# 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

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## 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 [1]. Past research has highlighted the importance of considering effects such as dependencies, common causes of failure and imprecision [2, 3, 4] 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 [5].

The survival signature was developed as a generalization of the systems signature [6] 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. [7]. Recent research showed that repairable systems [8], mission-stage-behaviour [9] and the combination of subsystems [10] 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 [11], dependent failures [12], imprecision [13] 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 [14] 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) [15]. 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 [16]. Then, the remaining entries are approximated using Monte Carlo simulation [17]. 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 2 presents the theory on the survival signature while Section 3 introduces percolation theory. The developed simulation algorithm is discussed in Section 4 including the application to toy examples and quantification of errors. Section 5 applies the proposed approach to more complex real world examples, followed by some concluding remarks in Section 6.

## 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 $\varphi : \{0,1\}^m \rightarrow \{0,1\}$. 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 $K \geq 2$ 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: $\underline{x} = (\underline{x}^1, \underline{x}^2, \ldots, \underline{x}^K)$. Each of these sub-vectors now indicate the states of all components of that specific type, for example $\underline{x}^k = (x_1^k, x_2^k, \ldots, x_{m_k}^k)$.

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) [5]. 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

$$\begin{aligned} \Phi(\underline{l} = \underline{0}) &= 0, \\ \Phi(\underline{l} = \underline{1}) &= 1, \\ \Phi(\underline{l}^a) \leq \Phi(\underline{l}^b) \text{ if } l_k^a \leq l_k^b,\ &\forall k \in (1, 2, \ldots, K), \end{aligned} \tag{1}$$

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 $k = 1, \ldots, K$. 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 $S_{l_1,\ldots,l_K}$. 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:

$$\Phi(\underline{l}) = \left[\prod_{k=1}^{K} \binom{m_k}{l_k}\right]^{-1} \times \sum_{\underline{x} \in S_{l_1,\ldots,l_K}} \varphi(\underline{x}), \tag{2}$$

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. 1 is presented in Table 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 $t$:

$$P(T_s > t) = \sum_{l_1=0}^{m_1} \ldots \sum_{l_K=0}^{m_K} \Phi(\underline{l})\ P\left(\bigcap_{k=1}^{K} \{C_t^k = l_k\}\right), \tag{3}$$

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

| $l_1$ | $l_2$ | $\Phi(l_1, l_2)$ | $l_1$ | $l_2$ | $\Phi(l_1, l_2)$ |
|---|---|---|---|---|---|
| 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: Survival signature of the system in Fig. 1.

a known cumulative distribution function $F_k(t)$, the probabilistic part of the survival function can be simplified to

$$\begin{aligned} P\left(\bigcap_{k=1}^{K}\{C_t^k = l_k\}\right) &= \prod_{k=1}^{K} P(C_t^k = l_k) = \cdots \\ \cdots &= \prod_{k=1}^{K}\left(\binom{m_k}{l_k} F_k(t)^{m_k - l_k}[1 - F_k(t)]^{l_k}\right). \end{aligned} \tag{4}$$

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 [11, 18].

In this work, application of the survival signature is restricted to systems consisting of binary components, in accordance with its original definition [5]. Generalization of the survival signature to multi-state systems is still actively being researched [19, 20].

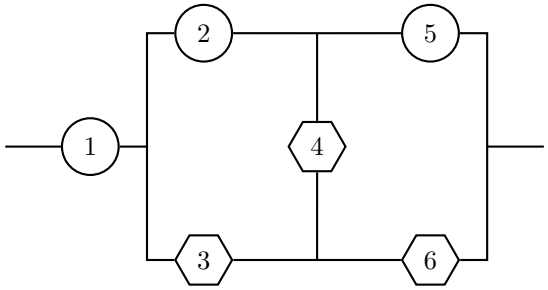


Figure 1: Example system with $K = 2$ component types and $m_1 + m_2 = 3 + 3 = 6$ components. The component types are represented by different shapes.

## 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 [21], 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 [22].

### *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* [23]. 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 [24] 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 $f_c$ [25]:

$$\begin{aligned} < s > &\sim |f - f_c|^{-\gamma} \text{ (avg. cluster size)}, \\ p_{\text{in}} &\sim (f - f_c)^{\beta} \text{ (prob. that random node is in cluster)}, \\ \xi &\sim |f - f_c|^{-\nu} \text{ (mean distance in cluster)}. \end{aligned} \tag{5}$$

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.

