How Many Diagnoses Do We Need?

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Abstract

A known limitation of many diagnosis algorithms is that the number of diagnoses they return can be very large. This raises the question of how to use such a large set of diagnoses. For example, presenting hundreds of diagnoses to a human operator (charged with repairing the system) is meaningless. In various settings, including decision support for a human operator and automated troubleshooting processes, it is sufficient to be able to answer a basic diagnostic question: is a given component faulty? We propose a way to aggregate an arbitrarily large set of diagnoses to return an estimate of the likelihood of a given component to be faulty. The resulting mapping of components to their likelihood of being faulty is called the system's health state. We propose two metrics for evaluating the accuracy of a health state and show that an accurate health state can be found without finding all diagnoses. An empirical study explores the question of how many diagnoses are needed to obtain an accurate enough health state, and a simple online stopping criterion is proposed.

Introduction

A diagnosis problem arises when a system does not behave as expected. A solution to a diagnosis problem is a *diagnosis*, which is a set of components that are assumed to have caused the system's abnormal behavior. Automated diagnosis has been studied in the artificial intelligence community for several decades, with several successful applications (Struss and Price 2003; Williams and Nayak 1996). One of the fundamental approaches to diagnosis is Model-Based Diagnosis (MBD). In MBD, a formal model of the diagnosed system is assumed specifying the expected behavior of the system. This model in conjunction with the observed behavior is used to deduce *diagnoses*.

If a diagnosis algorithm (DA) returns a single diagnosis, then the components that are faulty according to this diagnosis can be replaced. Unfortunately, in systems of non-trivial size it is often the case that many diagnoses can be deduced from the system model and observations. This may be due to having an insufficient number of observations, an inaccurate model of the diagnosed system, and computational limitations. In addition, some system models are not fully diagnosable, in the sense that some diagnoses are not separable by any observation (Provan 2001). In this work we explore the question of what can be done in such cases, where multiple diagnoses are found.

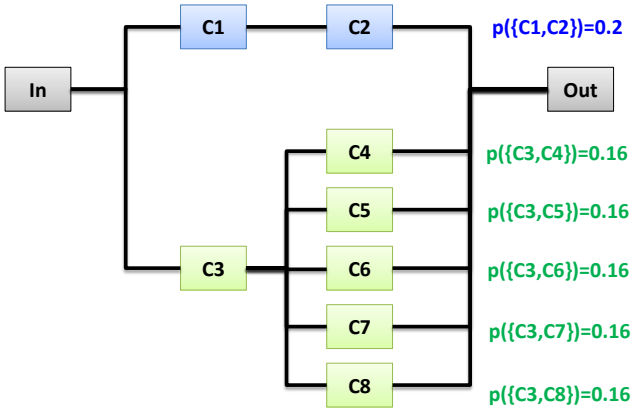


Figure 1: An example where viewing the most probable diagnosis can be more misleading than viewing the system's health state.

In some cases, additional diagnostic actions can be performed, e.g., probing internal components and performing additional system testing (Feldman, Provan, and van Gemund 2010b; de Kleer and Williams 1987; Shakeri et al. 2000). Such actions incur costs and they may still result in a large set of diagnoses. Consider a setting where the DA's output should be displayed to a human operator that will decide on subsequent actions. Clearly, a human operator cannot intelligently consider a list of hundreds of possible diagnoses.

Some DAs assign a score to every returned diagnosis, which estimates the likelihood of each diagnosis to be correct. Given the likelihood of each diagnosis to be correct, one may consider displaying only the most probable diagnoses. Figure 1, which is explained in greater detail later in this paper, shows an example where returning the most likely diagnosis is very misleading. The most likely diagnosis is that C_1 and C_2 are faulty, but it is actually most likely

that C_3 and one of the components after it is faulty. Thus, while showing a long list of diagnoses to a human operator is not helpful, focusing on a single diagnosis may miss important diagnostic information.

Our first contribution is in proposing to aggregate the set of diagnoses into a single vector containing for every component the likelihood that it is faulty. We call this vector the system's health state. To a human operator a system's health state provides a manageable view of which components are likely to be faulty. A notion similar to health states has been used for automated troubleshooting (Zamir, Stern, and Kalech 2014).

