Memory-Limited Model-Based Diagnosis*

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Abstract

Various model-based diagnosis scenarios require the computation of the most preferred fault explanations. Existing algorithms that are sound (i.e., output *only* actual fault explanations) and complete (i.e., can return *all* explanations), however, require exponential space to achieve this task. As a remedy, and to enable successful diagnosis both on memory-restricted devices and for memory-intensive problem cases, we propose two novel diagnostic search algorithms which build upon tried and tested techniques from the heuristic search domain. The first method, dubbed Recursive Best-First Hitting Set Search (RBF-HS), is based on Korf's well-known Recursive Best-First Search (RBFS) algorithm. We show that RBF-HS can enumerate an arbitrary predefined finite number of fault explanations in best-first order within linear space bounds, without sacrificing the desirable soundness or completeness properties. The second algorithm, called Hybrid Best-First Hitting Set Search (HBF-HS), is a hybrid between RBF-HS and Reiter's seminal HS-Tree. The idea is to find a trade-off between runtime optimization and a restricted space consumption that does not exceed the available memory.

We conducted extensive experiments on real-world diagnosis cases where we compared our approaches to Reiter's HS-Tree, a state-of-the-art diagnostic search that gives the same theoretical guarantees and is as general(ly applicable) as the suggested algorithms. For the computation of minimum-cardinality fault explanations, we find that *(1)* RBF-HS reduces memory requirements substantially in most cases by up to several orders of magnitude, *(2)* memory savings are significantly higher than potential runtime overheads for all non-trivial cases, *(3)* in more than a third of the cases, *both* memory savings *and* runtime savings are achieved, *(4)* given the runtime overhead is significant, using HBF-HS instead of RBF-HS reduces the runtime to values comparable with HS-Tree while keeping the used memory reasonably bounded. When computing most probable fault explanations, we observe that RBF-HS tends to trade memory savings more or less one-to-one for runtime overheads. Again, HBF-HS proves to be a reasonable remedy to cut down the runtime while complying with practicable memory bounds.

Notably, the suggested algorithms are broadly applicable to any model-based diagnosis problem, regardless of the used (monotonic) logical language to describe the

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diagnosed system and of the used inference mechanism. Moreover, the proposed methods are not restricted to model-based diagnosis, but suitable for hitting set computation problems in general.

Keywords: Hitting Set Computation, Sound Complete Best-First Diagnosis Computation, Linear Best-First Hitting Set Search, Model-Based Diagnosis, Fault Localization, Recursive Best First Search, Heuristic Search, Memory-Limited Diagnosis Search, Reiter's Hitting Set Tree, Sequential Diagnosis, Combinatorial Search

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1. Introduction

Model-based diagnosis [2, 3] is a popular, well-understood and domain-independent paradigm that has over the last decades found widespread adoption for troubleshooting systems as different as programs, circuits, physical devices, knowledge bases, spreadsheets, production plans, robots, vehicles, or aircrafts [4, 5, 6, 7, 8, 9, 10, 11, 12, 13]. The principle behind model-based diagnosis is to model the system to be diagnosed by means of a logical knowledge representation language. Beside general knowledge about the system, this *system description* includes a characterization of the normal behavior of all *system components* relevant to the diagnosis task. Logical theorem provers can then be used to verify if the predicted system behavior—deduced from the system description under the assumption that all components work nominally—is consistent with factual evidence (*observations*) about the real system behavior. In case of an inconsistency, the goal is to find the abnormal components responsible for the observed system misbehavior. An (irreducible) set of components whose assumed abnormality makes the system description consistent with the observations is called a *(minimal) diagnosis*. Typically, there are multiple minimal diagnoses for practical diagnosis problems, and it is an important issue to isolate the *actual diagnosis*, which pinpoints the actually faulty components, from other spurious candidates.

Over the last decades, various diagnosis search methods have been suggested, e.g., [14, 15, 16, 17, 18, 19, 20]. Motivated by different diagnosis scenarios and application fields, these algorithms feature greatly different properties. For instance, while some are designed to guarantee *soundness* and *completeness* (i.e., the computation of *only* and *all* minimal diagnoses), e.g., to ensure the localization of the actual diagnosis in critical applications (medicine [21], aircrafts [11], etc.), others drop one or both of these properties, e.g., to allow for higher diagnostic efficiency [22, 23]. Since the computation of all (minimal) diagnoses is intractable[2], all diagnosis searches have to focus on a (computationally feasible) subset of the diagnoses in general. This subset is commonly referred to as the *leading diagnoses* [25], and usually defined as the best minimal diagnoses according to some preference criterion such as minimal cardinality or maximal probability. Algorithms which enumerate diagnoses in order of preference are called *best-first*. One of the most general sound, complete and best-first algorithms

[2] Given a non-empty set of minimal diagnoses, deciding whether there is another minimal diagnosis, is NP-hard, even if theorem proving is in P [24]. Hence, computing all (minimal) diagnoses is NP-hard.

in literature is Reiter's seminal HS-Tree [2, 7, 17], because it is independent of the used (monotonic[3]) system description language and of the used theorem prover. The advantage of this generality is a *broad and flexible applicability* of the search algorithm over a wide range of diagnosis application domains. For example, in the field of knowledge base or ontology debugging, diagnosers have to deal with a myriad of different logics that are used to model and solve problems in various domains while achieving a trade-off between inference complexity and logical expressivity. The development of different (suitably adapted) diagnostic search techniques for all these cases would be hardly realizable. General algorithms like HS-Tree, on the other hand, can out of the box work with any of these logics and related theorem provers.

Traditional (sound and complete) best-first diagnosis search methods require an exponential amount of memory. The reason is that all paths in a search tree must be stored in order to guarantee that the best one is expanded in each iteration. This can prevent the application of best-first searches to a range of model-based diagnosis scenarios which, e.g., *(a)* pose substantial memory requirements on the diagnostic methods or *(b)* suffer from too little memory. One example for (a) are problems involving high-cardinality diagnoses, e.g., when two systems are integrated and a multitude of errors emerge at once [18, 26]. Manifestations of (b) are frequently found in today's era of the Internet of Things (IoT), distributed or autonomous systems, and ubiquitous computing, where low-end microprocessors, often with only a small amount of RAM, are incorporated into almost any device. Whenever such devices should perform (self-)diagnosing actions [27, 28], memory-limited diagnosis algorithms are a must [29, 30].

As a remedy, we introduce in this work two general diagnostic search algorithms that require either linear or (quasi-)restricted[4] memory while featuring all above-mentioned desirable search properties. In particular, our **contributions** are:

- We propose *Recursive Best-First Hitting Set Search (RBF-HS)*, a novel diagnostic search drawing on ideas used by Korf in his well-known *Recursive Best-First Search (RBFS)* algorithm [31].
- We show that RBF-HS can compute an arbitrary predefined finite number of minimal diagnoses in a sound, complete and best-first way within linear memory bounds, and that it can be generally applied to arbitrary diagnosis problems as per Reiter's theory of model-based diagnosis [2].
- We generalize RBF-HS, which acts on the maxim to use as little memory as possible, by integrating it with HS-Tree to a hybrid search method that remains sound, complete and best-first. The basic rationale behind this search, dubbed *Hybrid Best-First Hitting Set Search (HBF-HS)*, is to initially run HS-Tree as long as sufficient memory is still available (*optimize time*), and to then switch to RBF-HS to minimize the additional used memory (*optimize space*) in order to

[3] A logic is called *monotonic* iff all consequences (logical entailments) of any knowledge base $\mathcal{K}$ formulated over this logic remain valid for any extension of the knowledge base by a set of additional axioms β. Formally: $\mathcal{K} \models \alpha \implies \mathcal{K} \cup \beta \models \alpha$. Monotonicity is a vital requirement for the validity of the general theory of model-based diagnosis [2, 3].

[4] I.e., the user can set a memory limit, and the algorithm will only exceed this limit by an amount linear in the problem size. Empirically, we observe that this exceedence is always marginal in our experiments.

avoid running out of memory and preserve problem solvability.

Beside thorough theoretical complexity and correctness analyses, we present extensive empirical evaluations of the proposed techniques on real-world diagnosis cases where we demonstrate the broad applicability of our approaches on problems formulated in various different logics with high expressivities and hard reasoning complexities beyond NP-complete. The **main experiment results** are:

- *Minimal cardinality first:* When computing minimal diagnoses in ascending order of cardinality, we find that RBF-HS, compared to HS-Tree, *(1)* exhibits significant memory savings as opposed to no more than marginal runtime losses in most cases, *(2)* saves at least 50 % memory in 89 % of the cases, and at least 90 % in 56 % of the cases, where savings increase with increasing problem complexity, *(3)* saves *both* memory *and* runtime in more than 36 % of the cases, where runtime savings amount to up to more than 90 %, *(4)* scales to large numbers (100) of computed leading diagnoses and to problems involving high-cardinality minimal diagnoses while the ratio of space savings vs. times losses becomes even more favorable (by up to multiple orders of magnitude), and *(5)* in the rare cases where runtime overhead was significant, using HBF-HS instead of RBF-HS reduced the runtime to values comparable with HS-Tree while keeping the used memory reasonably bounded.
- *Maximal probability first:* When computing minimal diagnoses in descending order of probability, we find that RBF-HS tends to trade memory savings more or less one-to-one for runtime overheads (which has well-understood theoretical reasons that we discuss). Again, HBF-HS turns out to be a reasonable remedy to cut down the runtime while complying with practicable memory bounds.

The **organization of the paper** is as follows. To make this work self-contained, we repeat fundamental concepts from the fields of model-based diagnosis and heuristic search in Sec. 2. The RBF-HS algorithm is introduced and thoroughly discussed in Sec. 3. This includes a didactic approach which builds up RBF-HS from RBFS in a stepwise manner, an in-depth algorithm walkthrough describing its functioning, an illustration of the algorithm's workings on a simple but meaningful example, a time and space complexity analysis, as well as a proof of RBF-HS's properties and correctness. Furthermore, we briefly touch on applications and variations of RBF-HS and, in the course of this, introduce and describe HBF-HS as a generalization of RBF-HS and visualize it by means of an example in Sec. 4. We comment on related works in Sec. 5 from the perspective of both the model-based diagnosis and the heuristic search domain. Finally, Sec. 6 presents our experiments and reviews the obtained results, whereas concluding remarks and pointers to future work are given in Sec. 7.

2. Preliminaries

We first briefly characterize model-based diagnosis concepts used throughout this work, based on the framework of [7, 32] which is (slightly) more general [33] than Reiter's theory [2]. The main reason for using this more general framework is its ability to handle negative measurements (things that must *not* be true for the diagnosed

system) which are helpful, e.g., for diagnosing knowledge bases [32, 34, 35]. Next, we concisely review important notions from heuristic search and contrast classic path-finding with diagnosis search problems. This comparison should serve to facilitate the understanding of the presented development of the diagnosis computation procedure RBF-HS starting from the path-finding algorithm RBFS in Sec. 3.

