

APPLYING GRAPH THEORY AND LIFELINE RELIABILITY TO THE SYSTEM SURVIVAL SIGNATURE

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The recently introduced survival signature extends the concept of system signatures to multi-component systems - hereby providing a computationally efficient framework for analyzing the reliability of complex systems. However, for large systems the computation cost required is still large due to combinatoric effects, faster algorithms may depend on heuristic methods to prepare the network data, and Monte Carlo methods are required to be applied carefully due to the complex structure inherent to such systems. The application of recursive decomposition algorithms, inspired by the reliability assessment of lifeline networks, is proposed in this paper for the approximation of the survival signature. These algorithms not only provide a fast way to compute the 2-terminal reliability of a network, but also can be adjusted to provide proper upper and lower bounds for the entries in the survival signature.

Keywords: survival signature, reliability, complex networks, graphs.

1 Introduction

To assess the reliability of coherent systems of different types of components with independent and identically distributed failure times, the system survival signature has been presented as a powerful extension of the Samaniego signature. Usage of the survival signature allows analysis of systems with multiple types of components instead of only one in an intuitive way. The survival signature is used to decompose the survival function of the system into two functions: The survival signature carries solely information about the system's structure and is combined with terms containing information about the reliability of the individual component types.

Thus, for large systems, it can prove quite convenient to compute the survival signature beforehand as it does not change as long as the system's topology is untouched. This way the analysis of complex networks can be executed in computationally efficient ways. Additionally, this concept allows for dynamic testing of how different component reliabilities have on a system. Expanding the concept of the survival signature has already been done, e.g. for the implementation of replacement components in a system.

However, the computation of said survival signature is easier than the application of the Samaniego signature to multiple components (if that is possible at all), but is challenging still. To compute the survival signature exactly, all possible configurations of the system need to be evaluated. Despite the help of simplification techniques the combinatorial aspects of this problem tend to enlarge the computational effort. Additionally, every type of components multiplies the size of the survival signature by adding a dimension to the problem's size, invoking the 'curse of dimensionality'. In the case of the analysis using reliability block diagrams (RBD), the testing for working configurations boils down to the search of the 2-terminal reliability, which is NP-hard (Ball, 1980).

The computational and combinatorial hurdles in the computation process are subject to current research and various algorithms and techniques were recently presented to obtain the survival signature. In reference to Da et al. (2012), Coolen et al. (2014) introduce the separation of the system into subsystems, hereby reducing computation cost for the overall system. It is necessary to decompose the system in an efficient way to accomplish improvement in computation efficiency. It is also highlighted that not all elements of the survival signature may be necessary, depending on the information needed and the goal of the individual analysis. Reed (2017) presented a very fast algorithm to compute signatures that is based on ordered binary decision diagrams (OBDD). However, this approach is dependent on the existence of a OBDD representation of the system. This kind of data is not always available and may be obtained by heuristic methods and the approach may not be universally efficient.

The application of Monte Carlo methods cancels out the combinatorial computation by replacing it with sampling measurements. These can be improved up to a certain degree and offer further efficiency as the system's dimensions (i.e. component types) are coupled in reference to the system being functional or not. Nonetheless this does not solve the problem of the survival signature's size growing very fast with every component type added.

In this paper, two novel approaches to the survival signature are presented. The first allows the segmentation of the survival signature in regimes of high or low reliability entries using percolation theory. This can open up possibilities for dynamic simulation techniques, space fitting schemes or other methods relying on segmented partitions of a variable space. The second approach uses recursive decomposition algorithms to calculate the survival signature of reliability block diagrams from the 2-terminal reliability between signal source and sink. The algorithms presented by Wei Liu et al. (2009, 2012) not only provide efficient ways to accomplish these calculations, they can also be used to restrict computation time by introducing an error bound. As imprecise probabilities have already been introduced to the methodology of the survival signature, this approach offers possibilities for future research on the subject.

2 Methods

The state of a system consisting of a total of m components can be represented by the state vector $\underline{x} \in \{0,1\}^m$ with $x_i = 0$ denoting a dysfunctional and $x_i = 1$ a functional component i . The global structure function $\phi: \{0,1\}^m \rightarrow \{0,1\}$ yields information whether the system is in a working state ($\phi = 1$) or not ($\phi = 0$) for any possible \underline{x} .

Usually the systems are restricted to coherent systems. This refers to systems with structure functions that are not decreasing in any dimension of \underline{x} . This is reasonable as most systems are not becoming dysfunctional while gaining more functional components. Two additional assumptions are $\phi(\underline{0}) = 0$ and $\phi(\underline{1}) = 1$. These are intuitive, yet not necessary. However, in this paper the monotonicity of the system is assumed and thus these two conditions and the coherency of the system are assumed.

