simulations, e.g. line sampling [205] or subset simulation [137] require mappings to (and from) the standard normal space, and these are exposed through the to\_\_\_\_\_standard\_normal\_space! and to\_physical\_space! methods respectively. These operate on a DataFrame and as such can be applied to samples directly. The transformation is done in-place, i.e. no new DataFrame is returned. As such, in the following example, the samples end up exactly as they were in the beginning.

to\_standard\_normal\_space!(x, samples)
to\_physical\_space!(x, samples)

#### Dependencies

Uncertainty Quantification supports modelling of dependencies through copulas. By using copulas, the modelling of the dependence structure is separated from the modelling of the univariate marginal distributions. The basis for copulas is given by Sklar's theorem [59]. It states that any multivariate distribution H in dimensions  $d \ge 2$  can be separated into its marginal distributions  $F_i$  and a copula function C.

$$H(x_1, \dots, x_2) = C(F_1(x_1), \dots, F_d(x_d))$$
(7.1)

For a thorough discussion of copulas, see [61].

In line with Sklar's theorem we build the joint distribution of two dependent random variables by separately defining the marginal distributions.

```
x = RandomVariable(Normal(), :x)
y = RandomVariable(Uniform(), :y)
marginals = [x, y]
```

Next, we define the copula to model the dependence. UncertaintyQuantification supports Gaussian copulas for multivariate  $(d \ge 2)$  dependence as well as a list of Archimedean copulas for bivariate dependence. The Archimedean copulas are implemented as a wrapper around the *BivariateCopulas.jl* [206] package. Here, we define a Gaussian copula by passing the correlation matrix and then build the JointDistribution from the copula and the marginals.

```
cop = GaussianCopula([1 0.8; 0.8 1])
joint = JointDistribution(marginals, cop)
```

Figure 7.1 shows the samples drawn by sampling from the independent marginals and the joint distribution using the Gaussian copula.



Figure 7.1: 1000 samples drawn from the independent marginal distributions (a) and the dependent joint distribution (b).

#### 7.2.2 Models

In this section we present the models included in *UncertaintyQuantification*. A model, in its most basic form, is a relationship between a set of input variables  $x \in \mathbb{R}^{n_x}$  and an output  $y \in \mathbb{R}$ . Currently, most models are assumed to return single-valued outputs. However, as seen later, the **ExternalModel** is capable of extracting an arbitrary number of outputs from a single run of an external solver.

#### Model

A Model is essentially a native Julia function operating on the previously defined inputs. Building a Model requires two things: a Function, which is internally passed a DataFrame containing the samples and must return a Vector containing the model response for each sample, and a Symbol which is the identifier used to add the model output into the DataFrame.

Suppose we wanted to define a Model which computes the distance from the origin of two variables x and y as z. We first define the function and then pass it to the Model.

```
function z(df::DataFrame)
  return @. sqrt(df.x^2 + df.y^2)
end
m = Model(z, :z)
```

An alternative for a simple model such as this, is to directly pass an anonymous function to the Model.

 $m = Model(df \rightarrow sqrt.(df.x.^2 + df.y.^2), :z)$ 

After defining it, a Model can be evaluated on a set of samples by calling the evaluate! method. This will add the model outcome to the DataFrame. Alternatively, the reponse can be obtained as a vector, by calling the Model as a function.

```
samples = sample([x, y], MonteCarlo(1000))
evaluate!(m, samples) # add to the DataFrame
output = m(samples) # return a Vector
```

However, most of the time manual evaluation of the Model will not be necessary as it is done internally by whichever analysis is performed.

#### ParallelModel

With the basic Model it is up to the user to implement an efficient function which returns the model responses for all samples simultaneously. Commonly, this will involve vectorized operations as presented in the example. For more complex or longer running models, *UncertaintyQuantification* provides a simple ParallelModel. This model relies on the capabilites of the *Distributed* module, which is part of the standard library shipped with Julia. Without any present *workers*, the ParallelModel will evaluate its function in a loop for each sample. If one or more workers are present, it will automatically distribute the model evaluations. For this to work, *UncertaintyQuantification* must be loaded with the @everywhere macro in order to be loaded on all workers. In the following example, we first load *Distributed* and add four local workers. A simple model is then evaluated in parallel. Finally, the workers are removed.

```
using Distributed
addprocs(4) # add 4 local workers
@everywhere using UncertaintyQuantification
x = RandomVariable(Normal(), :x)
y = RandomVariable(Normal(), :y)
m = ParallelModel(df -> sqrt(df.x^2 .+ df.y^2), :z)
samples = sample([x, y], 1000)
evaluate!(m, samples)
rmprocs(workers()) # release the local workers
```

It is important to note, that the ParallelModel requires some overhead to distribute the

function calls to the workers. Therefore it performs significantly slower than the standard Model with vectorized operations for a simple function as in this example.