A health state can be derived from an arbitrarily large set of diagnoses and their likelihoods. In this work we investigate experimentally the relation between the accuracy of a health state and the number and type of diagnoses used to generate it. The second contribution of this work is in proposing two metrics for measuring the quality of a health state. The first metric is based on Euclidean distance from the optimal health state (where the true faults are known). The second metric views a health state as a classifier's model, and measures its quality according to the area under the curve (AUC) of a receiver operating characteristic (ROC) curve. Under both quality metrics, we observed empirically that the quality of a health state converges to a stable value without finding all diagnoses. This stable value is shown to be close to the best quality achievable, and that in most cases such a value can be obtained by considering only minimal cardinality diagnoses (diagnoses with a minimal number of faulty components). This supports the common diagnosis approach of focusing first on diagnoses with lower cardinality.

The empirical evaluation also shows that in most cases only a fraction of the set of minimal cardinality diagnoses is needed in order to reach a health state with a stable value. This result opens a great opportunity to develop DAs that determine online when to stop searching for more diagnoses (Feldman, Janssen, and van Gemund 2011). An online stopping condition for such an algorithm is proposed with promising preliminary results, suggesting future research.

Model Based Diagnosis

An MBD problem is specified as a triplet $\langle SD, COMPS, OBS\rangle$ where: SD is a model of the diagnosed system, $COMPS$ is a set of components, and OBS is an observation.

SD takes into account that some components might be abnormal (faulty). This is specified by an unary predicate $h(\cdot)$, such that $h(c)$ and $\neg h(c)$ denote that component c is healthy or faulty, respectively. Denoting the correct behavior of component c as a propositional formula, φ_c, SD is given formally as

$$SD = \bigwedge_{c \in COMPS} (h(c) \rightarrow \varphi_c)$$

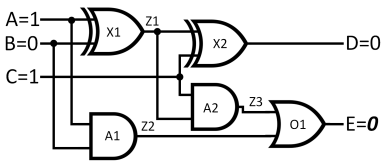
Namely, a healthy component follows its correct behavior. A diagnosis problem (DP) arises when the assumption that all components are healthy is inconsistent with the system description and observation (de Kleer and Williams 1987; Reiter 1987). System models can be classified into weak fault models (WFMs) and strong fault models (SFMs), where in WFMs only the nominal behavior a component is specified and in SFMs additional information is available about how faulty components behave. For ease of presentation, we assume in this paper a WFM, but all the theoretical results can be generalized to a SFM.

Figure 2 shows an example of an MBD problem, where the normal behavior would give output $E = 1$ but the observation had $E = 0$. DAs try to find *diagnoses*, which are subsets of $COMPS$ that explain the observation if assumed faulty.

Definition 1 (Diagnosis). *A set of components $\omega \subseteq COMPS$ is a* diagnosis *if the following term is consistent*

$$SD \wedge \bigwedge_{c \in \omega} \neg h(c) \ \wedge \bigwedge_{c \notin \omega} h(c) \ \wedge \ OBS$$

We say that ω is a minimal diagnosis *if no proper subset $\omega' \subset \omega$ is a diagnosis, and that ω is a* minimal cardinality diagnosis *if no other diagnosis $\omega' \subseteq COMPS$ exists such that $|\omega'| < |\omega|$.*



$COMPS = \{X_1, X_2, A_1, A_2, O_1\}$
$OBS = \{A, \neg B, C, \neg D, \neg E\}$

Figure 2: MBD: A full adder.

For the MBD problem in Figure 2, ω_1=$\{X_1, X_2\}$, ω_2=$\{O_1\}$, ω_3=$\{A_2\}$ are all the minimal diagnoses, and ω_2, ω_3 are all the minimal cardinality diagnoses. Some DAs search for subset-minimal diagnoses (Stern et al. 2012; de Kleer and Williams 1987; Williams and Ragno 2007) and other DAs search only for minimal cardinality diagnoses (Metodi et al. 2012; de Kleer 2009). Finding a single minimal cardinality diagnosis is an NP-hard problem (Selman and Levesque 1990) and finding more than one subset-minimal diagnosis is also NP-hard (Bylander et al. 1991). Even if limiting the output of a DA to only return minimal cardinality diagnoses, the number of returned diagnoses can still be exponential in the size of the diagnosis cardinality (the number of components assumed to be faulty). This occurs in practice in standard MBD benchmarks (Siddiqi 2011; Metodi et al. 2012). The question of how to manage such a large set of output diagnoses still holds, even if limiting the set of diagnoses to only include minimal cardinality diagnoses.