### *3.2. 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 [26]. For any graph, this can be expressed as

$$\kappa = \frac{< d^2 >}{< d >} > 2, \tag{6}$$

with $d$ being the node degree (sum of all connections going into a node), and $< d >$ and $< d^2 >$ 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

$$f_c = 1 - \frac{1}{\kappa - 1}, \tag{7}$$

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:

$$\sum_{k=1}^{K} l_k < (1 - f_c) \cdot \sum_{k=1}^{K} m_k \Rightarrow \Phi(\underline{l}) \approx 0. \tag{8}$$

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

Equations 6 and 8 have also been independently developed by Cohen et al. [27].

## 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. 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. 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 $w_{\underline{l}}$ by one. Next, update the approximation using

$$\Phi(\underline{l}) \approx \frac{w_{\underline{l}}}{n_{\underline{l}}} \tag{9}$$

and the current coefficient of variation by

$$c_{\underline{l}} = \frac{\sqrt{(\Phi(\underline{l}) - \Phi(\underline{l})^2)/n_{\underline{l}}}}{\Phi(\underline{l})}. \tag{10}$$

A pseudo-code implementation of the algorithm is presented in Algorithm 1. Note, that entries where the number of possible network states is smaller than $N$ are calculated analytically through Eq. 2.

Eq. 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 [28].

**Algorithm 1** Approximate survival signature entry

**function** APPROXIMATE($\underline{l}, \varphi, N, C$)
  $c, n, w, \Phi \leftarrow 0$ ▷ Initialise variables
  **while** $c > C$ **and** $n \leq N$ **do**
    $n \leftarrow n + 1$
    $s \leftarrow$ random network state for $\underline{l}$
    **if** $\varphi(s) = 1$ **then**
      $w \leftarrow w + 1$
    **end if**
    $\Phi \leftarrow w/n$
    $c \leftarrow \frac{\sqrt{(\Phi - \Phi^2)/n}}{\Phi}$
  **end while**
  **return** $\Phi,\ c$ ▷ 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. 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 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 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.

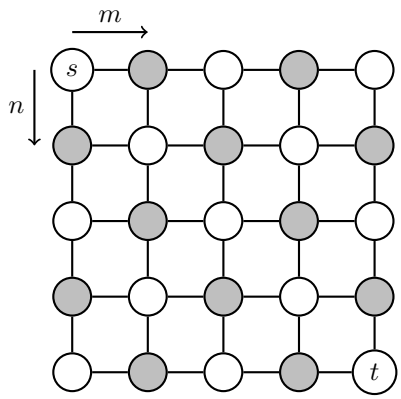


Figure 2: Simple grid network of size $5 \times 5$ with 25 nodes and 40 edges. The nodes labeled $s$ and $t$ are the source and target nodes.

### *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. 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. 8. Then, the absolute error

$$E_{f_c} = \|\Phi - \Phi_{f_c}\|_F \tag{11}$$

and relative error

$$\widetilde{E}_{f_c} = \frac{E_{f_c}}{\|\Phi\|_F} \tag{12}$$

made by excluding the entries below the threshold is calculated. The results are presented in Tab. 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

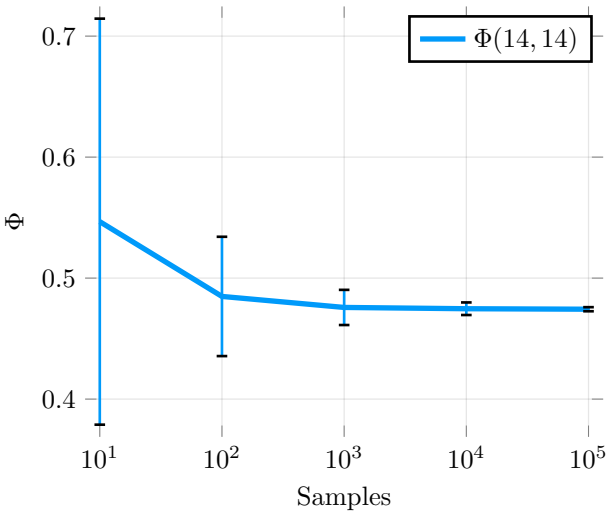


Figure 3: Convergence of the approximated signature entry $\Phi(14, 14)$ for the $6 \times 6$ network to the exact value of 0.4741594. The number of state vector evaluations needed for the exact solution is 9 363 600.