By using *ClusterManagers.jl* [207] to add the workers, the **ParallelModel** can easily be run on an existing compute cluster such as *Slurm*.

#### ExternalModel

The ExternalModel provides interaction with almost any third-party solver. The only requirement is, that the solver uses text-based input and output files in which the values sampled from the random variables can be injected for each individual run. The output quantities are then extracated from the files generated by the solver using one (or more) Extractor(s). This way, the simulation techniques included in this module, can be applied to advanced models in finite element software such as *OpenSees* or *Abaqus*.

The first step in building the ExternalModel is to define the folder where the source files can be found as well as the working directory. Here, we assume that the source file for a simple supported beam model is located in a subdirectory of our current working directory. Similarly, the working directory for the solver is defined. In addition, we define the exact files where values need to be injected, and any extra files required. No values will be injected into the files specified as extra. In this example, no extra files are needed, so the variable is defined as an empty String vector.

```
sourcedir = joinpath(pwd(), "demo/models")
sourcefiles = ["supported-beam.tcl"]
extrafiles = String[]
workdir = joinpath(pwd(), "supported-beam")
```

Next, we must define where to inject values from the random variables and parameters into the input files. For this, we make use of the *Mustache.jl* [208] and *Formatting.jl* [209] modules. The values in the source file must be replaced by triple curly bracket expressions of the form  $\{\{\{ :x \}\}\},$  where :x is the identifier of the RandomVariable or Parameter to be injected. For example, to inject the Young's modulus and density of an elastic isotropic material in *OpenSees*, one could write the following.

```
nDMaterial ElasticIsotropic 1 {{{ :E }}} 0.25 {{{ :rho }}}
```

This identifies where to inject the values, but not in which format. For this reason, we define a **Dict{Symbol**, **String**} which maps the identifiers of the inputs to a Python-style format string. In order to inject our values in scientific notation with eight digits, we use the format string ".8e". For any not explicitly defined **Symbol** we can include :\* as a fallback.

formats = Dict(:E => ".8e",:rho => ".8e", :\* => ".12e")

After formatting and injecting the values into the source file, it would look similar to this.

nDMaterial ElasticIsotropic 1 9.99813819e+02 0.25 3.03176259e+00

Now that the values are injected into the source files, the next step is to extract the desired output quantities. This is done using an Extractor. The Extractor is designed similarly to the Model in that it takes a Function and a Symbol as its parameters. However, where a DataFrame is passed to the Model, the working directory for the currently evaluated sample is passed to the function of the Extractor. The user defined function must then extract the required values from the file and return them. Here, we make use of the DelimitedFiles module to extract the maximum absolute displacement from the output file that OpenSees generated.

```
disp = Extractor(base -> begin
  file = joinpath(base, "displacement.out")
  data = readdlm(file, ' ')
  return maximum(abs.(data[:, 2]))
end, :disp)
```

An arbitrary number of Extractor functions can be defined in order to extract multiple output values from the solver.

The final step before building the model is to define the solver. The solver requires the path to the binary, and the input file. Optional command line arguments can be passed to the **Solver** through the **args** keyword. If the solver binary is not on the system path, the full path to the executable must be defined. Finally, the **ExternalModel** is assembled.

```
opensees = Solver(
   "OpenSees",
   "supported-beam.tcl";
   args = ""
)
ext = ExternalModel(
   sourcedir, sourcefiles, disp, opensees; formats=numberformats, workdir=workdir,
   → extras=extrafiles
)
```

A full example of how to run a reliability analysis of a model defined in *OpenSees* can be found in the demo files of *UncertaintyQuantification*.

#### 7.3 Reliability Analysis

Reliability analysis, as in the computation of the probability of failure of an engineering system, is facilitated through the simple method interface **probability\_of\_failure**. The method used to calculate this failure probability is selected internally based on the supplied arguments making use of Julia's multiple dispatch.

All methods to compute the probability of failure require the definition of a performance (limit-state) function g(x) where  $x \in \mathbb{R}^{n_x}$  is the set of input variables. By definition, failure of the system occurs for g(x) < 0. When implementing the limit-state, the Julia function operates on a **DataFrame** as seen with the Model. The **DataFrame** passed to the performance function includes the responses of all models.

#### 7.3.1 First order reliability method

In the *first-order reliability method* (FORM) [210, 211], the random variables are transformed into the uncorrelated standard normal space and the limit-state function is approximated by a first-order Taylor series expansion at the design point. The design point being the point on the limit-state closest to the origin in the standard normal space.