2.1. Model-Based Diagnosis

2.1.1. Diagnosis Problem

We assume that the diagnosed system, consisting of a set of components $\{c_1, \ldots, c_k\}$, is described by a finite set of logical sentences $\mathcal{K} \cup \mathcal{B}$, where $\mathcal{K}$ (possibly faulty sentences) includes knowledge about the behavior of the system components, and $\mathcal{B}$ (correct background knowledge) comprises any additional available system knowledge and system observations. More precisely, there is a one-to-one relationship between sentences[5] $ax_i \in \mathcal{K}$ and components c_i, where ax_i describes the normal behavior of c_i (*weak fault model*[6]). E.g., if c_i is an AND-gate in a circuit, then $ax_i := out(c_i) = and(in1(c_i), in2(c_i))$; $\mathcal{B}$ in this case might contain sentences stating, e.g., which components are connected by wires, or observed circuit outputs. The inclusion of a sentence ax_i in $\mathcal{K}$ corresponds to the (implicit) assumption that c_i is healthy. Evidence about the system behavior is captured by sets of positive (P) and negative (N) measurements [2, 3, 34]. Each measurement is a logical sentence; positive ones $p \in P$ must be true and negative ones $n \in N$ must not be true. The former can be, depending on the context, e.g., observations about the system, probes or required system properties. The latter model properties that must not hold for the system, e.g., if $\mathcal{K}$ is a biological knowledge base to be debugged, a negative test case might be "every bird can fly".[7] We call $\langle \mathcal{K}, \mathcal{B}, P, N \rangle$ a *diagnosis problem instance (DPI)*.

Example 1 *(Diagnosis Problem)* Tab. 1 depicts an example of a DPI, formulated in propositional logic. The "system" (which is the knowledge base itself in this case) comprises five "components" $c_1, \ldots, c_5$, and the "normal behavior" of c_i is given by the respective axiom $ax_i \in \mathcal{K}$. There is neither any background knowledge ($\mathcal{B} = \emptyset$) nor any positive measurements ($P = \emptyset$) available from the start. But, there is one negative measurement (i.e., $N = \{\neg A\}$), which postulates that $\neg A$ must *not* be an entailment of the correct system (knowledge base). Note, however, that $\mathcal{K}$ (i.e., the assumption that all "components" work normally) in this case does entail $\neg A$ (e.g., due to the axioms ax_1, ax_2) and therefore some axiom in $\mathcal{K}$ must be faulty (i.e., some "component" is abnormal). □

2.1.2. Diagnoses

Given that the system description along with the positive measurements (under the assumption $\mathcal{K}$ that all components are healthy) is inconsistent, i.e., $\mathcal{K} \cup \mathcal{B} \cup P \models \bot$,

[5] We refer to sentences by ax_i because sentences in a knowledge base are often referred to as *axioms*.

[6] *Weak fault models* define *only the normal behavior* of the system components, and do not specify any behavior in case components are at fault [36].

[7] This is a *negative* test case since there are, e.g., penguins which are birds, but cannot fly.

$\mathcal{K} =$	$\{ax_1 : A \rightarrow \neg B$	$ax_2 : A \rightarrow B$	$ax_3 : A \rightarrow \neg C$
	$ax_4 : B \rightarrow C$	$ax_5 : A \rightarrow B \vee C$	$\}$
$\mathcal{B} = \emptyset$	$P = \emptyset$		$N = \{\neg A\}$

Table 1: Example DPI stated in propositional logic.

or some negative measurement is entailed, i.e., $\mathcal{K} \cup \mathcal{B} \cup P \models n$ for some $n \in N$, some assumption(s) about the normality of components, i.e., some sentences in $\mathcal{K}$, must be retracted. We call such a set of sentences $\mathcal{D} \subseteq \mathcal{K}$ a *diagnosis* for the DPI $\langle \mathcal{K}, \mathcal{B}, P, N \rangle$ iff $(\mathcal{K} \setminus \mathcal{D}) \cup \mathcal{B} \cup P \not\models x$ for all $x \in N \cup \{\bot\}$. We say that $\mathcal{D}$ is a *minimal diagnosis* for dpi iff there is no diagnosis $\mathcal{D}' \subset \mathcal{D}$ for dpi. The set of minimal diagnoses is representative of all diagnoses under the weak fault model [37], i.e., the set of all diagnoses is equal to the set of all supersets of minimal diagnoses. Therefore, diagnosis approaches often restrict their focus to only minimal diagnoses. We furthermore denote by $\mathcal{D}^*$ the (unknown) *actual diagnosis* which pinpoints the actually faulty axioms, i.e., all elements of $\mathcal{D}^*$ are in fact faulty and all elements of $\mathcal{K} \setminus \mathcal{D}^*$ are in fact correct.

Example 2 *(Diagnoses)* For our DPI in Tab. 1 we have four minimal diagnoses, given by $\mathcal{D}_1 := [ax_1, ax_3]$, $\mathcal{D}_2 := [ax_1, ax_4]$, $\mathcal{D}_3 := [ax_2, ax_3]$, and $\mathcal{D}_4 := [ax_2, ax_5]$.[8] For instance, $\mathcal{D}_1$ is a minimal diagnosis as $(\mathcal{K} \setminus \mathcal{D}_1) \cup \mathcal{B} \cup P = \{ax_2, ax_4, ax_5\}$ is both consistent and does not entail the given negative measurement $\neg A$. □

2.1.3. Diagnosis Probability Model

In case useful meta information is available that allows to assess the likeliness of failure for system components, the probability of diagnoses (of being the actual diagnosis) can be derived. Specifically, given a function pr that maps each sentence (system component) $ax \in \mathcal{K}$ to its failure probability $0 < pr(ax) < 1$, the probability $pr(X)$ of a diagnosis candidate[9] $X \subseteq \mathcal{K}$ (under the common assumption of independent component failure) is computed as the probability that all sentences in X are faulty, and all others are correct, i.e.,

$$pr(X) := \prod_{ax \in X} pr(ax) \prod_{ax \in \mathcal{K} \setminus X} (1 - pr(ax)) \tag{1}$$

Example 3 *(Diagnosis Probabilities)* Reconsider the DPI depicted in Tab.1 and let the fault probabilities $\langle pr(ax_1), \ldots, pr(ax_5) \rangle = \langle .1, .05, .1, .05, .15 \rangle$. Then, we can

[8] In this work, we always denote diagnoses by square brackets.

[9] Note that the probability (of being equal to the actual diagnosis) of some $X \subseteq \mathcal{K}$ which is not a diagnosis is trivially zero. Nevertheless, it is reasonable to define the probability pr for such sets as well. The reason is that the diagnostic search strategies discussed in this work will grow diagnosis candidates stepwise, starting from the empty set, and it can make a substantial difference (in terms of performance) which of those candidates are further explored when. To this end, the probability of these candidates will provide a valuable guidance.

compute the probabilities of all minimal diagnoses from Example 2 as $\langle pr(\mathcal{D}_1), \ldots, pr(\mathcal{D}_4)\rangle = \langle .0077, .0036, .0036, .0058\rangle$. For instance, $pr(\mathcal{D}_1)$ is calculated as $0.1 * (1-0.05) * 0.1 * (1-0.05) * (1-0.15)$. The normalized diagnosis probabilities would then be $\langle .37, .175, .175, .28\rangle$. Note, this normalization makes sense if not all diagnoses, but only *minimal* diagnoses are of interest, which is usually the case in model-based diagnosis applications for complexity reasons. □

2.1.4. Conflicts

Instrumental for diagnosis computation is the notion of a conflict [2, 3]. A conflict is a set of healthiness assumptions for components c_i that cannot all hold given the current knowledge about the system. More formally, $\mathcal{C} \subseteq \mathcal{K}$ is a *conflict* for the DPI $\langle \mathcal{K}, \mathcal{B}, P, N\rangle$ iff $\mathcal{C} \cup \mathcal{B} \cup P \models x$ for some $x \in N \cup \{\bot\}$. We call $\mathcal{C}$ a *minimal conflict* for dpi iff there is no conflict $\mathcal{C}' \subset \mathcal{C}$ for dpi.

Example 4 *(Conflicts)* For our running example, dpi, in Tab. 1, there are four minimal conflicts, given by $\mathcal{C}_1 := \langle ax_1, ax_2\rangle, \mathcal{C}_2 := \langle ax_2, ax_3, ax_4\rangle, \mathcal{C}_3 := \langle ax_1, ax_3, ax_5\rangle$, and $\mathcal{C}_4 := \langle ax_3, ax_4, ax_5\rangle$.[10] For instance, $\mathcal{C}_4$, in CNF equal to $(\neg A \vee \neg C) \wedge (\neg B \vee C) \wedge (\neg A \vee B \vee C)$, is a conflict because adding the unit clause (A) to this CNF yields a contradiction, which is why the negative test case $\neg A$ is an entailment of $\mathcal{C}_4$. The minimality of the conflict $\mathcal{C}_4$ can be verified by rotationally removing from $\mathcal{C}_4$ a single axiom at the time and controlling for each so obtained subset that this subset is consistent and does not entail $\neg A$. □

Literature offers a variety of algorithms for conflict computation, e.g., [38, 39, 40, 41]. Given a DPI $dpi = \langle \mathcal{K}, \mathcal{B}, P, N\rangle$ as input, one call to such an algorithm returns one minimal conflict for dpi. All algorithms require an appropriate theorem prover that is used as an oracle to perform consistency checks over the logic by which the DPI is expressed. In the worst case, none of the available algorithms has a lower time complexity than $O(|\mathcal{K}|)$ [40]. The performance of diagnosis computation methods depends largely on the complexity of consistency checking for the used logic and on the number of consistency checks executed. Since consistency checking is often NP-complete or beyond for practical problems [42, 43, 44], and diagnostic algorithms have no influence on the used system description language, it is pivotal to keep the number of conflict computations at a minimum.

2.1.5. Relationship between Conflicts and Diagnoses

Conflicts and diagnoses are closely related in terms of a hitting set and a duality property [2]:

Hitting Set Property Let $dpi = \langle \mathcal{K}, \mathcal{B}, P, N\rangle$ be a DPI. Then $\mathcal{D}$ is a (minimal) diagnosis for dpi iff $\mathcal{D}$ is a (minimal) hitting set of all minimal conflicts for dpi.
(X is a *hitting set* of a collection of sets $\mathbf{S}$ iff $X \subseteq \bigcup_{S_i \in \mathbf{S}} S_i$ and $X \cap S_i \neq \emptyset$ for all $S_i \in S$)

[10] In this work, we always denote conflicts by angle brackets.

Duality Property Given a DPI $dpi = \langle \mathcal{K}, \mathcal{B}, P, N \rangle$, X is a diagnosis (or: contains a minimal diagnosis) for dpi iff $\mathcal{K} \setminus X$ is not a conflict (or: does not contain a minimal conflict) for dpi.

Example 5 *(Conflicts vs. Diagnoses)* Let us again consider our example DPI from Tab. 1. Regarding the Hitting Set Property, e.g., the minimal diagnosis $\mathcal{D}_1$ (see Example 2) is a hitting set of all minimal conflict sets because each conflict (see Example 4) contains ax_1 or ax_3. It is moreover a *minimal* hitting set since the elimination of ax_1 implies an empty intersection with, e.g., $\mathcal{C}_1$, and the elimination of ax_3 means that, e.g., $\mathcal{C}_4$ is no longer hit. Thus, given the collection $\mathbf{C}$ of all minimal conflicts, we can determine all the minimal diagnoses as the collection of minimal hitting sets of $\mathbf{C}$.