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 | N | $E_{f_c}$ | $\widetilde{E}_{f_c}$ |
|---|---|---|---|---|---|
| $5 \times 5$ | 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 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

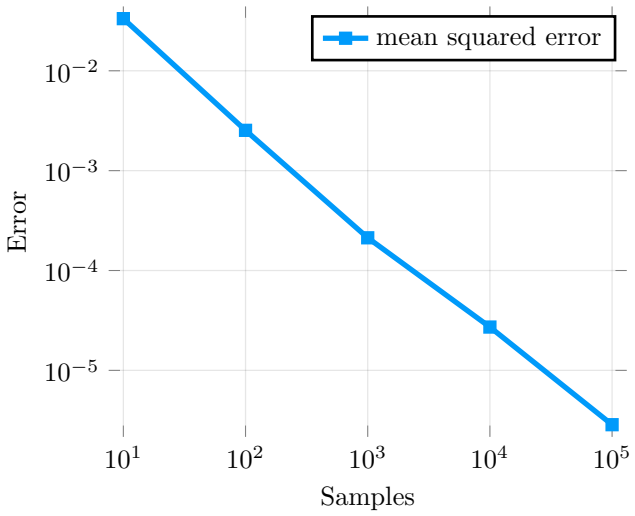


Figure 4: Evolution of the mean squared error when approximating the survival signature entry $\Phi(14, 14)$ for the 6×6 network with increasing sample size.

large-scale networks should be studied more closely in the future.

### *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 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

$$E_{mc} = \|\Phi_{f_c} - \Phi_{mc}\|_F \tag{13}$$

and relative error

$$\widetilde{E}_{mc} = \frac{E_{mc}}{\|\Phi_{f_c}\|_F} \tag{14}$$

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 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 | $n_\varphi$ | $E_{mc}$ | $\widetilde{E}_{mc}$ |
|---|---|---|---|---|
| $5 \times 5$ | $2^{25}$ | 399256 | 0.0207 | 0.0056 |
| $5 \times 6$ | $2^{30}$ | 862400 | 0.0347 | 0.0085 |
| $6 \times 6$ | $2^{36}$ | 2099933 | 0.0451 | 0.0086 |

Table 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 $n_\varphi$.

### *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 and Eq. 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. 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 $\widetilde{E}_P = \|P - P_{mc}\|_F \,/\, \|P\|_F$ 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. 4.

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

Table 4: Absolute and relative errors resulting from a reliability analysis using the approximated survival signatures.

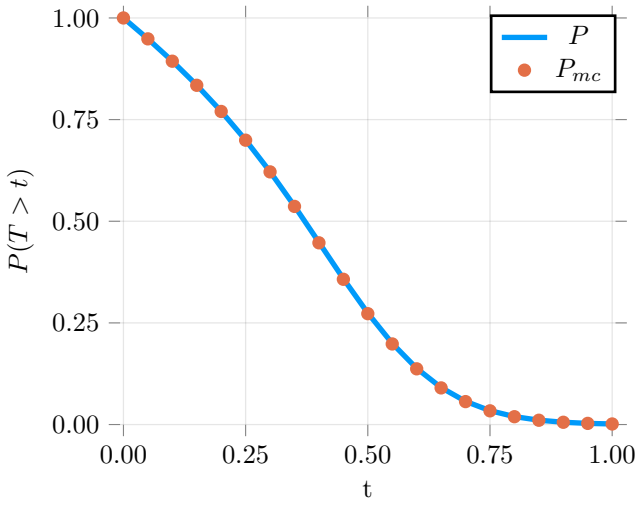


Figure 5: Survival functions of the $6 \times 6$ network. The approximated reliability of the network denoted by $P_{mc}$ closely matches the analytical solution $P$.

## 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 4.

### *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 [29]. The network consists of 29 nodes that are split into two component types based on their bus type. Load buses

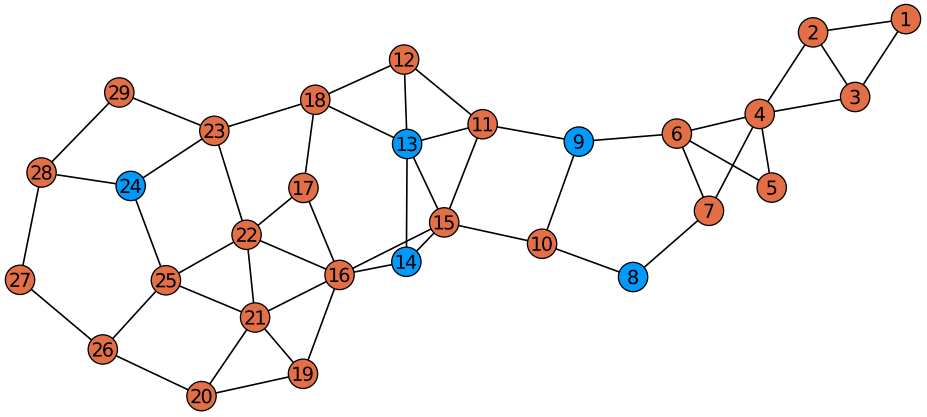


Figure 6: Topology of the electricity transmission network used in example 1. Components of type 1 are shown in blue. Components of type 2 are shown in orange. The locations of the nodes in the figure are not related to their actual geographical location.