Health States

Given a large set of diagnoses, a reasonable question that a human operator might ask is "what is the likelihood that a component C is faulty?" This is helpful, for example, to decide which component to replace first. In addition, being able to estimate the likelihood of each component being faulty is helpful in troubleshooting algorithms (Zamir,

Stern, and Kalech 2014; Heckerman, Breese, and Rommelse 1995).

Definition 2 (Health State). *A health state is a vector $H \in [0,1]^{|COMPS|}$ where the i^{th} element of H, denoted $H[i]$, is an estimate of the likelihood that component $C_i \in COMPS$ is faulty.*

Next, we show how a health state can be generated from a set of diagnoses (found by a DA).

Let Ω be a set of diagnoses found by a DA, and let $p : \Omega \rightarrow [0,1]$ be a probability distribution over the diagnoses in Ω, such that $p(\omega)$ corresponds to the probability $\omega \in \Omega$ is correct. Many DAs prioritize the diagnoses in Ω, and some return a score for each diagnosis to denote how likely it is to be correct (Abreu et al. 2009). A common method to generate such a score is by considering a prior probability on the fault of each component (without considering the observations), and assuming that components fail independently. This is a common assumption in MBD (de Kleer and Williams 1987; Williams and Ragno 2007). Thus, a score of a diagnosis ω would be $\prod_{C_i \in \omega} pr(C_i)$, where $pr(C_i)$ is the prior probability that C_i is faulty. Converting diagnoses scores to a valid probability distribution simply requires normalizing their sum to one:

$$p(\omega) = \frac{\prod_{C_i \in \omega} pr(C_i)}{\sum_{\omega' \in \Omega} \prod_{C_i \in \omega'} pr(C_i)}$$

Other methods to generate a probability distribution p over Ω may also exist.

Given Ω and p, we can derive a health state as follows:

$$H[i] = \sum_{\omega \in \Omega} p(\omega) \cdot \mathbb{1}_{C_i \in \omega} \quad (1)$$

where $\mathbb{1}_{C_i \in \omega}$ is the indicator function defined as:

$$\mathbb{1}_{C_i \in \omega} = \begin{cases} 1 & C_i \in \omega \\ 0 & \text{otherwise} \end{cases}$$

If Ω contains all diagnoses and the uncertainty over the true state of the world is accurately represented by p, then the health state generated by Equation 1 is accurate.[1] In this paper we only consider generating a health state from Ω and p using Equation 1, and refer to this simply as *generating a health state from Ω and p*.

We argue that presenting a human operator with a health state is more meaningful and helpful than a long list of diagnoses. A human operator cannot reason effectively about a long list of diagnoses. One might consider presenting a short list of only the most probable diagnoses to the operator. This approach, however, may be misleading. For example, consider the system depicted in Figure 1, and assume that a DA has returned five diagnoses $\{C_3, C_4\}, \{C_3, C_5\}, \{C_3, C_6\}, \{C_3, C_7\}, \{C_3, C_8\}$ with a probability of 0.16 each, and another diagnosis $\{C_1, C_2\}$ with a probability of 0.2. Table 1 lists the health state generated from these diagnoses. The most probable diagnosis is $\{C_1, C_2\}$, having a probability of 0.2. The health state, however, point at C_3 as the component that is most likely to be faulty, having $H[3] = 0.8$.

[1]Note that since there is only a single diagnosis that is correct in a given state of the world, then there is no notion of probability dependance between diagnoses.

	ω_1	ω_2	ω_3	ω_4	ω_5	ω_6	H[i]
C_1	1	0	0	0	0	0	**0.2**
C_2	1	0	0	0	0	0	**0.2**
C_3	0	1	1	1	1	1	**0.8**
C_4	0	1	0	0	0	0	**0.16**
C_5	0	0	1	0	0	0	**0.16**
C_6	0	0	0	1	0	0	**0.16**
C_7	0	0	0	0	1	0	**0.16**
C_8	0	0	0	0	0	1	**0.16**
p	0.2	0.16	0.16	0.16	0.16	0.16	