Assume two random variables  $x_1 \sim N(200, 20)$  and  $x_2 \sim N(150, 10)$  with the failure domain being

$$F = \{(x_1, x_2) : x_2 > x_1\}.$$
(7.2)

The following script will compute the failure probability using FORM. The solution is obtained using the Hasofer-Lind-Rackwitz-Fiessler (HL-RF) algorithm.

```
form = FORM()
x1 = RandomVariable(Normal(200, 20), :x1)
x2 = RandomVariable(Normal(150, 10), :x2)
function g(df)
return df.x1 .- df.x2
end
pf, beta, dp = probability_of_failure(g, [x1, x2], form)
```

The returned quantities are the probability of failure  $p_f \approx 0.012673$ , the reliability index  $\beta \approx 2.23606$  and the design point  $dp \approx (160, 160)$ . In this case, the **probability\_of\_failure** function is called without a separate model, which can be included as the first input if desired. The **FORM** struct holds no information and its sole purpose is to dispatch to the correct method.

Currently *UncertaintyQuantification* only implements the HL-RF algorithm to compute the design point. To circumvent the algorithm's known shortcomings, we plan to add an alternative method, where the design point identification is solved as an optimization problem, in the future.

#### 7.3.2 Monte Carlo Simulation

The probability of failure can also be approximated by a variety of Monte Carlo simulation techniques. The module includes standard Monte Carlo simulation as well as a number of quasi-Monte Carlo simulation methods such as Latin hypercube sampling or Sobol' sampling. In order to compute the probability of failure for the simple example presented in the previous subsection through standard Monte Carlo simulation, we need only replace the FORM struct with a MonteCarlo struct. The only parameter necessary to construct the MonteCarlo object is the desired number of samples to be used.

```
mc = MonteCarlo(10000)
pf, c, samples = probability_of_failure(g, [x1, x2], mc)
```

The probability of failure obtained from the simulation is  $p_f = 0.0129$  with a coefficient of variation of 0.87475 which agrees with the results obtained by FORM in the previous section. In difference to FORM, any of the Monte Carlo methods will return the the coefficient of variation and the evaluated samples instead of the reliability index and the design point.

To run the simulation with quasi-Monte Carlo techniques, simply replace the MonteCarlo struct.

```
pf, c, samples = probability_of_failure(g, [x1, x2],

→ LatinHypercubeSampling(10000))
pf, c, samples = probability_of_failure(g, [x1, x2], HaltonSampling(10000))
pf, c, samples = probability_of_failure(g, [x1, x2], SobolSampling(10000))
```

UncertaintyQuantification provides some advanced Monte Carlo methods, namely LineSamp J ling and SubSetSimulation. For a more complex example using SubSetSimulation to estimate small failure probabilies, see Section 7.6.1.

#### 7.4 Sensitivity Analysis

This section presents the methods for both local and global sensitivity analysis included in *UncertaintyQuantification*. Sensitivity analysis examines how the uncertainty of the model output can be attributed to the uncertainty of the inputs [212]. There are two major areas of sensitivity. Where local sensitivity analysis considers the influence of inputs in a certain point, global sensitivity analysis considers the complete input space.

#### 7.4.1 Local Sensitivity Analysis

UncertaintyQuantification provides the computation of gradients for local, derivative based, sensitivity analysis through the gradient method. For a set of input variables and models the gradient can be calculated by passing a DataFrame of reference points to evaluate. The gradient method will return a new DataFrame of the same size, containing the gradients. Internally, finite difference methods are used to approximate the gradients.

grads = gradient(model, inputs, reference, output)

Gradients can alternatively be estimated after transformation to the standard normal space. However, this is mainly provided in order to find the important direction required for line sampling [136].

grads = gradient\_in\_standard\_normal\_space(model, inputs, reference, output)

#### 7.4.2 Global Sensitivity Analysis

For global sensitivity analysis [212] Uncertainty Quantification provides Sobol' indices, a form of variance based sensitivity analysis. This type of sensitivity analysis quantifies how much of the variance of a model output can be attributed to each of the inputs. Two main sensitivity measures are defined. For a model  $Y = f(X_1, X_2, \ldots, X_n)$ , the first order index is defined by

$$S_i = \frac{V_{X_i}(E_{\mathbf{X}_{\sim i}}(Y|X_i))}{V(Y)},\tag{7.3}$$

where  $\mathbf{X}_{\sim i}$  represents all input variables except *i*. The first order index captures the effect of varying  $X_i$  alone. The total effect index captures also the variance caused by all interactions of  $X_i$  with other variables. It is defined as

$$S_{T_i} = \frac{E_{\mathbf{X}_{\sim i}}(V_{X_i}(Y|\mathbf{X}_{\sim i}))}{V(Y)}.$$
(7.4)