Concerning the Duality Property, e.g., $\mathcal{D}_4$ is a diagnosis because $\mathcal{K} \setminus \mathcal{D}_4 = \{ax_1, ax_3, ax_4\}$ is not a conflict (this can be easily verified by checking that no minimal conflict in Example 4 is a subset of this set), or, equivalently, $(\mathcal{K} \setminus \mathcal{D}_4) \cup \mathcal{B} \cup P = \{ax_1, ax_3, ax_4\}$ is both consistent and does not entail $\neg A$. Inversely, e.g., $\mathcal{C}_2$ is a conflict since $\mathcal{K} \setminus \mathcal{C}_2 = \{ax_1, ax_5\}$ is not a diagnosis (again, this can be easily seen by verifying that no minimal diagnosis in Example 2 is a subset of this set), or, equivalently, $(\mathcal{K} \setminus (\mathcal{K} \setminus \mathcal{C}_2)) \cup \mathcal{B} \cup P = \mathcal{C}_2 \cup \mathcal{B} \cup P = \{ax_2, ax_3, ax_4\}$ entails the negative measurement $\neg A$. □

2.2. Search

2.2.1. Path-Finding Problem

A *path-finding problem instance (PPI)* [45] can be characterized as a tuple $\langle S_0, \mathsf{succ}(), \mathsf{goal}(), g() \rangle$ where S_0 is a distinguished *initial state*, $\mathsf{succ}()$ is a *successor function* that returns all directly reachable neighbor states of any given state, $\mathsf{goal}()$ is a Boolean *goal test* that returns $true$ iff a given state is a goal state, and $g()$ is a *cost function* that assigns a real-valued cost to any given sequence of states (called *path*). A *solution* to a PPI is a path from the initial state to some goal state, and the objective is often to find an *optimal solution*, i.e., one with the least costs among all solutions.

Example 6 *(Path-Finding Problem)* An intuitive instance of a path-finding problem is the task of searching for the (shortest) route between two cities, say Berlin and Vienna. In this case, we would define $S_0 := Berlin$, $\mathsf{succ}()$ to return all (major) cities reachable from a given city by a direct motorway, $g()$ to return the summed up (motorway-)distances through all cities along a given path, and $\mathsf{goal}()$ to return $false$ for all cities except for $Vienna$. □

2.2.2. Search Algorithms

Various algorithms exist to tackle PPIs, which usually produce a systematic search tree. Each search tree is a tree composed of nodes and edges, where the root node n_0 corresponds to the state S_0, and from a node n corresponding to state S there are $|\mathsf{succ}(S)|$ emanating edges to other nodes, each of which represents one of the states in $\mathsf{succ}(S)$. For a node n that represents a state S, we also say that n's *node label* is S. The creation of child nodes from a current leaf node n by means of $\mathsf{succ}()$ is called

expansion of n. Inversely, the creation of a child node n when its parent is expanded is called *generation* of n. Importantly, *each generated node* n *stores a pointer to its parent* to allow for the reconstruction of the path to n in case it is a goal. If there are specific (named) *actions* that can be taken in a state S, each of which results in some successor state in $\mathsf{succ}(S)$, the respective action name is often used as an *edge label* between S and the successor node reached through this action. Note that one and the same state can occur multiple times in a search tree, depending on the used algorithm. In general, different ways of constructing the search tree—i.e., in which order nodes are selected for expansion, and how much about the tree construction "history" (e.g., already expanded nodes) is stored —yield a variety of search methods with different properties regarding *completeness* (will a solution be found whenever one exists?), *best-first property*[11] (will the best solution be found first?), as well as *time and space complexity* (how much time and memory will the algorithm need to find a solution?). Search algorithms that solve PPIs usually stop after the first path to a goal state is found.

2.2.3. Informed Search

If problem-specific information beyond the mere PPI is (not) available to an algorithm, the problem is called *(un)informed*. If applicable, such problem-specific information is normally given as a *heuristic function* $h(\mathsf{n})$ which assigns to each node n a non-negative real value as an estimation of the cost of the best path from n's state to some goal state. This heuristic value $h(\mathsf{n})$ can then be combined with the costs $g(\mathsf{n})$ already incurred to reach n, in terms of $f(\mathsf{n}) := g(\mathsf{n}) + h(\mathsf{n})$, which estimates the overall cost of the path from the start to some goal state via node n.

Example 7 *(Heuristic Function)* Recall the route planning task from Example 6. For this problem, a simple heuristic function is given by the straight-line distance between a particular city n and the closest destination city (goal state). □

Example 8 *(Search Algorithms)* Important uninformed search strategies are depth-first, breadth-first, uniform-cost and iterative deepening search; popular informed search methods are A* and IDA* [45]. Each of them maintains a queue of nodes that is sorted in a specific way, where the first node of this queue is chosen for expansion at each step. Each expanded node is deleted from the queue and its generated successors are added to it in a way the defined sorting is preserved. Whenever a node is expanded whose state satisfies the $\mathsf{goal}()$ test, the respective path is returned and the search terminates.

Now, depth-first search maintains a LIFO queue, breadth-first search a FIFO queue, and uniform-cost search and A*, respectively, a queue sorted in ascending order by $g()$ and $f()$. Iterative deepening and IDA* run in iterations, executing one depth-first search per iteration. At this, each iteration uses an incremented depth-limit $l = 1, 2, \ldots$ (iterative deepening) or an incremented cost-limit equal to the best known node from the last iteration that has not been expanded (IDA*). A depth-limit (cost-limit) k means that no successors are generated for any node at tree depth k (with cost $> k$). □

[11] Often also referred to as *optimality* [45].

2.2.4. Diagnosis Search Algorithms

Given a DPI $\langle \mathcal{K}, \mathcal{B}, P, N \rangle$, a diagnosis search algorithm[12] is characterized by the definition of a *node processing procedure*. The latter is divided into two parts, *node labeling* and *node assignment*. A generic diagnosis search algorithm then works as follows:

- Start with a queue including only the root node $\emptyset$.
- While the queue is non-empty and not enough minimal diagnoses have been found,[13] poll the first node n from the queue and *process* it. That is, *compute a label* L for n, and *assign* n (or potentially its successors) to an appropriate node class (e.g., solutions, non-solutions) based on L.

Different specific diagnosis search algorithms are obtained by (re)defining *(i)* the sorting of the queue and *(ii)* the node processing procedure, which means specifying how nodes are labeled, and to which collections nodes are assigned.

Example 9 *(Reiter's HS-Tree)* To make this more concrete, let us examine how (i) and (ii) is realized in Reiter's seminal HS-Tree [2]:
Sorting of the queue: Depending on the desired preference criterion to be optimized, either a FIFO-queue is used (breadth-first search; *minimum-cardinality diagnoses first*) or the queue is kept sorted in descending order of $pr(\mathsf{n})$, cf. Eq. 1 (uniform-cost search; *most probable diagnoses first*).
Node labeling: The following checks are executed in the given order, and a label is returned as soon as the first check is positive.

(non-minimality) Is n a superset of some already found diagnosis? If yes, return $L = closed$.

(duplicate) Is there another node equal to n in the queue? If yes, return $L = closed$.

(reuse label) Is there a conflict $\mathcal{C}$ among the already used node labels such that $\mathsf{n} \cap \mathcal{C} = \emptyset$? If yes, return $L = \mathcal{C}$.

(compute label) Compute a minimal conflict for $\langle \mathcal{K} \setminus \mathsf{n}, \mathcal{B}, P, N \rangle$. If some set $\mathcal{C}$ is computed, return $L = \mathcal{C}$. If 'no conflict' is output, return $L = valid$.

Node assignment: If n's computed label

$L = \langle ax_1, \ldots, ax_k \rangle$ (a minimal conflict), then k new successor nodes $\mathsf{n}_1, \ldots, \mathsf{n}_k$ are generated and added to the queue, where $\mathsf{n}_i = \mathsf{n} \cup \{ax_i\}$.

$L = valid$, then n is a solution and added to the collection of minimal diagnoses.

$L = closed$, then n is irrelevant or a proven non-solution and not added to any collection, i.e., it is discarded.

Note, apart from guiding the node assignment, there is no purpose of a node's label L. Thus, in the queue, only nodes are stored, but not the labels along their paths. In a separate collection, already used node labels are recorded due to the *reuse label* check (see above).

[12] Albeit literature offers a variety of different diagnosis computation paradigms (cf. Sec. 5), we discuss only the formulation as a hitting set finding problem, which suffices for the purposes of this work.

[13] Of course, various other stop conditions are possible, e.g., a timeout or a maximal amount of consumed memory.

Remark: In order for this algorithm to be sound, complete and best-first

- the function for conflict computation used in *(compute label)* must be sound (if a set is returned, it is a conflict), complete (a conflict is returned whenever there is one), and must return only *minimal*[14] conflicts, and
- the probability model $pr(ax)$ for $ax \in \mathcal{K}$ needs to be *cost-adjusted*, i.e., $pr(ax) < 0.5$ for all $ax \in \mathcal{K}$.[15] (Clearly, this condition is not needed if minimum-cardinality diagnoses are to be computed, where a FIFO-queue is used.) □

2.2.5. Diagnosis Search vs. Path-Finding

The main properties that distinguish diagnosis search from path-finding are:

(I) PPI-formulation does not suffice as an input: Although the problem of searching for minimal diagnoses for a DPI can be stated as a PPI—where $S_0 = \emptyset$, $\mathsf{succ}()$ gets a *labeled* node n with label L and returns the successors of n if L is a set, and $\emptyset$ else, $\mathsf{goal}(\mathsf{n})$ returns $true$ iff n is a diagnosis, and $g(\mathsf{n}) := pr(\mathsf{n})$ as per Eq. 1—this characterization is not a sufficient basis to run a diagnosis search. What is missing is the definition of a *node labeling* and a *node assignment* strategy (see above). Importantly, these missing building blocks decide over the soundness, completeness and best-first property of the diagnosis search. By contrast, for path-finding, the PPI includes all relevant information for the problem to be directly solved by an off-the-shelf path-finding algorithm (cf. Example 8).

(II) States, nodes and paths coincide: In diagnosis search, the state of a search tree node n corresponds to n itself (i.e., to a set of ax_i-elements). So, no distinction between states and nodes is made. When viewing successor node generation performed by $\mathsf{succ}(\mathsf{n})$ as an application of actions, then the only possible action at any node n would be "add one element ax_i from n's label L to n". When the label ax_i is assigned to the edge pointing from n to its child node $\mathsf{n} \cup \{ax_i\}$, nodes (and states) can be seen as representatives of the (edge labels along the) paths in the search tree.

(III) Solutions are sets, not paths: Solutions to a diagnosis search problem are nodes (*sets* of edge labels along a tree path) which are minimal diagnoses for the given DPI. Unlike in path-finding problems, the order of labels along the path does not matter.

(IV) Multiple solutions are sought: In diagnosis search, it is usually of interest to find multiple solutions, i.e., after the first solution is determined, the search must be (correctly) continuable until sufficient solutions are found.