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. 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 Section 4, has little meaning for this network. Instead, the so called network efficiency [30] as defined in Eq. 15 is used to measure the state of the network for a given state vector.

$$E(G) = \frac{1}{n(n-1)} \sum_{i \neq j \in G} \frac{1}{d(i,j)} \tag{15}$$

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

$$\varphi(\underline{x}) = \frac{E(G(\underline{x}))}{E(G)} < 0.5. \tag{16}$$

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 [31].

Survival signature approximations are performed with increasing sample sizes and compared to the exact solution to prove convergance. Figure 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 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 11 069 s for the full combinatorial evaluation.

### *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 [32]. 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. 8. The same structure function as in example 1 is applied to the network, see Eq. 16.

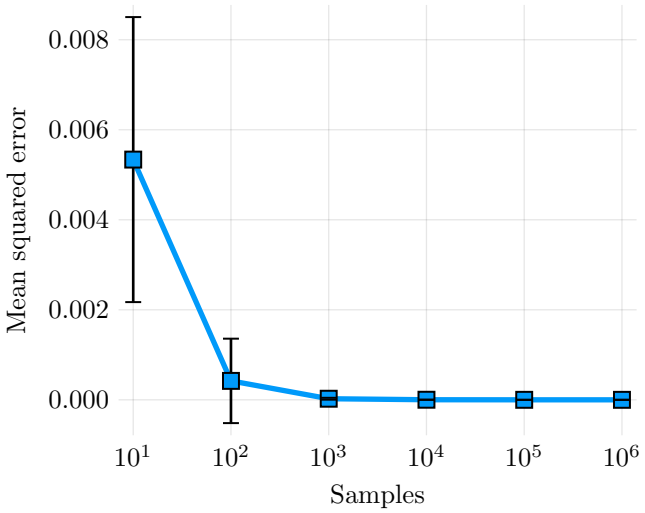


Figure 7: Evolution of the mean squared error resulting from approximation of the survival signature for the network shown in Fig. 6 with increasing number of samples used.

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. 7. The approximation of a single survival signature is essentially the same as computing a probability of failure. The minimum number of samples $N$ required to estimate a probability of failure or in this case survival signature entry $\Phi(\underline{l})$ is defined by

$$N \leq \frac{1}{c^2 \cdot \Phi(\underline{l})}, \tag{17}$$

where $c$ is the desired coefficient of variation [1]. This shows that the per entry

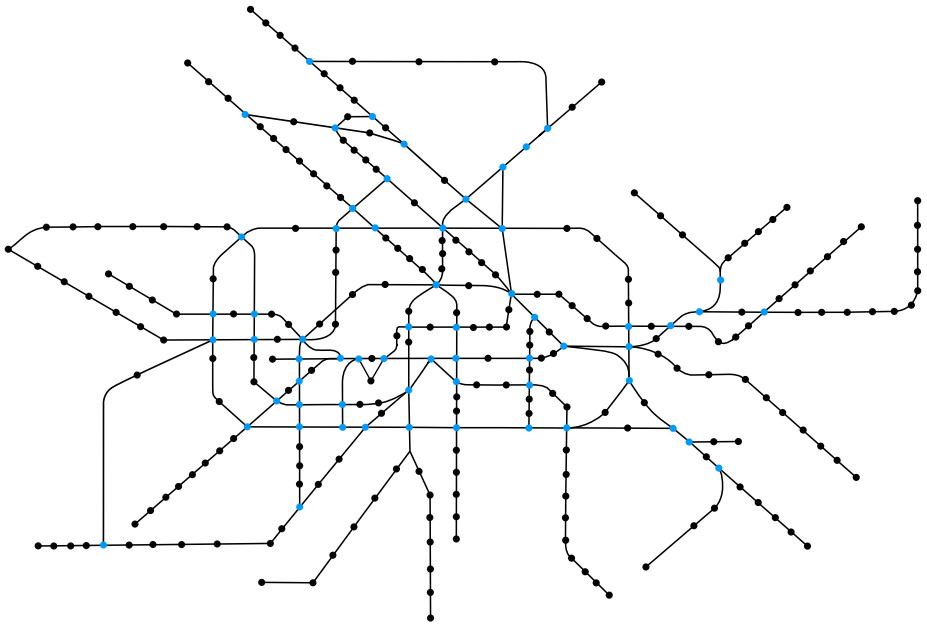

Figure 8: Topology of the Berlin metro system with 306 nodes. Nodes highlighted in blue represent stations with more than two connections. Adapted from [32].

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 [33] or subset simulation [34] could drastically improve efficency.

## 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 prohibts 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 analyze 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.

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