To compute simulation based Sobol' indices we must first define the inputs and model as with all the previous examples. The indices can then be approximated by calling the **sobolindices** function. Quasi-Monte carlo methods like **SobolSampling** usually lead to better results than brute force Monte Carlo. The Sobol' indices for multiple models of the same inputs can be computed simultaneously by passing vectors of models and output symbols to the method.

```
# single model/output
indices = sobolindices(model, inputs, :y, SobolSampling(2000))
# multiple models/outputs
indices = sobolindices([m1, m2], inputs, [:y1, :y2], SobolSampling(2000))
```

The Sobol' indices are estimated according to Jansen (1999) [213] and Saltelli (2010) [214]. Bootstrapping is used to quantify the standard error of the estimators. For a complete example of how to compute Sobol' indices, see Section 7.6.2.

#### 7.5 Metamodelling

When dealing with complex, long running models, a single run of the model can take hours to days. In these cases, it is infeasible to run any analysis requiring a large number of samples. Quantities such as Sobol' indices for sensitivity analysis simply can not be computed. In these cases we can apply so called *metamodels* or *surrogate models*. These models are constructed from a small selection of evaluations of the true model and aim to approximate it as closely as possible. The metamodel itself is easy to evaluate and enables the analyses which where inaccessible for the original model.

The metamodels currently included in *UncertaintyQuantification* are the response surface methodology, polyharmonic splines and polynomial chaos expansion. Several designs of experiments (central composite design, Box-behnken design, factorial design), are provided to fit response surface models.

#### 7.5.1 Polyharmonic spline

As a simple example we are going to construct a polyharmonic spline metamodel for a simple one-dimensional test function. A polyharmonic spline [215] is a combination of a low degree polynomial term and polyharmonic radial basis functions of the form

$$s(x) = \sum_{i=1}^{N} w_i \varphi(|\mathbf{x} - \mathbf{c}_i|) + \mathbf{v}^T \begin{bmatrix} 1\\ \mathbf{x} \end{bmatrix}.$$
 (7.5)

The radial basis functions are  $\varphi(r) = r^p, p = 1, 3, 5, ...,$  and  $\varphi(r) = r^p \ln(r), p = 2, 4, 6, ...,$ with degree p and  $r = |\mathbf{x} - c_i| = \sqrt{(\mathbf{x} - \mathbf{c}_i)^T (\mathbf{x} - \mathbf{c}_i)}$ . The N center points to interpolate are denoted by  $\mathbf{c}_i$ .

The test function [216] is defined on  $x \in [0, 1]$  as

$$f(x) = (6x - 2)^2 \sin(12x - 4).$$
(7.6)

To start, we set up the necessary input and the model. We sample 20 values of x using Sobol' sampling and evaluate the model for the sampled points. By using a quasi-Monte Carlo sampling scheme we make sure that the sampled points have adequate coverage of the input space. Figure 7.2: Polyharmonic spline metamodel compared to the true function.

```
x = RandomVariable(Uniform(0, 1), :x)
m = Model(df -> (6 .* x .- 2) .^ 2 .* sin.(12 .* x .- 4), :y)
data = sample(x, SobolSampling(20))
evaluate!(m, data)
```

In order to construct the polyharmonic spline (and determine the required weights  $\mathbf{w}$  and  $\mathbf{v}$ ), the sampled points are passed to the constructor along with the desired degree p = 2 and the Symbol of the output to fit the metamodel to.

```
ps = PolyharmonicSpline(data, 2, :y)
```

A plot comparing the metamodel to the original function and the sampled points can be seen in Figure 7.2. With just 20 sampled points, the spline is able to accurately approximate the test function.

#### 7.6 Numerical Examples

This section presents a few more complex examples than the ones presented in the previous sections.

#### 7.6.1 Estimation of small failure probabilities

Subset simulation [see 137] is an advanced Monte Carlo simulation technique for the estimation of small failure probabilities. Here we solve a simple problem [taken from 217, page 9] where the response y depends on two independent random variables  $x_1$  and  $x_2$  following a standard normal distribution. The simple linear model is defined by

$$y(x_1, x_2) = x_1 + x_2 \tag{7.7}$$

with the failure domain

$$F = \{(x_1, x_2) : x_1 + x_2 > 9\}.$$
(7.8)

The analytical probability of failure can be calculated as

$$p_f = 1 - \Phi(\frac{9}{\sqrt{2}}) \approx 1 \times 10^{-10},$$
(7.9)

where  $\Phi$  is the standard normal cumulative density function.