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[14] If the minimality of computed conflicts is not guaranteed, the algorithm becomes generally incomplete, and a directed acyclic graph version [17] must be used to reestablish completeness.

[15] This condition [7] is fairly benign as it can be established from any probability model pr. In fact, a *cost-adjusted* probability measure pr_{adj} is obtained by simply choosing an arbitrary fixed $c \in (0, 0.5)$ and by setting $pr_{adj}(ax) := c \cdot pr(ax)$ for all $ax \in \mathcal{K}$. Observe that this adjustment does not affect the relative probabilities in that $pr_{adj}(ax)/pr_{adj}(ax') = k$ whenever $pr(ax)/pr(ax') = k$, i.e., no information is lost in the sense that the fault probability order of components will remain invariant.

Intuitively, the cost adjustment is necessary to ensure that the algorithm, when exploring nodes in descending order of probability, will have already visited all nodes $\mathsf{n} \subset \mathsf{n}'$ whenever it visits a node n' (cf. Eq. 1). This property is necessary for the algorithm's soundness (computation of only *minimal* diagnoses).

(V) Search for maximal-cost solutions: In diagnosis search, one wants to calculate the maximal-cost (i.e., most probable or maximal cardinality^{-1}) solutions whereas path-finding is usually about finding a minimal-cost solution.

(VI) Stricter conditions on cost function: Like for path-finding, the used cost function must fulfill certain criteria in order for soundness, completeness and the best-first feature to be guaranteed. While it is common for (uninformed) path-finding problems to specify the cost function $f()$ in a way the path costs amount to the sum of the action (or: step) costs along the path, the cost function $f(\mathsf{n}) := pr(\mathsf{n})$ as per Eq. 1 used for diagnosis search cannot be seen as a sum of step costs. As a consequence, it suffices in the former case to make sure step costs are non-negative ($f()$ is said to be *monotonic* in this case), as opposed to the latter case, where the *cost-adjustment* (see Example 9) is necessary (and it does not suffice that merely $pr(ax_i) > 0$ for all $ax_i \in \mathcal{K}$). This cost-adjustment makes the function $f(\mathsf{n}) := pr(\mathsf{n})$ *anti-monotonic*, i.e., $f(\mathsf{n}_i) \geq f(\mathsf{n}_j)$ whenever n_j is a successor of n_i (i.e., $\mathsf{n}_i \subset \mathsf{n}_j$).[16] Note that anti-monotonicity when searching for maximal-cost solutions (as for diagnosis search, cf. *(V)*) has the same implications as monotonicity when searching for minimal-cost solutions (as for path-finding problems).

(VII) Soundness is not trivial: Whereas in path-finding any path whose end state satisfies the goal test is a valid solution to the PPI, in diagnosis search an appropriate combination of suitable goal test, node labeling, node assignment and cost function is necessary to ensure soundness, i.e., that each found solution is indeed a minimal diagnosis for the given DPI.

3. Recursive Best-First Hitting Set Search (RBF-HS)

3.1. Deriving RBF-HS from RBFS

3.1.1. RBFS: The Basis

Korf's RBFS algorithm [31] provides the inspiration for RBF-HS. Historically, the main motivation that led to the engineering of RBFS was the problem that best-first searches by that time required exponential space. The idea behind RBFS is to trade (more) time for (much less) space. To this end, RBFS implements a scheme that can be synopsized as

- *(complete and best-first):* always expand current globally-best node while remembering current globally-second-best node,
- *(undo and forget to keep space linear):* backtrack and explore second-best node if none of the child nodes of best node is better than second-best,
- *(remember utility of forgotten subtrees to keep the search progressing):* before deleting a subtree in the course of backtracking, store cost of subtree's best node,
- *(restore utility at regeneration to avoid redundancy):* whenever a subtree is re-explored, use this stored cost value to update node costs in the subtree.

[16] In fact, $f(\mathsf{n})$ is even *strictly* anti-monotonic ($f(\mathsf{n}_i) > f(\mathsf{n}_j)$) as $0 < pr(ax) < 1$ holds for all $ax \in \mathcal{K}$ (this can be easily seen from Eq. 1).

Algorithm 1 RBFS

Input: PPI $ppi := \langle S_0, \mathsf{succ}(), \mathsf{goal}(), g() \rangle$ and a heuristic function $h()$ (if ppi is an uninformed problem, then $h(\mathsf{n}) := 0$ for all nodes n)
Output: a path from S_0 to some goal state, if a goal state is reachable from S_0 by means of successive applications of the $\mathsf{succ}()$ function; *null* otherwise

```
1:  procedure RBFS(ppi, h())
2:      solution ← null
3:      n_0 ← MAKENODE(S_0)                          ▷ MAKENODE creates a tree node for the given state
4:      RBFS'(n_0, f(n_0), ∞)                        ▷ f(n) := g(n) + h(n)
5:      return solution

6:  procedure RBFS'(n, F(n), bound)
7:      if goal(STATE(n)) then                       ▷ STATE returns the state associated with the given node
8:          solution ← GETPATHTO(n)                  ▷ GETPATHTO returns sequence of states from root node to given node
9:          exit procedure
10:     Child_Nodes ← [ ]
11:     for S_i ∈ succ(STATE(n)) do
12:         Child_Nodes ← ADD(MAKENODE(S_i), Child_Nodes)   ▷ ADD(e, C) adds element e to collection C
13:     if Child_Nodes = [ ] then
14:         return ∞                                 ▷ n is hopeless, i.e., is no goal and has no children
15:     for n_i ∈ Child_Nodes do
16:         if f(n) < F(n) then                      ▷ if true, n was already expanded before
17:             F(n_i) ← max(F(n), f(n_i))
18:         else
19:             F(n_i) ← f(n_i)
20:     if |Child_Nodes| = 1 then                    ▷ ADDDUMMYNODE adds a newly created "dummy" node n_d...
21:         Child_Nodes ← ADDDUMMYNODE(Child_Nodes)  ▷ ...with F(n_d) = ∞ to the given collection
22:     Child_Nodes ← SORTINCREASINGBYF(Child_Nodes)  ▷ sort Child_Nodes in descending order of F-value
23:     n_1 ← GETANDDELETEFIRSTNODE(Child_Nodes)     ▷ n_1 . . . best child
24:     n_2 ← GETFIRSTNODE(Child_Nodes)              ▷ n_2 . . . 2nd-best child
25:     while F(n_1) ≤ bound ∧ F(n_1) < ∞ do
26:         F(n_1) ← RBFS'(n_1, F(n_1), min(bound, F(n_2)))
27:         Child_Nodes ← INSERTSORTEDBYF(n_1, Child_Nodes)   ▷ insert n_1 s.t. sorting by F-value is preserved
28:         n_1 ← GETANDDELETEFIRSTNODE(Child_Nodes)  ▷ n_1 . . . best child
29:         n_2 ← GETFIRSTNODE(Child_Nodes)           ▷ n_2 . . . 2nd-best child
30:     return F(n_1)
```

As a result, RBFS is complete and best-first and works within linear-space bounds.

3.1.2. RBFS: Briefly Explained

RBFS is presented by Alg. 1. In a nutshell, it works as follows [45]. Initial node costs are the f-values computed from $g()$ and $h()$, and *backed-up node costs* are named F-values. Initially, all backed-up node costs are the nodes' initial costs. Starting from the root node corresponding to S_0, the principle is to follow the best (lowest F) path downwards (recursive RBFS'-calls, line 26). At each downward step, the variable $bound$ is used to keep track of the (backed-up) cost of the best alternative path available from any ancestor of the current node (note, this is the *globally* best alternative path). If the current node exceeds $bound$, the recursion unwinds back to the alternative path. As the recursion unwinds, the cost of each node along the path is replaced with a (new) backed-up cost value, which is the best (backed-up) cost of its child nodes (cf. line 30). In this way, RBFS always remembers the backed-up cost of the best leaf in the forgotten subtree and can therefore decide whether it is worth reexpanding the subtree at some later time (this decision is made through the condition of the while-loop). When expanding a subtree rooted at node n, which has already been expanded and forgotten before (condition in line 16 is true) and whose initial cost (f-value) appears

more promising than the algorithm knows from a previous iteration and the stored backed-up cost $F(\mathsf{n})$ it actually is, the F-value of child nodes n_i of n is not tediously learned again by RBFS, but directly updated by means of n's F-value (see line 17). If some node is recognized to correspond to a goal state, the path to this node is returned and RBFS' terminates (lines 7–9).

3.1.3. From RBFS to RBF-HS: Necessary Modifications

In order to transform a path-finding into a diagnosis search algorithm, we have to make adequate amendments to the former with due regard to all differences between both paradigms discussed in bullets *(I)–(VII)* in Sec. 2. Next, we list and explain the main modifications necessary to derive RBF-HS from RBFS (line numbers given refer to the respective locations of the changes *in the RBF-HS algorithm*, i.e., in Alg. 2).

(Mod1) A node labeling (line 12 and LABEL procedure) and a node assignment (lines 13–19) strategy have to be added. Importantly, the goal test (check, whether a node is a minimal diagnosis, lines 39, 42 and 44) as well as the preparation of nodes for expansion (i.e., the provision of a minimal conflict, line 43 or 49) is part of these two code blocks. Note, it is crucial for achieving soundness, completeness and the best-first property that node labeling and node assignment are properly engineered. *Justification:* Bullet *(I)* on page 11.

(Mod2) Differentiation between nodes, states and paths is no longer necessary, which is why the functions MAKENODE (generates node from state), STATE (extracts state from node), and GETPATHTO (returns path from root to node) can be omitted. This becomes evident in line 9 (root node is simply equal to initial state $\emptyset$; cf. line 3 in Alg. 1), line 16 (a *set* n is added to the solutions $\mathbf{D}$; cf. line 8 in Alg. 1), line 20 and EXPAND function (successors are generated directly from the *node* n; cf. line 12 in Alg. 1), and lines 39, 42 and 45 (goal test performed on node, not state; cf. line 7 in Alg. 1). *Justification:* Bullets *(II)* and *(III)* on page 11.

(Mod3) The requirement that *multiple* solutions are generally desired in diagnosis search is handled in lines 17–19. Note, it is essential to return $-\infty$ (i.e., the worst possible cost) as the backed-up F-cost of the solution node n in order to allow the search to continue in a well-defined and correct way. More precisely, this will cause the F-value of n's best sibling node to be propagated upwards. As a consequence, the backed-up value for any subtree including n will be the so-far found best cost over all nodes in this subtree *except for* n. In fact, any backed-up value $F^* := F(\mathsf{n}) > -\infty$ would prevent RBF-HS' from terminating and thus would make it incomplete (intuitively, at some point all other nodes would have a value lower than F^* and the algorithm would loop forever exploring n again and again). *Justification:* Bullet *(IV)* on page 11.

(Mod4) Since solutions of maximal cost are stipulated in diagnosis search, all occurrences of $<$, $\leq$, $\min$, $\max$, ∞, SORTINCREASINGBYF have to be switched to $>$, $\geq$, $\max$, $\min$, $-\infty$, SORTDECREASINGBYF, respectively. *Justification:* Bullet *(V)* on page 12.