Table 1: Diagnoses and health state for Figure 1

While a health state is an informative aggregation of a given set of diagnoses, some information contained in the set of diagnoses it was generated from, is lost. This lost information is the dependencies between the different components. For example, consider again the diagnoses in Figure 1. The component C_1 is only a member of a single diagnosis $\{C_1, C_2\}$. Thus, repairing only C_1 without repairing C_2 is not likely to fix the system. This relation between C_1 and C_2 is lost in the aggregated perspective of a health state. Automated troubleshooting algorithms (Feldman, Provan, and van Gemund 2010b; de Kleer and Williams 1987; Shakeri et al. 2000) might make use of such additional relation information and might thus prefer as input a list of diagnoses over a health state.

Evaluating a Health State

Due to computational limitations, DAs often cannot return all the diagnoses for a given diagnosis problem. In addition, the diagnosis likelihood function p is often a (usually rough) approximation. This raises the question of how accurate is a health state that is generated by Ω and p that are returned in practice by DAs. A complementing question is how many diagnoses should a DA return in order to generate a health state that is accurate enough.

To answer these questions, a metric is needed to measure the quality of a generated health state. Next, we present two such metrics.

Distance-based Metric

The first health state metric is computed with respect to the offline optimal health state, denoted by H^* and defined as follows:

$$H^*[i] = \begin{cases} 1 & C_i \text{ is faulty} \\ 0 & \text{otherwise} \end{cases}$$

A given health state can be evaluated by its "distance" from H^*. Health states, including H^*, are real valued vectors. Thus, there are several distance metrics that can be used to measure the distance between a given health state and H^*. We chose to use a simple Euclidean distance for this pur-

pose

$$\sqrt{\sum_{C_i \in COMPS} (H[i] - H^*[i])^2}$$

Lower Euclidean distance indicates a better health state, and zero Euclidean distance indicates that Ω contains a single diagnosis consisting of exactly the faulty components (i.e., the correct diagnosis).

AUC-based Metric

The second health state metric we propose is based on viewing a diagnosis problem as a classification problem whose output is which components are classified as faulty. The health state is then considered as a classifier model, such that a component C_i is classified as faulty if $H[i] \geq T$, where T is a threshold parameter that can be tuned to control the sensitivity and specificity of the resulting classifier. Thus, setting $T = 0$ would classify all components as faulty, while $T = 1$ would only classify as faulty the components that are faulty for certainty, according to the health state (these are the components that are members of all the diagnoses in Ω).

For a given T, it is then possible to measure the true/false positives/negatives, and compute the true positive rate (TPR) and false positive rate (FPR). By varying T the receiver operating characteristic (ROC) curve can be drawn, which is the curve resulting from plotting the TPR against the FPR for a range of T values. A common measure for evaluating classifiers with such a threshold parameter is by measuring the area under the ROC curve, denoted as AUC (Mitchel 1997). AUC values range from zero to one, where the best AUC value is one.

Both the Euclidean and AUC metrics can be used to evaluate health states. Thus, they can also be used to compare DAs by comparing the quality of the health state they generate. Next, we use these health state metrics to study experimentally the relation between the number of diagnoses found and the quality of the resulting health state.

Experimental Results

System	$\|COMPS\|$	Obs.	$\|\Omega\|$	Max minc
74181	65	49	439	5
74182	19	50	146	5
74283	36	30	521	3
c499	202	19	90	3
c880	383	13	169	3

Table 2: Details of the used systems and observations.

As a case study, we performed experiments on a standard Boolean circuit benchmark taken from the "synthetic track" in the annual DXC diagnosis competition of 2009.[2] From the set of systems in the DXC benchmark, we used the 74xxx, c499, and c880 systems. To have a diverse set of observations, we used a randomly selected set of observations per minimal cardinality, taken from the DXC benchmark.

[2]See details in the DXC 09 website: http://sites.google.com/site/dxcompetition2009/.

For each observation we run a DA that searches for all subset-minimal diagnoses in order of increasing cardinality. The DA was halted when all subset-minimal diagnoses were found or after running for 15 minutes. The resulting set of subset-minimal diagnoses were sorted by cardinality, starting from the minimal cardinality diagnoses. Let Ω_i be the set of the first i diagnoses according to this sorting and let H_i denote the health state generated from the diagnoses in Ω_i. Table 2 lists the number of components, observations, found diagnoses, and maximal minimal cardinality for the systems in our experiment.