The components consist of K different types, while each set of components of type $k \in \{1, 2, \dots, K\}$ consists of m_k elements and the sum of all m_k equals the number of components $\sum_k m_k = m$. The amount of components of type k functional in the system are denoted as l_k . This leads to $C(m_k, l_k)$ combinations of component type k under the assumption of independent failure of all components. Then the set $S(\underline{l})$ is the collection of all state vectors \underline{x} that fulfill the condition that $\underline{l} = (l_1, l_2, \dots, l_K)$ components are working.

The system's *survival signature* $\Phi(l_1, l_2, \dots, l_K)$ is now defined as the probability that the system functions if exactly l_k components of type k are functional. The survival signature is an array of K dimensions with $m_k + 1$ entries in each dimension (including the case that none of the components of that type function). For components with exchangeable random failure times the survival signature is given by

$$\Phi(l_1, l_2, \dots, l_K) = \left[\prod_{k=1}^K C(m_k, l_k) \right]^{-1} \times \sum_{\underline{x} \in S(\underline{l})} \phi(\underline{x}). \quad (2.1)$$

The survival signature can be applied to the computation of the *survival function* $S(t) = P(T_s > t)$ of the system. It yields the probability that a random failure time T_s of the system follows a specific point in time t . Under the assumption of component type failure times independently and identically distributed (*iid*) with respect to a known CDF $F_k(t)$, the survival function of the system observed is found to be

$$S(t) = \sum_{l_1=0}^{m_1} \dots \sum_{l_K=0}^{m_K} \left[\Phi(\underline{l}) \times \prod_{k=1}^K \binom{m_k}{l_k} [F_k(t)]^{m_k - l_k} [1 - F_k(t)]^{l_k} \right]. \quad (2.2)$$

Eq. (2.1) and (2.2) clearly show that - for exact computation - many different states need to be evaluated and that the size of the survival signature itself is growing multilinearly.

2.1 Partitioning the survival signature

A common way to show how the functionality of a system depends on the component configuration is the *reliability block diagram* (RBD). A RBD displays a working state if a signal path exists from a specified source block to a target (or sink) block. Between these two blocks all components of the system are integrated in a block diagram. These RBD can be interpreted as networks known from graph theory, with the components acting as nodes (or vertices) and the connections as the representative edges (also known as arches or links).

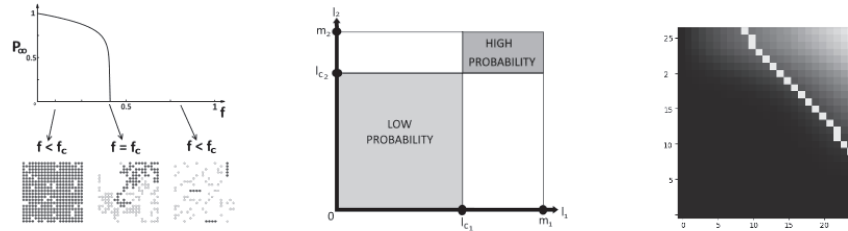


Figure 1. Critical threshold of a percolation process (left); partitioning of a survival signature into regimes using the critical percolation threshold (middle); partition of the Berlin Metro network, 78% of the probability mass is confined to 23% of the survival signature (right).

Percolation theory is describing the characteristics and behaviour of giant connected clusters in graphs. Common objects of interest are the *critical fraction* f_c and the probability P_∞ that a giant connected cluster exists. Most networks tend to retain a giant connected cluster under random removal of a fraction of nodes. However, once the fraction taken away exceeds a critical value, the giant connected cluster desintegrates into several smaller components (see figure 1).

Usually the existence of a giant connected cluster is not of relevance for a RBD. However, the existence of a giant connected cluster indicates a high probability for the existence of a path from one side of the network to the other. Thus a connection from source to sink in the RBD is very likely to occur if less than the critical amount of components is taken as dysfunctional. Further inference from the percolation behaviour of a network is difficult, as the computation for percolation is highly influenced by the topology of the network. This is true for analytical solutions as well as for computational results. Nonetheless the critical fraction can easily be derived *for any arbitrary network*.