(Mod5) The used probability measure pr needs to be cost-adjusted. For any given model that assigns some failure probability $pr(ax) \in (0, 1)$ to each $ax \in \mathcal{K}$, this can be achieved as explained in footnote 15. *Justification:* Bullet *(VI)* on page 12.

(Mod6) To achieve soundness (only minimal diagnoses are added to the solutions $\mathbf{D}$ in line 16), the following provisions are made. The function f is cost-adjusted (since pr is cost-ajusted and $f := pr$, cf. inputs of Alg. 2) which implies, by the sorting of Child_Nodes (line 28), that minimal diagnoses will be found prior to non-minimal ones (cf. bullet *(VI)*). Moreover, the LABEL function is designed such that only nodes n can be labeled $valid$ for which no already-found diagnosis exists which is a subset of n (goal test, part 1, line 39), and which is evidentially a diagnosis (goal test, part 2, line 45). Finally, the node assignment ensures that only nodes labeled $valid$ can be assigned to the solution list $\mathbf{D}$ (line 16).[17] *Justification:* Bullet *(VII)* on page 12.

3.2. RBF-HS Algorithm Walkthrough

3.2.1. Inputs and Output

RBF-HS is depicted by Alg. 2.[18] It accepts the following arguments: a DPI $dpi = \langle \mathcal{K}, \mathcal{B}, P, N \rangle$, a probability measure pr (see Sec. 2), and a stipulated number ld of minimal diagnoses to be returned.[19] It outputs the ld (if existent) minimal diagnoses of maximal probability wrt. pr for dpi. To effect that diagnoses of minimum cardinality (instead of maximal probability) are preferred, the probability model must satisfy $pr(ax) := c$ for all $ax \in \mathcal{K}$ for some arbitrary fixed $c \in (0, 0.5)$. Note, this has the same effect as defining $pr(\mathsf{n}) := 1/|\mathsf{n}|$ for all nodes n in the search tree.

3.2.2. Trivial Cases

At the beginning (line 2), RBF-HS initializes the solution list of found minimal diagnoses $\mathbf{D}$ and the list of already computed minimal conflicts $\mathbf{C}$. Then, two trivial cases are checked, i.e., whether no diagnoses exist for dpi (lines 4–5), or if the empty set is the only diagnosis for dpi (lines 6–7). Note, the former case applies iff the empty set is a conflict for dpi, which implies that $\mathcal{K} \setminus \emptyset = \mathcal{K}$ is not a diagnosis for dpi by the Duality Property (cf. Sec. 2), which in turn means that no diagnosis can exist since diagnoses are subsets of $\mathcal{K}$ and each superset of a diagnosis must be a diagnosis as well (weak fault model, cf. Sec. 2). The latter case holds iff there is no conflict at all for dpi, i.e., in particular, $\mathcal{K}$ is not a conflict, which is why $\mathcal{K} \setminus \mathcal{K} = \emptyset$ is a diagnosis by the Duality Property, and consequently no other *minimal* diagnosis can exist.

If none of these trivial cases is given, the call of FINDMINCONFLICT (line 3) returns a non-empty minimal conflict $\mathcal{C}$ (line 8 is reached), which entails by the Hitting Set Property (cf. Sec. 2) that a non-empty (minimal) diagnosis will exist. For later reuse (recall from Sec. 2.1: conflict computation is an expensive operation), $\mathcal{C}$ is added to the computed conflicts $\mathbf{C}$, and then the recursive sub-procedure RBF-HS' is called (line 9). The arguments passed to RBF-HS' are the root node $\emptyset$, its f-value, and the initial bound set to $-\infty$.

[17] This argumentation does *not* prove the soundness (cf. Theorem 2 for a full proof), but aims to emphasize the non-trivial premises for soundness in diagnosis search, as opposed to path-finding.

[18] Our implementation of RBF-HS can be accessed at https://bit.ly/2Gp3XwX.

[19] The shortcut ld refers to "leading diagnoses".

Algorithm 2 RBF-HS

Input: tuple $\langle dpi, pr, ld \rangle$ comprising

- a DPI $dpi = \langle \mathcal{K}, \mathcal{B}, P, N \rangle$
- a probability measure pr that assigns a failure probability $pr(ax) \in (0, 1)$ to each $ax \in \mathcal{K}$ (cf. Sec. 2), where pr is cost-adjusted (cf. footnote 15); *note:* the cost function $f(\mathsf{n}) := pr(\mathsf{n})$ as per Eq. 1 for all tree nodes $\mathsf{n} \subseteq \mathcal{K}$
- the number ld of leading minimal diagnoses to be computed

Output: list $\mathbf{D}$ where $\mathbf{D}$ is the list of the ld (if existent) most probable (as per pr) minimal diagnoses wrt. dpi, sorted by probability in descending order

procedure RBF-HS(dpi, pr, ld)
  $\mathbf{D} \leftarrow [\,],\ \mathbf{C} \leftarrow [\,]$
  $\mathcal{C} \leftarrow$ FINDMINCONFLICT(dpi)
  if $\mathcal{C} = \emptyset$ **then**
    return $\mathbf{D}$
  if $\mathcal{C}$ = 'no conflict' **then**
    return $[\emptyset]$
  $\mathbf{C} \leftarrow$ ADD($\mathcal{C}, \mathbf{C}$)
  RBF-HS'($\emptyset, f(\emptyset), -\infty$) ▷ $\emptyset$ is the root node
  return $\mathbf{D}$

procedure RBF-HS'($\mathsf{n}, F(\mathsf{n}), bound$)
  $L \leftarrow$ LABEL(n)
  if $L = closed$ **then**
    return $-\infty$
  if $L = valid$ **then**
    $\mathbf{D} \leftarrow$ ADD($\mathsf{n}, \mathbf{D}$) ▷ new minimal diagnosis found
    if $|\mathbf{D}| \geq ld$ **then**
      exit procedure
    return $-\infty$
  Child_Nodes $\leftarrow$ EXPAND(n, L)
  for $\mathsf{n}_i \in$ Child_Nodes **do**
    if $f(\mathsf{n}) > F(\mathsf{n})$ **then** ▷ if $true$, n was already expanded before
      $F(\mathsf{n}_i) \leftarrow \min(F(\mathsf{n}), f(\mathsf{n}_i))$
    else
      $F(\mathsf{n}_i) \leftarrow f(\mathsf{n}_i)$
  if |Child_Nodes| = 1 **then** ▷ add dummy node n_d with $F(\mathsf{n}_d) = -\infty$
    Child_Nodes $\leftarrow$ ADDDUMMYNODE(Child_Nodes)
  Child_Nodes $\leftarrow$ SORTDECREASINGBYF(Child_Nodes)
  $\mathsf{n}_1 \leftarrow$ GETANDDELETEFIRSTNODE(Child_Nodes) ▷ n_1 . . . best child
  $\mathsf{n}_2 \leftarrow$ GETFIRSTNODE(Child_Nodes) ▷ n_2 . . . 2nd-best child
  while $F(\mathsf{n}_1) \geq bound\ \wedge\ F(\mathsf{n}_1) > -\infty$ **do**
    $F(\mathsf{n}_1) \leftarrow$ RBF-HS'($\mathsf{n}_1, F(\mathsf{n}_1), \max(bound, F(\mathsf{n}_2))$)
    Child_Nodes $\leftarrow$ INSERTSORTEDBYF(n_1, Child_Nodes)
    $\mathsf{n}_1 \leftarrow$ GETANDDELETEFIRSTNODE(Child_Nodes) ▷ n_1 . . . best child
    $\mathsf{n}_2 \leftarrow$ GETFIRSTNODE(Child_Nodes) ▷ n_2 . . . 2nd-best child
  return $F(\mathsf{n}_1)$

procedure LABEL(n)
  for $\mathsf{n}_i \in \mathbf{D}$ **do**
    if $\mathsf{n} \supseteq \mathsf{n}_i$ **then** ▷ goal test, part 1 (is n non-minimal?)
      return $closed$ ▷ n is a non-minimal diagnosis
  for $\mathcal{C} \in \mathbf{C}$ **do**
    if $\mathcal{C} \cap \mathsf{n} = \emptyset$ **then** ▷ cheap non-goal test (is n not a diagnosis?)
      return $\mathcal{C}$ ▷ n is not a diagnosis; reuse $\mathcal{C}$ to label n
  $L \leftarrow$ FINDMINCONFLICT($\langle \mathcal{K} \setminus \mathsf{n}, \mathcal{B}, P, N \rangle$)
  if L = 'no conflict' **then** ▷ goal test, part 2 (is n diagnosis?)
    return $valid$ ▷ n is a minimal diagnosis
  else ▷ n is not a diagnosis
    $\mathbf{C} \leftarrow$ ADD($L, \mathbf{C}$) ▷ L is a *new* minimal conflict ($\notin \mathbf{C}$)
    return L

procedure EXPAND($\mathsf{n}, \mathcal{C}$)
  Succ_Nodes $\leftarrow [\,]$
  for $e \in \mathcal{C}$ **do**
    Succ_Nodes $\leftarrow$ ADD($\mathsf{n} \cup \{e\}$, Succ_Nodes)
  return Succ_Nodes

3.2.3. Recursion: Principle

The basic principle of the recursion is very similar as sketched above for RBFS. That is, always explore the open node with best F-value in a depth-first manner, until the best node has worse costs than the globally best alternative node (whose cost is always stored by $bound$). Then backtrack and propagate the best F-value among all child nodes up at each backtracking step. Based on their latest known F-value, the child nodes at each tree level are re-sorted in best-first order of F-value. When re-exploring an already explored, but later forgotten, subtree, the cost of nodes in this subtree is, if necessary, updated through a cost inheritance from parent to children. In this vein, a re-learning of already learned backed-up cost-values, and thus repeated and redundant work, is avoided. Exploring a node in RBF-HS means labeling this node and assigning it to an appropriate collection of nodes based on the computed label (cf. Sec. 2.2.4 and Example 9). The recursion is executed until either $\mathbf{D}$ comprises the desired number ld of minimal diagnoses or the hitting set tree has been explored in its entirety.

3.2.4. Recursion: Structure

To get a better impression of RBF-HS' on a more abstract, structural level before delving into the details, it is instructive to look upon RBF-HS' as a succession of the following blocks:

- node labeling (line 12),
- node assignment (lines 13–19),
- node expansion (line 20),
- node cost inheritance (lines 21–25),
- child node preparation (lines 26–28), and
- recursive child node exploration (lines 29–36).

3.2.5. Recursion: Details

The first argument passed to RBF-HS' (line 9 or 32) is the node n it will process.

Node Labeling. As a first step, n is labeled by the LABEL function (line 12).

Node Assignment. The computed label is then handled very similarly as in case of Reiter's HS-Tree (cf. Example 9), i.e., $closed$ nodes are discarded, $valid$ ones added to $\mathbf{D}$, and those labeled by a conflict L are expanded by the EXPAND function (line 20). In addition, since a value has to be returned by each recursive RBF-HS'-call (cf. line 32) in order for the recursion to be properly resumed, the (worst possible) backed-up F-value $-\infty$ is returned for nodes without successors (labels $closed$ and $valid$). Intuitively, the value $-\infty$ can be interpreted as "this node is hopeless or already explored". The rationale behind this is to avoid a misleading of the algorithm towards re-exploring such nodes once their costs would be better than those of all other nodes. In fact, any F-value larger than $-\infty$ would even imply the algorithm's non-termination and thus incorrectness, cf. **(Mod3)** on page 14.