First, we examine whether the quality of a health state, measured by either Euclidean distance or AUC, converges to a stable value as more diagnoses are considered. Let $eval(H_i)$ be the quality of a health state H_i according to one of the proposed health state metrics. The value of a health state H_i was regarded as stable if there is no $j > i$ such that the quality of H_j is different from that of H_i by more than ϵ, where ϵ is a parameter. For a given observation, we quantified the rate at which a health state converges to a stable value by counting the number of diagnoses required until the health state was stable. Formally, the convergence rate of a given observation and corresponding set of diagnoses Ω is the minimal $i \in [1, |\Omega|]$ for which $|eval(H_j)\text{-}eval(H_i)| \leq \epsilon$ for every $j > i$. In the results below we normalized the convergence rate by dividing them by $|\Omega|$.

$\epsilon \setminus$ System	74181	74182	74283	c499	c880
0	1.00	1.00	1.00	1.00	1.00
0.1	0.14	0.48	0.11	0.20	0.34
0.2	0.05	0.09	0.03	0.17	0.28
0.3	0.01	0.04	0.01	0.06	0.02
0.4	0.01	0.03	0.01	0.06	0.02

Table 3: Norm. convergence rate for the AUC metric.

$\epsilon \setminus$ System	74181	74182	74283	c499	c880
0	1.00	1.00	1.00	1.00	1.00
0.1	0.01	0.12	0.01	0.02	0.01
0.2	0.01	0.03	0.00	0.02	0.01
0.3	0.01	0.02	0.00	0.02	0.01
0.4	0.01	0.02	0.00	0.02	0.01

Table 4: Norm. convergence rate for the Euclidean metric.

Tables 3 and 4 show the average normalized convergence rate for AUC and Euclidean distance metrics, respectively, for a range of ϵ values. A value of zero corresponds to cases where the health state generated by the first diagnosis, is stable. This occurs in very small systems and high values of ϵ. The row $\epsilon = 0$ serves as a baseline, as convergence for $\epsilon = 0$ is only reached once all diagnoses are found. As can be seen, for both AUC and Euclidean distance metrics it is possible to reach a stable health state for every evaluated $\epsilon > 0$ without finding all diagnoses. For example, consider normalized convergence rate using the AUC metric for system 74181. A health state that is at most 0.1 far from the health state obtained with all diagnoses can be generated by finding only

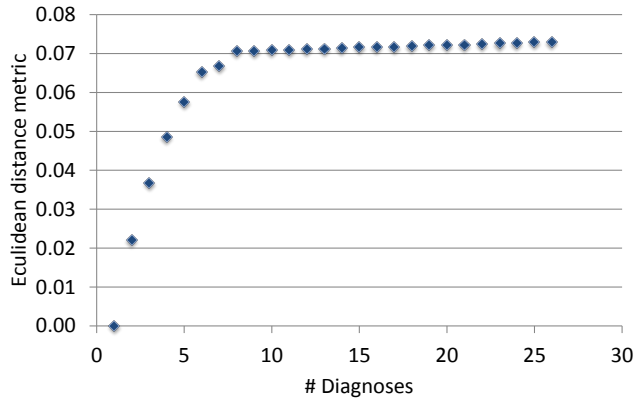


Figure 3: An example where more diagnoses degrades the quality of the health state.

14% of the diagnoses. This suggests that intelligent DAs can halt early and obtain a useful health state.

Interestingly, the health state generated from all the found diagnoses is not necessarily better than the health state obtained by considering only a subset of the diagnoses. For example, Figure 3 shows the health state quality, measured using the Euclidean distance metric, as a function of the number of diagnoses found for a specific observation. In this observation, the health state starts at the optimal value (zero distance from H^*). This is since the correct diagnosis happened to be the first diagnosis that was found. As more diagnoses are found, the health state's quality degrades. Thus, considering more diagnoses is not always helpful.

$\epsilon \setminus$ System	74181	74182	74283	c499	c880
Oracle	0.92	0.92	0.91	1.00	0.83
Online	0.85	0.87	0.80	0.97	0.77
0	0.82	0.90	0.84	0.94	0.78
0.1	0.82	0.88	0.86	0.94	0.79
0.2	0.78	0.83	0.83	0.91	0.77
0.3	0.76	0.76	0.76	0.84	0.70
0.4	0.73	0.72	0.74	0.83	0.70

Table 5: AUC values after convergence.