The condition for a giant connected cluster to occur is the *Molloy-Reed criterion*: Each node inside the connected component must, on average, connect to two other nodes. Starting from the conditional probability that a node i with degree k_i (degree meaning here the number of connections of the node to other nodes) is connected to another node that is inside the cluster, one can obtain the Molloy-Reed criterion

$$2 < \kappa = \frac{\langle k^2 \rangle}{\langle k \rangle} \quad (2.3)$$

as necessary condition for the existence of a giant connected cluster (Cohen, 2000). Comparing the degree distributions (and their corresponding moments $\langle k \rangle$ and $\langle k^2 \rangle$ before and after the removal of a fraction of nodes and applying eq (2.3) yields a functional description of the critical fraction that only depends on κ (Cohen, 2000),

$$f_c = 1 - \frac{1}{\kappa - 1}. \quad (2.4)$$

This critical fraction can now be applied to the survival signature: The critical value $l_c = f_c \cdot (l_1, l_2, \dots, l_k)$ and the monotonicity of the system guarantee that the regions above these values are more or equally likely to function than not. The overall effectiveness of the partitioning can be quantified using $E = P_A \cdot A^{-1}$, the ratio of the percentage amount of probability mass inside the segment P_A and the relative size of the high probability segment A . As the entries of the signature serve as linear coefficients in eq. (2.2), this area is of high interest. A high value for E corresponds to high probabilities in a small subsection of the survival signature.

2.2 Two-node lifeline reliability

The analysis of networks consisting of lifeline networks (e.g. gas pipe networks, electricity grids or water supply networks) is usually concerned with the robustness of such networks under various types of failures. Liu and Li (2012) provided an efficient set of algorithms to calculate the two-node reliability (between a source and a sink) of lifeline networks recursively. Two of these methods are PRDA and CRDA (path-based and cut-based recursive decomposition algorithm). They can easily be applied to node reliability as well as to connection reliability.

Each component i (in this work, only node reliability will be analysed to stay in coherence with the example systems found in Coolen et al. (2014)) is assigned a reliability p_i under sudden environmental changes. Further assumptions are mutual independent reliabilities of the components and the simultaneous failure of the components. If every node of component type k is assigned the reliability of $p_i = l_i \cdot m_k^{-1}$, this provides an analogy to the uniform sampling of l_k out of m_k components over multiple iterations.

After the assignment of component reliabilities, both algorithms make use of the survival function as boolean representation. They decompose the network into disjoint minimal cuts (DMC) and disjoint minimal paths (DMP). Starting with *one* single DMP (A_i) (or DMC C_i), more instances of DMC (or DMP) can be found by merging nodes into the source, reducing the network with each computation step and thus simplifying computations. As the two-node reliability R can be expressed as functions of the probabilities of the DMC and DMP,

$$\begin{aligned} R_c &= 1 - \sum_i P(C_i), \\ R_a &= \sum_i P(A_i), \end{aligned} \quad (2.5)$$

each iteration of the algorithm provides an upper and lower bound of the reliability (Fratta and Montanari, 1973). Thus, R can be approximated by $R_a < R < R_c$ and $R \approx 0.5 \cdot (R_a + R_c)$.

3 Results

The critical fraction partitioning was tested for two large sample networks (Berlin Metro system, Moreno High-School network (Coleman, 1964)). The Berlin Metro sample network consists of 52 nodes with the source and sink choosen from the networks periphery. All nodes were randomly assigned a component type for each run. The high probability region yields on average 96 ± 8 % of all probability mass, whereas it is on average only 56 ± 5 % the size of the whole array. For the Moreno High-School network (treated the same way), an average of 87 ± 10 % of probability mass was found in 77 ± 7 % of the signature.

The PRDA and CRDA yield the same results if all DMC and DMP are evaluated. For large networks however, the computational times vary heavily if an accuracy interval of size $R_c - R_a$ is desired. This is due to low or high probabilities being approximated faster from different directions depending on the chosen algorithm. In this study all DMC and DMP were evaluated. The three example systems presented in Coolen and Coolen-Maturi (2014) were used to compare the results by the lifeline algorithms with exact solutions for survival signatures (see table 1).

Table 1. Computation times for the lifeline algorithms

Network name	CRDA computation time (s)	PRDA computation time (s)	Average abs. error [%]
Coolen Example 1 ($K = 2$)	0.012	0.022	5.7
Coolen Example 2 ($K = 3$)	0.023	0.031	7.0
Coolen Example 3 ($K = 3$)	0.013	0.048	5.6

4 Discussion

Partitioning of the survival signature not only shows that the probability mass is concentrated in a small subsection. It shows that with higher dimensionality the size of this subset shrinks relative to the overall size. This clarifies whether different methods should be applied to the individual sections of the signature array. The computation of the critical fraction is highly efficient, as it only demands summation over the adjacency matrix to obtain node degrees.

Usage of the two-node lifeline reliability offers possibilities to signature computation. However, for larger signatures it is still suffering from the ‘curse of dimensionality’, as the algorithms are to be applied to each entry of the signature. For medium-sized networks the two-node reliability is a possible and novel approach that can be fine-tuned to the computational needs, as the algorithm for each signature entry can be stopped as soon a desired accuracy of $R_c - R_a$ is reached.

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