Notably, nodes with F-value equal to $-\infty$ *can* be considered again (given their parent nodes are expanded again), but, if so, they are directly labeled $closed$ in line 40 because they are either equal to or proper supersets of some node in $\mathbf{D}$. Equality

holds for nodes originally labeled $valid$, which are therefore in $\mathbf{D}$; the superset property is given in case of nodes originally labeled $closed$, for which there was already a proper subset in $\mathbf{D}$ and thus there still must be one (note: no elements are ever deleted from $\mathbf{D}$ in Alg. 2). This (*inexpensive*) catching of re-explored nodes at the very beginning of LABEL is critical since the FINDMINCONFLICT operation later in LABEL involves costly theorem prover calls, and must thus be performed as rarely as possible (cf. Sec. 2.1.4).

Node Expansion. Whenever n is neither a $closed$ nor a $valid$ node, it is labeled by a minimal conflict L and its successors $\mathsf{Child\_Nodes}$ are created via a call of the EXPAND function (line 20). The result of this node expansion are $|L|$ nodes, generated as $\mathsf{n} \cup \{ax_i\}$ for each $ax_i \in L$ (line 53).

Node Cost Inheritance.[20] Next, the F-value of each of the newly-generated child nodes n_i is set (lines 21–25). Note, this is necessary at each node expansion since a (child) node's F-value exists only as long as the node is in memory; is it no longer stored after a node is discarded through a backtracking step of the algorithm. Intuitively, the ideal F-value would be: *(a)* the original f-value for child nodes never explored before, for which there cannot be a "learned" F-value yet, *(b)* the last known F-value for child nodes already explored before.

Basically, there are two possibilities how RBF-HS may specify the F-value of a child node n_i: either the F-value of the parent n is inherited to the child node, or n_i's (original) f-value is used. In fact, the algorithm first checks whether n has already been explored before, which is true if $f(\mathsf{n}) > F(\mathsf{n})$ (line 22).

In case $f(\mathsf{n}) > F(\mathsf{n})$, the child nodes can be partitioned into those that have been explored before, and those that have not. For the latter class, we have $F(\mathsf{n}) \geq f(\mathsf{n}_i)$, which involves that each non-explored child node keeps its original f-cost ($\min$ in line 23). For the former class, it indeed holds that $F(\mathsf{n}) < f(\mathsf{n}_i)$, which is why all already-explored nodes inherit the F-value of the parent n ($\min$ in line 23). Note, the child nodes' last known F-value (before they were discarded) might have been lower than the inherited $F(\mathsf{n})$ because only *one* F-value is remembered by the algorithm when a subtree is forgotten; however, $F(\mathsf{n})$ is at least to some extent lower than $f(\mathsf{n}_i)$ which implies that at least some "fraction" of n_i's already learned backed-up cost is restored by the inheritance.

Alternatively, given $f(\mathsf{n}) = F(\mathsf{n})$ (note that $f(\mathsf{n}) \leq F(\mathsf{n})$ for all nodes n is an invariant throughout RBF-HS'), n can, but does not need to, have been explored already. If n has not yet been explored, then clearly none of its child nodes n_i can have been explored either, which is why it is reasonable to set the F-value of all children to their f-value (line 25). Otherwise, i.e., if n has already been explored before, then the latest backed-up value $F(\mathsf{n})$ (which was necessarily less than $f(\mathsf{n})$) must have been forgotten in the course of backtracking steps (which *is* possible, e.g., if one of n's siblings had a greater F-value than n at the point where RBF-HS' backtracked after exploring n's parent node). Now, since the f-value of each node is greater than the f-value of any

[20] For a detailed argumentation why the assertions about the f- and F-costs of nodes made in this paragraph hold, please consider the proof of Theorem 2.

of its successors (anti-monotonicity of f, cf. bullet *(VI)* on page 12), it must hold that *(a)* $F(\mathsf{n}) = f(\mathsf{n}) > f(\mathsf{n}_i)$ for all child nodes n_i of n, and *(b)* any solution in a subtree rooted at some n_i will have cost lower than or equal to $f(\mathsf{n}_i)$. Since the "learned" F-value for any node should not be a worse estimate of the cost of a solution in the respective subtree than the original estimation given by the node's f-value, it does not make sense to set the F-value of any child node n_i to the value $F(\mathsf{n})$ ($> f(\mathsf{n}_i)$). Hence, it is most plausible also in this case to set the F-value of all children to their original f-value (line 25).

Child Node Preparation. Once all nodes in Child_Nodes have been assigned their F-value, Child_Nodes is prepared for node exploration (while-loop, line 31) in the following way: First, if there is only a single node in Child_Nodes, then a second "dummy" node is added. The reason for this is that lines 30 and 35 require a second node to be present in Child_Nodes. In order not to compromise the correctness of RBF-HS, the F-value of this dummy node has to be set to the worst possible value $-\infty$ (cf. argumentation for *Node Assignment* above). Second, the nodes in Child_Nodes are sorted in descending order of F-value, such that exactly the nodes with the highest and second-highest F-value are extracted from Child_Nodes in lines 29 and 34, respectively.

Recursive Child Node Exploration. Now, as the child nodes have been generated, their F-costs have been set, and the list Child_Nodes has been prepared for being processed, the final block of RBF-HS' involves the best-first exploration of nodes in Child_Nodes by means of the algorithm's while-loop. Throughout the iteration of the loop, the variables n_1 and n_2 always comprise the best and second-best node, respectively, among Child_Nodes, according to their (backed-up) F-value. This is guaranteed by lines 33, 34, and 35, where INSERTSORTEDBYF inserts a node to a list such that the sorting of the list according to F is preserved. The while-loop is iterated by always exploring the best node n_1 through a recursive call of RBF-HS' (line 32) as long as the current n_1's F-value is better than $bound$. The latter stores the maximal F-value over all child nodes of all ancestors of n_1 (see the $\max$ which determines the bound at each recursive downward step in line 32). This value at the same time corresponds to the maximal F-value of *any* alternative node in the entire hitting set tree, which in turn is greater than or equal to the f-value (i.e., the probability pr) of *any* existing solution other than n_1 (see the proof of Theorem 2 for a precise argumentation why these things hold). Hence, the use of $bound$ as a ruler of backtracking actions guarantees that the most probable (remaining) solution is always found first (next). At the point where all nodes in Child_Nodes have an F-value lower than $bound$, the while-loop is exited and the currently best F-value among the nodes in Child_Nodes is returned, i.e., propagated upward to their parent node n. Note, in the course of the recursive explorations of the subtrees rooted at nodes in Child_Nodes throughout the iteration of the while-loop, solutions might be located and added to $\mathbf{D}$.

Termination. Whenever $\mathbf{D}$ is extended, a check is run which tests if the list of solutions $\mathbf{D}$ has already reached the stipulated size ld (line 17). If so, the RBF-HS' procedure terminates (line 18). Otherwise, i.e., if there are fewer than ld minimal diagnoses existent for the tackled DPI, RBF-HS' terminates once all nodes in the hitting set tree

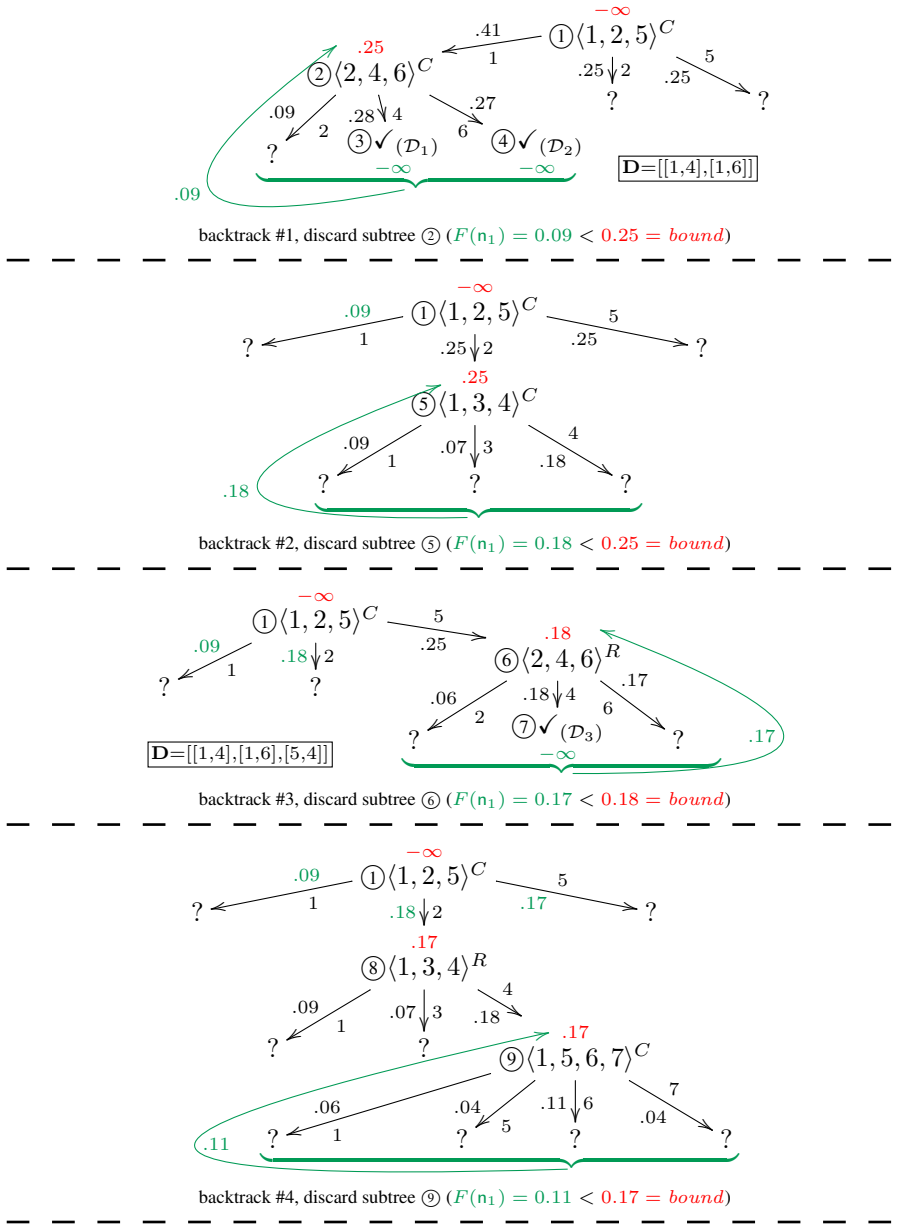
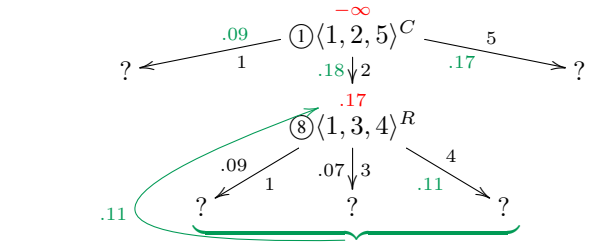
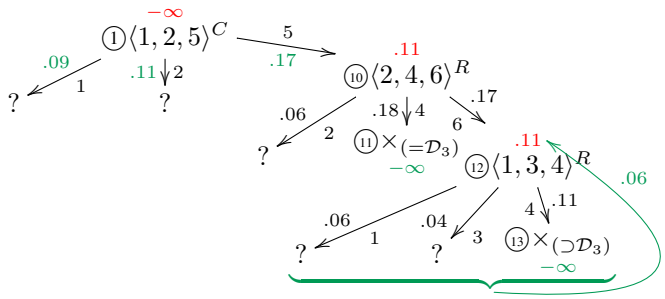


Figure 1: RBF-HS executed on example DPI (part I), cf. Example 10.