$\epsilon \setminus$ System	74181	74182	74283	c499	c880
Oracle	0.14	0.22	0.18	0.05	0.06
Online	0.17	0.25	0.22	0.07	0.07
0	0.17	0.23	0.21	0.07	0.06
0.1	0.21	0.28	0.27	0.08	0.09
0.2	0.21	0.34	0.29	0.08	0.09
0.3	0.21	0.36	0.29	0.08	0.09
0.4	0.21	0.36	0.29	0.08	0.09

Table 6: Euclidean distance values after convergence.

Table 5 and 6 show the average AUC and Euclidean distance metrics, respectively, of the stable health state reached for a range of ϵ values. In addition, each table contains two special rows, marked as "Oracle" and "Online". The values in the "Oracle" row are the (AUC or Euclidean distance) values of the best health states obtained by adding diagnoses sequentially, i.e., the best $eval(H_i)$ for every $i \in [1, |\Omega|]$. The values in the "Online" row are the (AUC or Euclidean distance) values obtained using an online stopping criterion that is described and discussed below.

First, corresponding with the example in Figure 3, even for $\epsilon = 0$ the obtained health state was not as good as the health state obtained by the oracle. The converged health states for low ϵ values are, however, very close to it. In addition, consider the impact of increasing ϵ on the AUC and Euclidean distance values. The results show that increasing ϵ results in health state of poorer quality, i.e., lower AUC and higher Euclidean distance. Thus, while the health state generated by the oracle is better than the converged health state, it is still true that health states generated from more diagnoses tend to have higher quality, on average.

Online Stopping Criterion

The convergence described above are detected in post-hoc, as one needs to know the true faults to compute the AUC and Euclidean distance. A main application for health states is to be used as a termination criterion for DAs that generate multiple diagnoses (Feldman, Janssen, and van Gemund 2011). Such a stopping criterion is especially needed in stochastic DAs (Feldman, Provan, and van Gemund 2010a), which are known to work well in practice but require parameter tuning. One such stopping condition can be to halt when the Euclidean distance of two subsequent health states (H_i and H_{i+1}) are below a predefined threshold δ. The "Online" rows in Table 5 and 6 show the average AUC and Euclidean distances, respectively, obtained by using this online stopping criterion for $\delta = 0.1$. We emphasize that checking this stopping condition does not require computing any health state evaluation metric (neither Euclidean distance nor AUC), since the stopping condition measures distance between subsequent health states and not distance to H^* (since H^* is not available online).

As can be seen, the quality of the resulting health state is slightly less than those obtained by the "Oracle", but is comparable to the quality obtained by the stable health state for $\epsilon = 0.1$. Note that the number of diagnoses needed to reach an online termination for $\delta = 0.1$ is at most one more than the number of diagnoses needed to reach a stable health state for $\epsilon = 0.1$. Thus, these results suggest that online simple stopping can be used efficiently to halt DAs and obtain a high quality health state.

Finding Minimal Cardinality Diagnoses

Many DAs have focused on finding only minimal cardinality diagnoses. Next, we evaluate the impact of the minimal cardinality diagnoses on the quality of the resulting health state. For more than 70% of the observations in all the 74xxx systems, the health state has converged without requiring any diagnosis that is not of minimal cardinality. Thus, in most cases, limiting the DA to find only minimal cardinality diagnoses seems to be a reasonable choice. Moreover, a high quality health state can be found with only a subset

of all minimal cardinality diagnoses. Table 7 shows the ratio of minimal cardinality diagnoses (where 1 corresponds to all minimal cardinality diagnoses) required, on average, to reach a stable health state. As can be seen, even for $\epsilon = 0.1$, only a fraction of the minimal cardinality diagnoses are needed to reach a stable health state. For example, only 17% of the minimal cardinality diagnoses are needed to generate a health state that is stable for $\epsilon = 0.1$ for the 74181 system under the Euclidean distance metric.