In order to solve this problem, we start by creating the two standard normal random variables and group them in a vector inputs.

```
x1 = RandomVariable(Normal(), :x1)
x2 = RandomVariable(Normal(), :x2)
inputs = [x1, x2]
```

Next we define the model as

 $y = Model(df \rightarrow df.x1 + df.x2, :y)$ 

where the first input is our function (which must accept a DataFrame) and the second the Symbol for the output variable.

To estimate a failure probability we need a performance function. This function, which accepts a DataFrame similar to the Model, must return a vector which is negative if a failure occurs for a sample. Here, a failure occurs if y exceeds 9.

```
function g(df::DataFrame)
  return 9 .- df.y
end
```

Finally, we create the SubSetSimulation object and compute the probability of failure using a standard Gaussian proposal PDF. The value for the target probability of failure at each intermediate level is set to 0.1.

```
subset = SubSetSimulation(1000, 0.1, 10, Normal())
pf, cov, samples = probability_of_failure(y, g, inputs, subset)
```

Alternatively, instead of using the standard Subset simulation algorithm (which internally uses Markov Chain Monte Carlo), we can use **SubSetInfinity** to compute the probability of failure, see [218]. Here we use a standard deviation of 0.5 to create the proposal samples for the next level.

```
subset = SubSetInfinity(1000, 0.1, 10, 0.5)
pf, cov, samples = probability_of_failure(y, g, inputs, subset)
```

Figure 7.3 shows the samples at each level of the two Subset simulations. Both methods are able to estimate the small probability of failure with the MCMC based method yielding  $p_f \approx 5.3912e - 10$  and Subset- $\infty p_f \approx 3.13212e - 11$ . The plots show, that Subset- $\infty$  required two extra levels to approximate the probability of failure. However, due to the numerical demand of the Markov chains, Subset- $\infty$  runs about twice as fast for this example.



Figure 7.3: Samples at the different levels for the two Subset simulations. Both simulations have been started from the same seed samples at the first level.

#### 7.6.2 Global Sensitivity Analysis of the Ishigami function

The Ishigami function [219] given by

$$f(x) = \sin(x_1) + a\sin(x_2)^2 + bx_3^4\sin(x_1), \tag{7.10}$$

with  $x_i \sim U(-\pi,\pi)$  for i = 1, 2, 3, is often used to benchmark global sensitivity analysis methods. It shows strong nonlinearity and has an interesting dependence on  $x_3$ . The parameter *a* is typically set to 7 while *b* is either 0.1 [220] or 0.05 [221].

The following script will estimate the first order and total effect Sobol' indices of the Ishigami function using 10000 samples drawn from the Sobol' sequence. Using a quasi-Monte Carlo method instead of the brute force method improves convergence of the Sobol' indices.

```
x = RandomVariable.(Uniform(-pi,pi), [:x1, :x2, :x3])
a = Parameter(7, :a)
b = Parameter(0.1, :b)
function ishigami(df)
return @. sin(df.x1) + df.a * sin(df.x2)^2 + df.b * df.x3^4 * sin(df.x1)
end
m = Model(ishigami, :y)
sobol = sobolindices(m, [x..., a, b], :y, SobolSampling(10000))
```

The Sobol' indices computed for the Ishigami function using 10000 samples are shown in

The analytical solutions $S_i$ and $ST_i$ are included for comparison.							
$x_i$	$\hat{S}_i$	$\sigma_{\hat{S}_i}$	$S_i$	$\hat{S_{T_i}}$	$\sigma_{\hat{S_{T_i}}}$	$S_{T_i}$	
$x_1$	0.291419	0.00964169	0.3138	0.536946	0.0129737	0.5574	
$x_2$	0.436318	0.0102289	0.4424	0.439057	0.0130688	0.4424	
$x_3$	-0.004927	0.0101326	0.0	0.243939	0.0130147	0.2436	
	0.	6	I	First O	rder		

**Table 7.1:** Approximated first order and total effect Sobol' indices of the Ishigami function with estimated standard errors. The analytical solutions  $S_i$  and  $S_{T_i}$  are included for comparison.



Figure 7.4: First order and total effect Sobol' indices of the Ishigami function.

Figure 7.4 and Table 7.1.  $S_3$  being slightly negative can be attributed to numerical inaccuracies. Note also the interesting dependence on  $x_3$ . While  $S_3$  suggests no influence on the function at all,  $S_{T_3}$  proves that  $x_3$  has significant influence through interactions.