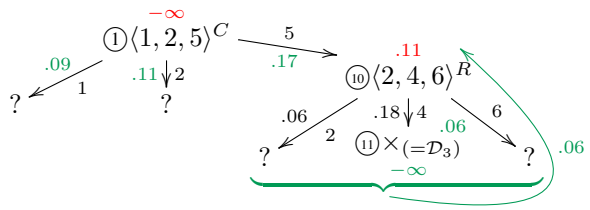
have been explored and assigned the backed-up value $-\infty$, which is why all recursive while-loops must stop (condition in line 31). In any case, RBF-HS finally returns $\mathbf{D}$ (line 10).



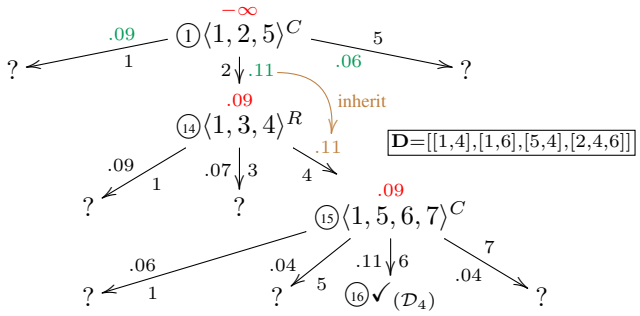
backtrack #5, discard subtree ⑧ ($F(\mathsf{n}_1) = 0.11 < 0.17 = bound$)



backtrack #6, discard subtree ⑫ ($F(\mathsf{n}_1) = 0.06 < 0.11 = bound$)



backtrack #7, discard subtree ⑩ ($F(\mathsf{n}_1) = 0.06 < 0.11 = bound$)



exit procedure ($|\mathbf{D}| = 4 \geq 4 = ld$) ⇒ return $\mathbf{D}$

Figure 2: RBF-HS executed on example DPI (part II), cf. Example 10.

3.2.6. Sub-Procedures

To make the algorithm description complete, we subsequently explain the workings of the sub-procedures called throughout RBF-HS:

- FINDMINCONFLICT(dpi) receives a DPI $dpi = \langle \mathcal{K}, \mathcal{B}, P, N \rangle$ and outputs a minimal conflict $\mathcal{C} \subseteq \mathcal{K}$ if one exists, and 'no conflict' else. A well-known algorithm that can be used to implement this function is QUICKXPLAIN [38, 39].
- ADD(x, L) takes an object x and a list of objects L as inputs, and returns the list obtained by appending the element x to the end of the list L.
- ADDDUMMYNODE(L) takes a list of nodes L, appends an artificial node n with $f(\mathsf{n}) := -\infty$ to L, and returns the result.
- GETANDDELETEFIRSTNODE(L) accepts a sorted list L, deletes the first element from L and returns this deleted element.
- GETFIRSTNODE(L) accepts a sorted list L and returns L's first element.
- SORTDECREASINGBYF(L) accepts a list of nodes L, sorts L in decending order of F-value, and returns the resulting sorted list.
- INSERTSORTEDBYF(n, L) accepts a node n and a list of nodes L sorted by F-value, and inserts n into L in a way the sorting of L by F-value is preserved.

Finally, the LABEL function can be seen as a series of the following blocks:

- *non-minimality* check (lines 38–40),
- *reuse label* check (lines 41–43), and
- *compute label* operations (lines 44–49).

Note that this LABEL function of RBF-HS' is equal to the one used in Reiter's HS-Tree (cf. Example 9), except that the *duplicate* check is obsolete in RBF-HS'. The reason for this is that there cannot ever be any duplicate (i.e., set-equal) nodes in memory at the same time during the execution of RBF-HS. This holds because for all potential duplicates $\mathsf{n}_i, \mathsf{n}_j$, we must have $|\mathsf{n}_i| = |\mathsf{n}_j|$, but equal-sized nodes must be siblings (depth-first tree exploration) which is why n_i and n_j must contain $|\mathsf{n}_i| - 1$ equal elements (same path up to the parent of $\mathsf{n}_i, \mathsf{n}_j$) and one necessarily different element (label of edge pointing from parent to n_i and n_j, respectively).

3.3. RBF-HS Exemplification

The following example illustrates the workings of RBF-HS.

Example 10 *(RBF-HS) Inputs.* Consider a defective system with seven components, described by $dpi := \langle \mathcal{K}, \mathcal{B}, P, N \rangle$, where $\mathcal{K} = \{ax_1, \ldots, ax_7\}$ and no background knowledge or any positive or negative measurements are initially given, i.e., $\mathcal{B}, P, N = \emptyset$. Let $\langle pr(ax_1), \ldots, pr(ax_7) \rangle := \langle .26, .18, .21, .41, .18, .40, .18 \rangle$ (note: pr is already cost-adjusted since the probability of each $ax_i \in \mathcal{K}$ is less than 0.5, cf. footnote 15). In addition, let all minimal conflicts for dpi be $\langle ax_1, ax_2, ax_5 \rangle$, $\langle ax_2, ax_4, ax_6 \rangle$, $\langle ax_1, ax_3, ax_4 \rangle$, and $\langle ax_1, ax_5, ax_6, ax_7 \rangle$. Assume we want to use RBF-HS to find the $ld := 4$ most probable diagnoses for dpi (e.g., because we surmise the actual diagnosis to be amongst the most likely candidates). To this end, the arguments dpi, pr and ld are passed to RBF-HS (Alg. 2) as input arguments.

Illustration (Figures). The way of proceeding of RBF-HS is depicted by Figs. 1 and 2. In the figures, we use the following notation. Axioms ax_i are simply referred to by i (in node and edge labels). Numbers ⓚ indicate the chronological node labeling (expansion) order. Recall that nodes in Alg. 2 are sets of (integer) edge labels along tree branches. E.g., node ⑨ in Fig. 1 corresponds to the node $\mathsf{n} = \{ax_2, ax_4\}$, i.e., to the assumption that components c_2, c_4 are at fault whereas all others are working properly. The probability $pr(\mathsf{n})$ (i.e., the original f-value) of a node n is shown by the black number from the interval $(0, 1)$ that labels the edge pointing to n, e.g., the cost of node ⑨ is 0.18. We tag minimal conflicts $\langle \dots \rangle$ that label internal nodes by ^{C} if they are freshly computed (*expensive*; FINDMINCONFLICT call, line 44), and by ^{R} if they result from a reuse of some already computed and stored (see list $\mathbf{C}$ in Alg. 2) minimal conflict (*cheap*; reuse label check; lines 41–43). Leaf nodes are labeled as follows: "?" is used for open (i.e., generated, but not yet labeled) nodes; $\checkmark_{(\mathcal{D}_i)}$ for a node labeled $valid$, i.e., a minimal diagnosis named $\mathcal{D}_i$, that is not yet stored in $\mathbf{D}$; $\times_{(Expl)}$ for a node labeled $closed$, i.e., one that constitutes a non-minimal diagnosis or a diagnosis that has already been found and stored in $\mathbf{D}$; $Expl$ is an explanation for the non-minimality in the former, and for the redundancy of node in the latter case, i.e., $Expl$ names a minimal diagnosis in $\mathbf{D}$ that is a proper subset of the node, or it names a diagnosis in $\mathbf{D}$ which is equal to node, respectively. Whenever a new diagnosis is added to $\mathbf{D}$ (line 16), this is displayed in the figures by a box that shows the current state of $\mathbf{D}$. For each expanded node, the value of the $bound$ variable relevant to the subtree rooted at this node is denoted by a red-colored value above the node. By green color, we show the backed-up F-value returned in the course of each backtracking step (i.e., the best known probability of any node in the respective subtree). Further, f-values that have been updated by backed-up F-values are signalized by green-colored edge labels, see, e.g., in Fig. 1, the left edge emanating from the root node of the tree has been reduced from 0.41 (f-value) to 0.09 (F-value) after the first backtrack. Finally, F-values of parents inherited by child nodes (line 23) are indicated by brown color, see the edge between node ⑭ and node ⑮ in Fig. 2.

Discussion and Remarks. Initially, RBF-HS starts with an empty root node, labels it with the minimal conflict $\langle 1, 2, 5\rangle$ at step ①, generates the three corresponding child nodes $\{1\}, \{2\}, \{5\}$ shown by the edges originating from the root node, and recursively processes the best child node (left edge, f-value 0.41) at step ②. The $bound$ for the subtree rooted at node ② corresponds to the best edge label (F-value) of any open node other than node ②, which is 0.25 in this case. In a similar manner, the next recursive step is taken in that the best child node of node ② with an F-value not less than $bound = 0.25$ is processed. This leads to the labeling of node $\{1, 4\}$ with F-value $0.28 \geq bound$ at step ③, which reveals the first (provenly most probable) diagnosis $\mathcal{D}_1 := [1, 4]$ with $pr(\mathcal{D}_1) = 0.28$, which is added to the solution list $\mathbf{D}$. Note that $-\infty$ is at the same time returned for node ③. After the next node has been processed and the second-most-probable minimal diagnosis $\mathcal{D}_2 := [1, 6]$ with $pr(\mathcal{D}_2) = 0.27$ has been detected, the by now best remaining child node of node ② has an F-value of 0.09 (leftmost node). This value, however, is lower than $bound$. Due to the best-first property of RBF-HS, this node is not explored right away because $bound$ suggests that there are more promising unexplored nodes elsewhere in the tree which have to

be checked first. To keep the memory requirements linear, the current subtree rooted at node ② is discarded before a new one is examined. Hence, the first backtrack is executed. This involves the storage of the best (currently known) F-value of any node in the subtree as the backed-up F-value of node ②. This newly "learned" F-value is signalized by the green number (0.09) that by now labels the left edge emanating from the root. Analogously, RBF-HS proceeds for the other nodes, whereas the used $bound$ value is always the best value among the $bound$ value of the parent and all sibling's F-values. Please also observe the F-value inheritance that takes place when node $\{2,4\}$ is generated for the third time (node ⑮, Fig. 2). The reason for this is that the original f-value of $\{2,4\}$ is 0.18 (see top of Fig. 1), but the meanwhile "learned" F-value of its parent $\{2\}$ is 0.11 and thus smaller. This means that $\{2,4\}$ must have already been explored and the *de-facto* probability of any (minimal) diagnosis in the subtree rooted at $\{2,4\}$ must be less than or equal to 0.11.