Systems	AUC			
ϵ	0.1	0.2	0.3	0.4
74181	0.71	0.46	0.27	0.25
74182	0.71	0.51	0.39	0.36
74283	0.56	0.40	0.27	0.26

Systems	Euclidean			
ϵ	0.1	0.2	0.3	0.4
74181	0.17	0.15	0.15	0.15
74182	0.56	0.32	0.29	0.29
74283	0.10	0.07	0.07	0.07

Table 7: Fraction of minimal cardinality diagnoses required to reach convergence.

Note that the results above do not mean that an efficient DA would limit itself to only minimal cardinality. Future work would perform a comprehensive evaluation of existing DAs and how fast do they produce a high quality health state.

Related Work

Many approaches and algorithms for MBD have been proposed. A classic approach to MBD, implemented in DAs like GDE (de Kleer and Williams 1987) and CDA* (Williams and Ragno 2007), finds diagnoses in a two stage process. First, conflict sets are identified, each of which includes at least one fault. Then, a hitting set algorithm is used to extract diagnoses from this set of conflict sets. Others have proposed a compilation-based approach, using Binary Decision Diagrams (BDDs) (Torasso and Torta 2006) or Decomposable Negation Normal Form (DNNF) (Darwiche 2001). A DA based on a greedy stochastic approach was also proposed (Feldman, Janssen, and van Gemund 2011). All these DAs may potentially return a large set of diagnoses. Thus, they are orthogonal to our work, as a health state can be generated from the set of diagnoses, regardless of the DA used.

Keren et al. (2011) present an alternative approach to diagnosis that combines MBD with multi-label classification. They propose to build a classifier that maps symptoms (observations) of the system to possible faults. The major advantage of this approach is in reducing significantly the online computational complexity; The learning process of the relations between observations and the diagnosis is performed in advance offline. Afterward (online), a diagnosis can be computed immediately by using the classifier that was learned offline. Unlike other DAs mentioned above, this machine learning approach to diagnosis returns a single diagnosis and not a set of diagnoses. Similar to the AUC metric we used to evaluate health states, the output of this machine learning based DA is also measured using standard classification metrics such as false positives and false negatives. A key difference is that we do not propose a new DA that returns a single diagnosis, but propose a general approach for aggregating a set of diagnoses that can be applied for a wide range of DAs

Maier et al. (2011) pointed out that often AI problems lie at the intersection of the fields of MBD and probabilistic reasoning and that probabilistic reasoning can be a promising alternative to the MBD approaches. They proposed an automatic translation from a first-order model-based diagnosis formalism, namely Probabilistic hierarchical constraint automata (PHCA) (Williams, Chung, and Gupta 2001), to statistical relational models. Similar to our approach, they also remark that solutions to AI problems in engineering domains need to be compactly represented for the needs of engineers. There are several key differences between their work and ours. First, by "compactly represented" they mean auto-generating low-level representation, such as Bayesian networks, that can be used as input to off-the-shelf tools used by Engineers. We aim to find a simpler representation of the diagnoses, that can even be understood by a human operator. Moreover, their approach focused on finding the connections and dependencies between components, while we do not consider the logical model of the system and directly aggregate the output of the DA – the diagnoses and their likelihood – to health states. An interesting future work would be to explore whether more informed health states can be generated by considering the systems' internal structure.

Discussion, Conclusion and Future Work

We proposed an alternative form of output for DAs called the health state. A health state maps every component to a probability that it is faulty. We argue that a health state is for many cases a more reasonable output than a single or k most probable diagnoses since it contains aggregated information over all the found diagnoses. Thus, it provides an overview of the state of the system that is readable by a human operator and can be useful for an automated troubleshooter.

A method was presented for generating a health state from a set of diagnoses. Two metrics were proposed to measure the quality of generated health states. Empirically, we observe that for both quality metrics the quality of health states, on average, tends to converge to a relatively high value as more diagnoses are considered. Moreover, in many cases only a subset of all minimal cardinality diagnoses was needed in order to reach convergence. Lastly, we propose a simple stopping criterion that can be used online by a DA to identify when a health state of high quality is reached and the search can halt. Future research would research this direction in depth, considering ideas form the optimal stopping problem (Peskir and Shiryaev 2006) and studying how the accuracy of diagnosis likelihoods (the p function) and component priors affect the convergence speed and efficiency of stopping conditions. Another research question that arises from our work is how to quantify the amount of information lost by using health states instead of the set of diagnoses returned from the DA.

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