Computing thousands of model evaluations will be impossible for a complex model. To work around this problem, we can build an accurate metamodel of our model and use it to compute the Sobol' indices as seen in the next section.

#### 7.6.3 Metamodelling and Global Sensitivity Analysis

It is entirely possible to build a metamodel such as a response surface or polyharmonic spline based on a few model evaluations and use it to compute the Sobol' indices similarly to the previous section. However, a unique property of the polynomial chaos expansion (PCE) [222] is that it provides the Sobol' indices as a byproduct as they can be calculated from the coefficients of the PCE. Consider again the Ishigami function. In order to build a PCE metamodel we must first define the polynomial basis to be used.

We begin by selecting the degree p = 8 and the Legendre polynomials as a basis for the three input variables. Then we assemble the **PolynomialChaosBasis** from the combinations of degree up to p of our basis functions.

	$\hat{S}_i$	$\hat{S_{T_i}}$
$x_1$	0.312994	0.555787
$x_2$	0.444213	0.444213
$x_3$	5.10399e-32	0.242794

 Table 7.2: First order and total effect Sobol' indices of the Ishigami function estimated from the polynomial chaos expansion.

```
p = 8
bases = [LegendreBasis(), LegendreBasis(), LegendreBasis()]
psi = PolynomialChaosBasis(bases, p)
```

Internally, UncertaintyQuantification will perform an isoprobabilistic transformation of the inputs to the support of the basis functions (in this case [0, 1] for all inputs). Next, the PCE metamodel is built using Gauss quadrature and the Sobol' indices are computed directly from the polynomial chaos expasion.

```
pce, samples = polynomialchaos(inputs, m, psi, :y, GaussQuadrature())
sobol = sobolindices(pce)
```

The resulting indices are presented in Table 7.2. No errors are estimated when computing the Sobol' indices from a polynomial chaos expansion. With just 729 model evaluations for p = 8 one can see that the results are much closer to the analytical solution than using 10000 samples with the true model. Note, that the number of required quadrature nodes grows quickly with increasing degree and the number of inputs. This issue can be eleviated by applying sparse quadrature grids. However, the implementation of sparse quadrature and other methods of estimating the PCE coefficients in *UncertaintyQuantification* is still ongoing.

#### 7.7 Conclusion

This paper presented a new framework for uncertainty quantification called *UncertaintyQuantification.jl.* The framework has been developed as a module in the Julia programming language making use of its modern features. This work serves as an introduction to the framework. We presented its basic usage and outlined how to perform a few key analyses including reliability analysis, sensitivity analysis and metamodelling.

Ongoing development of the framework is focused on improving existing methods such as extending the polynomial chaos expansion with sparse quadratures, as well as adding more algorithms. Features currently in development include more metamodels like Kriging and artificial neural networks, global sensitivity analysis with dependent inputs and the propagation of imprecise probabilities through probability boxes.

### 7 UncertaintyQuantification.jl: A new Framework for Uncertainty Quantification in Julia

The source code of the framework is released under the MIT license and publicly available on Github. Contributions from other researchers are very welcome.

## 8 Conclusions and outlook

This chapter summarizes the key developments presented in this thesis and provides an outlook into the direction of future research.

#### 8.1 Conclusions

This dissertation discusses several important improvements to the survival signature ecosystem. New methodologies are presented, where copulas are used to model dependent failures while Monte Carlo simulation and surrogate models allow for efficient approximation of the survival signature. These methods, when combined, allow for the efficient numerical reliability analysis of complex coupled networks. The individual contributions are summarized next.

The first publication presented focuses on modelling dependencies in networks and interdependencies between different networks for the reliability analysis. Based on the separation of probabilistic and structural information inherent to the survival signature, this new method proposes to model the dependencies using copulas in the probabilistic part of the survival function. Failures cascade between networks solely based on the component failures sampled from the copulas. Pair-copula construction through vine copulas is suggested to model highdimensional multivariate failure time distributions. In addition, the inclusion of imprecise probabilities in the copulas and the marginal distributions is presented. The concept has been applied successfully to an example based on the IEEE reliability test system.

Instead of the probabilistic modelling of component failures, the second contribution focuses on efficiently deriving the survival signature for large networks. The proposed method is divided into two steps. First, large parts of the survival signature can be excluded as negligible through the application of percolation theory. In the second step, the remaining entries are approximated using Monte Carlo simulation. The errors of both steps in comparison to the analytical solution are quantified using simple toy examples. It is shown, that the new method is able to accurately approximate the survival signature with a significant reduction in numerical effort. Finally, to demonstrate scalability to larger systems, the approach is applied to a network based on the Berlin S- and U-Bahn systems. With this new method, systems with hundreds of components can be analysed through the survival signature where previously the computational demand was prohibitive.

Expanding on this approximation method, the third and fourth publications develop a

surrogate model for the survival signature instead of fully approximating it. First, a radial basis function network is constructed based on a few initial data points estimated through the previous Monte Carlo technique. Next, this surrogate model is adaptively refined until it provides an accurate representation of the survival signature. In the final step, the uncertainty associated with the Monte Carlo simulation is propagated through an interval predictor model into the final survival signature. With only a few computed signature entries, this new method is able to accurately predict bounds on the survival signature and therefore the reliability. In comparison to the method based only on Monte Carlo simulation, this new technique provides another significant reduction in numerical demand. In the presented examples, a survival signature with 119556 entries is accurately predicted with only 406 evaluated data points.

The fifth contribution extends a framework for resilience decision-making to multidimensional problems and substructured systems. The resilience of large systems can be efficiently quantified by computing the survival signature for the subsystems and deriving failure rates from the survival functions. The proposed approach can analyse systems with thousands of components. Simulations for different endowment configurations are often computationally demanding. This requirement is reduced greatly by exploiting the separation property of the survival signature and modifying only the probability structures of the component failure times.

The sixth and final paper introduces a new framework for uncertainty quantification. This new framework, developed in the modern Julia programming language, offers generalized algorithms for reliability analysis, sensitivity analysis, and numerous metamodelling approaches. It is open to the public and encourages contributions from the research community.

#### 8.2 Outlook

The methods presented in this dissertation are able to efficiently estimate the reliability of large dependent networks. However, several potential areas for improvement have been identified during their development and are presented here.

In regard to modelling dependencies with copulas, especially vine copulas, it has been shown that constructing the copula model is a complex task. Alternative methods for modelling multivariate distributions could prove beneficial. For example, the recently presented class of Sliced-Normal [149] distributions allows for the characterization of complex dependencies with little modelling effort and could serve as a potential replacement of the copula model.

An area of interest for the approximation of the survival signature is the reduction of samples required to accurately estimate a single entry, which both presented methods will benefit from. Advanced Monte Carlo methods such as line sampling [136] or subset simulation [137, 217] suggest great potential and should be investigated.

In addition, for the surrogate model approach, different refinement schemes for the radial basis function network should be compared. Moreover, the current assumptions made for the number of centers and spread of the basis functions are rough and can certainly be optimized in the future. Optimal centers and spread can potentially lead to the method requiring even less data points for an accurate representation of the true survival signature.

The current development focus for the *UncertaintyQuantification.jl* framework lies on feature parity with OpenCOSSAN and the implementation of completely new algorithms. Areas of special interest are the inclusion of more surrogate models such as Kriging and artificial neural networks, reliability based optimization, and the efficient propagation of imprecise probabilities.

# 9 List of publications

### Journal articles

- Behrensdorf, J., Broggi, M. and Beer, M. 'Interval Predictor Model for the Survival Signature Using Monotone Radial Basis Functions'. In: ASCE-ASME Journal of Risk and Uncertainty in Engineering Systems, Part A: Civil Engineering (2023). Submitted
- Salomon, J., Behrensdorf, J., Winnewisser, N., Broggi, M. and Beer, M. 'Multidimensional Resilience Decision-Making for Complex and Substructured Systems'. In: *Resilient Cities* and Structures. Resilience of Civil Infrastructure to Multiple Hazards and Climate Change 1.3 (2022), pages 61–78. DOI: 10.1016/j.rcns.2022.10.005
- Behrensdorf, J., Regenhardt, T.-E., Broggi, M. and Beer, M. 'Numerically Efficient Computation of the Survival Signature for the Reliability Analysis of Large Networks'. In: *Reliability Engineering & System Safety* 216 (2021), page 107935. DOI: 10.1016/j.r ess.2021.107935
- Yang, L., Wang, P., Wang, Q., Bi, S., Peng, R., Behrensdorf, J. and Beer, M. 'Reliability Analysis of a Complex System with Hybrid Structures and Multi-Level Dependent Life Metrics'. In: *Reliability Engineering & System Safety* 209 (2021), page 107469. DOI: 10.1016/j.ress.2021.107469
- Behrensdorf, J., Broggi, M. and Beer, M. 'Reliability Analysis of Networks Interconnected With Copulas'. In: ASCE-ASME Journal of Risk and Uncertainty in Engineering Systems, Part B: Mechanical Engineering 5.4 (2019), 041006 (9 Pages). DOI: 10.1115/1.4044043

#### **Book contributions**

- Salomon, J., Behrensdorf, J. and Beer, M. 'Resilienz Baulicher Infrastruktur Sicher Und Wirtschaftlicher Durch Dick Und Dünn'. In: 26. Dresdner Baustatik - Seminar - "Realität-Modellierung-Tragwerksplanung". Institut für Statik und Dynamik der Tragwerke, TU Dresden, 2022
- Behrensdorf, J., Broggi, M. and Beer, M. 'Efficient Reliability and Risk Analysis of Complex Interconnected Systems'. In: *Resilience Engineering for Urban Tunnels*. Amer-

ican Society of Civil Engineers, 2018, pages 43–54. ISBN: 978-0-7844-1513-9. DOI: 10.1061/9780784415139.ch04

## **Conference** papers

- Behrensdorf, J., Broggi, M. and Beer, M. 'Imprecise Survival Signature Approximation Using Interval Predictor Models'. In: 2023 IEEE Symposium Series on Computational Intelligence. Submitted. Mexico City, Mexico, 2023
- Behrensdorf, J., Gray, A., Broggi, M. and Beer, M. 'UncertaintyQuantification.jl.: A New Framework for Uncertainty Quantification in Julia'. In: *Proceedings of the 5th ECCOMAS Thematic Conference on Uncertainty Quantification in Computational Sciences and Engineering (UNCECOMP 2023)*. Edited by M. Papadrakakis, V. Papadopoulos and G. Stefanou. Athens, Greece, 2023
- Bittner, M., Behrendt, M., Behrensdorf, J. and Beer, M. 'Epistemic Uncertainty Quantification of Localised Seismic Power Spectral Densities'. In: Probabilistic Safety Assessment and Management PSAM 16. Honolulu, USA, 2022
- Salomon, J., Behrensdorf, J., Winnewisser, N., Broggi, M. and Beer, M. 'Resilience Decision-Making for Complex and Substructured Systems'. In: *Proceedings of the 8th International Symposium on Reliability Engineering and Risk Management*. Edited by M. Beer, E. Zio, K.-K. Phoon and B. M. Ayyub. Singapore: Research Publishing Services, 2022, pages 530–537. DOI: 10.3850/978-981-18-5184-1\_MS-16-191-cd
- Salomon, J., Behrensdorf, J., Broggi, M., Weber, S. and Beer, M. 'Multidimensional Resilience Decision-Making On A Multistage High-Speed Axial Compressor'. In: *Proceedings of the 29th European Safety and Reliability Conference*. Edited by M. Beer and E. Zio. Singapore: Research Publishing Services, 2019, pages 1357–1364. DOI: 10.3850/978-981-11-2724-3\_0992-cd
- Behrensdorf, J., Brandt, S., Broggi, M. and Beer, M. 'Efficient Approximation of the Survival Signature for Large Networks'. In: *Proceedings of the 6th International Symposium* on Reliability Engineering and Risk Management. Singapore: Research Publishing Services, 2018, pages 661–666. ISBN: 978-981-11-2726-7. DOI: 10.3850/978-981-11-2726-7\_CRR1 4
- Behrensdorf, J., Broggi, M. and Beer, M. 'Imprecise Reliability Analysis of Complex Interconnected Networks'. In: Safety and Reliability - Safe Societies in a Changing World. 28th European Safety and Reliability Conference. Edited by S. Haugen, A. Barros, C. Gulijk, T. Kongsvik and J. E. Vinnem. London: CRC Press, 2018, pages 2589–2594. ISBN: 978-1-351-17466-4. DOI: 10.1201/9781351174664-325

### 9 List of publications

 Behrensdorf, J., Broggi, M., Brandt, S. and Beer, M. 'Numerically Efficient Reliability Analysis of Interdependent Networks'. In: *Safety and Reliability. Theory and Applications*. 27th European Safety and Reliability Conference. Edited by M. Cepin and R. Bris. London: CRC Press, 2017. DOI: 10.1201/9781315210469-298

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# Curriculum Vitae

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#### Education

since $04/2017$	PhD student
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04/2014 - 09/2016	Master of Science, Computational Engineering
	Thesis: Comparing isogeometric mesh generation techniques for
	curve-to-area parametrization
	Leibniz Universität Hannover
10/2009 - 03/2014	Bachelor of Science, Computational Engineering
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	Thesis: Konzeptionierung und softwaretechnische Umsetzung einer
	Prüfstandsimulation für Schulungszwecke

## Work experience

since 09/2016	Research assistant
	Institute for Risk and Reliability, Leibniz Universität Hannover
07/2015 - 09/2016	Student assistant
	Institute for Risk and Reliability, Leibniz Universität Hannover
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