Output. Finally, RBF-HS immediately terminates as soon as the ld-th (in this case: fourth) minimal diagnosis $\mathcal{D}_4$ is located and added to $\mathbf{D}$. The list $\mathbf{D}$ of minimal diagnoses arranged in descending order of probability pr is returned. □

3.4. RBF-HS Complexity Analysis

3.4.1. Time Complexity

We can distinguish between two sources of time complexity inherent in RBF-HS:

(t1) logical consistency checking, and
(t2) tree construction and management.

As to *(t1)*, both the *hardness* and the *number of* performed consistency checks are of relevance.

First, the *hardness of consistency checks* executed by RBF-HS depends on the knowledge representation language adopted to model the diagnosed system and thus cannot be generally assessed. It might range from polynomial in the case of Horn logic over NP-complete for propositional system descriptions to even much harder, such as (2)NEXPTIME-complete for some Description Logics [46] (cf. our evaluation dataset in Sec. 6). Note, despite these somewhat discouraging theoretical complexities, experience with real-world diagnosis cases has shown that practical runtimes for consistency checks are often reasonable, even for interactive scenarios and very expressive logics [18, 32, 42, 43, 44, 47].

Regarding the *number of consistency checks*, in contrast, we are able to derive the upper bound $O(|\mathcal{K}|(|\mathbf{minC}| + |ld|))$ where $\mathbf{minC}$ denotes the set of all minimal conflicts for the DPI dealt with. To see why this holds, observe that

- the only place where RBF-HS issues consistency checks is in line 44 (FINDMINCONFLICT),
- each FINDMINCONFLICT call either yields a minimal conflict (line 49) or a minimal diagnosis (line 46),
- RBF-HS terminates once the desired ld minimal diagnoses have been found,
- each minimal conflict is actually computed *only once* (but it might be reused multiple times by means of the stored list of conflicts $\mathbf{C}$), and

- one call of FINDMINCONFLICT requires $O(|\mathcal{K}|)$ consistency checks in the worst case [40] if a minimal conflict $\mathcal{C}$ is returned, and only a single check if a minimal diagnosis is found (i.e., 'no conflict' is output).

Hence, no more than $|\mathbf{minC}|+|ld|$ calls of FINDMINCONFLICT, each issuing no more than $|\mathcal{K}|$ consistency checks, can be made throughout the execution of RBF-HS.

Factor *(t2)* is somewhat harder to estimate, as one and the same node might be explored multiple times (cf., e.g., node $\{2,4\}$, which is processed three times in our Example 10). Essentially, there are two main aspects that affect this factor: *(i)* The larger the number of *different* f-values among all nodes is and *(ii)* the higher the distribution of promising nodes in the search tree is, the more backtrackings and node re-explorations RBF-HS will do [48]. In the worst case, each node has a different f-value and, when sorting all nodes according to their f-value, any two neighbors in this sorting are in different subtrees of the root node. In such scenario, $O(n)$ node explorations have to be executed per newly expanded node, where n is the number of all nodes in the complete hitting set tree (as constructed by HS-Tree). The reason for this is that each node expansion requires forgetting the entire last explored subtree of the root and expanding another one until the newly expanded node is reached. Since n nodes will be explored overall (as many as HS-Tree explores[21]), we have a resulting complexity of $O(n^2)$ (cf. the analogue argumentation in [48] for RBFS). However, this scenario is only possible when most probable diagnoses are sought.

In the minimum-cardinality case, we can deduce[22] from the findings of [31] that RBF-HS explores $O(n)$ nodes, i.e., for sufficiently large problem size, no more than a constant number as many as HS-Tree does. Intuitively, the plausibility of this can be verified by considering (i) and (ii). As to (i), we have only d different node costs in the minimum-cardinality case where d is the size of the last-found diagnosis. Regarding (ii), it is straightforward to see that the next explored node of any node n will be the sibling of n's closest ancestor[23] which has not been processed in the current iteration.[24] Thus, each next-best node will be "close" to the current node and a minimum number of backtracking steps will have to be performed to reach the next-best node from the

[21] This holds under the assumption that HS-Tree does not close duplicate nodes, i.e., the *(duplicate)* criterion is left out, cf. Example 9. In this case, it will explore exactly the same nodes as RBF-HS (which, by construction, cannot eliminate duplicates, cf. Sec. 3.2.6), except that the latter might explore nodes more than once. Note that we have observed in diverse experiments with HS-Tree that it usually runs faster if the duplicate-check is omitted, because the latter has to explore a potentially exponential-sized collection of nodes at (almost) each processing of a node. The correctness of HS-Tree is not harmed by this modification.

[22] [31] derived this for RBFS in comparison to breadth-first search. We can transfer this result to RBF-HS and HS-Tree (without duplicate check, cf. footnote 21) for the following reasons: First, HS-Tree performs exactly a breadth-first search when minimum-cardinality diagnoses are sought, due to the f-cost of any node n being reciprocal to its cardinality (tree-depth) $|\mathsf{n}|$ in this case, cf. Sec. 3.2.1. Second, the fact that RBF-HS and HS-Tree usually execute until multiple solutions are found (while RBFS and breadth-first search terminate with the finding of the first solution) is not detrimental to the analysis in [31] as its result is independent of the goal function. In other words, if k diagnoses should be found, the k-th found diagnosis is interpreted as the first goal node (and the first $k-1$ diagnoses are simply interpreted as non-goal nodes without successors).

[23] n itself is defined to belong to the set of ancestors of n.

[24] Like [31], we define an *iteration of RBF-HS* as "the interval of time when those nodes being expanded for the first time are all of the same cost."

current one.

3.4.2. Space Complexity

First, the space complexity of Korf's original RBFS algorithm, that acts as a basis for RBF-HS, is linear [31], i.e., in $O(bd)$ where b is the maximal number of successor states of any state (a.k.a. branching factor) and d the maximal length of any path in the search space. Second, no amendments to the recursive (depth-first) nature of RBFS have been made while deriving RBF-HS (cf. Sec. 3.1.3). Third, RBF-HS stores computed minimal conflicts and minimal diagnoses, information RBFS does not need. In RBF-HS, recorded conflicts allow for a more efficient labeling of nodes (reuse instead of recalculation), whereas the storage of diagnoses is essential for the algorithm's correctness and moreover trivially necessary as diagnoses constitute exactly the solutions which should finally be returned.

Hence, the space complexity of RBF-HS is affected by three factors:

(s1) $|\mathbf{D}|$ (number of stored minimal diagnoses),
(s2) $|\mathbf{C}|$ (number of stored minimal conflicts), and
(s3) the space required to store the search tree.

Factor *(s1)* is bounded by the fixed input argument ld, which is arbitrarily preset by the user of RBF-HS, and thus in $O(1)$.[25] Factor *(s2)* is bounded by $|\mathbf{minC}|$ where $\mathbf{minC}$ is the set of all minimal conflicts for the considered DPI. Analogously to RBFS, factor *(s3)* is bounded by $|\mathcal{C}_{\max}| * |\mathbf{minC}|$ where $\mathcal{C}_{\max}$ is the minimal conflict for DPI with maximal cardinality. The explanation for this is that

- no node can have more than $|\mathcal{C}_{\max}|$ child nodes (reason: exactly k successors result from a node-labeling conflict of size k; no other ways of successor generation exist in RBF-HS),
- no node (set of edge labels along tree path) can include more than $|\mathbf{minC}|$ elements (reason: any node including $|\mathbf{minC}|$ elements must hit all minimal conflicts and thus must be a diagnosis; diagnoses are labeled $valid$ or $closed$ and never further expanded by RBF-HS), and
- at any tree depth, only a single node can be expanded at one particular point in time (reason: depth-first recursion, line 32).

All in all, given finite ld, we thus have a space complexity of $O(|\mathcal{C}_{\max}| * |\mathbf{minC}|)$ which can be interpreted as branching factor times maximal depth, equivalently as for RBFS.

Experience in the diagnosis field suggests that usually[26] the number of minimal

[25] Note, if $ld := \infty$ is specified, which means that the intention is to find *all* minimal diagnoses for the given DPI, then ld is not in $O(1)$, but conditioned by the number of minimal diagnoses existent. Obviously, the existence of a generally linear algorithm to accomplish that task is theoretically impossible since the mere maintenance of the collection of (potentially exponentially many) solutions $\mathbf{D}$ might require more than linear space.

[26] Still, we see in [25] that there are systems (from the domain of digital circuits) that include exceptionally long connected chains of components which altogether determine some system output. If such an output is observed to be wrong, this long component chain gives rise to a large number of minimal conflicts, which in this case does depend on the system size $|\mathcal{K}|$.

conflicts does not depend on (or: grow with) the size of the diagnosed system. There are small systems with a higher number of minimal conflicts, as well as there are huge systems with negligible numbers of minimal conflicts. So, from an empirical perspective it appears to be in many cases justified to interpret $|\mathbf{minC}|$ to be in $O(1)$. This assumption implies that RBF-HS is linear in the size of the DPI $\langle \mathcal{K}, \mathcal{B}, P, N \rangle$, because clearly $|\mathcal{C}_{\max}| \leq |\mathcal{K}|$ due to $\mathcal{C}_{\max} \subseteq \mathcal{K}$ (cf. Sec. 2.1.4). Note, if both b and d are assumed to be not in $O(1)$ (i.e., are dependent on the problem size), then also the original RBFS algorithm loses its linear space bounds.

3.4.3. Summary

Synopsized, our complexity results derived in Secs. 3.4.1 and 3.4.2 are:

Theorem 1 (Time and Space Complexity)**.** *Let $dpi = \langle \mathcal{K}, \mathcal{B}, P, N \rangle$ be an arbitrary DPI, ld the number of diagnoses to be computed, n the number of nodes expanded by HS-Tree (without the duplicate criterion) for dpi and ld, t_{CC} the worst-case time of a consistency check for dpi, $\mathbf{minC}$ the set of all minimal conflicts for dpi, and $\mathcal{C}_{\max}$ the conflict of maximal size for dpi. Further, let $TPT := t_{CC}|\mathcal{K}|(|\mathbf{minC}| + |ld|)$ (theorem proving time). Finally, assume that $ld \in O(1)$ and $\mathbf{minC} \in O(1)$. Then:*

- Time Complexity: *RBF-HS requires time in $O(n + TPT)$ for the computation of ld minimum-cardinality diagnoses for dpi; and time in $O(n^2 + TPT)$ for the computation of ld most probable diagnoses for dpi.*
- Space Complexity: *RBF-HS requires space in $O(|\mathcal{K}|)$.*

3.5. RBF-HS Correctness

The following theorem shows that RBF-HS is correct. The proof can be found in Appendix A.

Theorem 2 (Correctness)**.** *Let* FINDMINCONFLICT *be a sound and complete method for conflict computation, i.e., given a DPI, it outputs a minimal conflict for this DPI if a minimal conflict exists, and 'no conflict' otherwise. RBF-HS is sound, complete and best-first, i.e., it computes* all *and* only *minimal diagnoses* in descending order of probability *as per the cost-adjusted probability measure pr.*

3.6. RBF-HS: Potential Impact and Synergies with Other Techniques

Beside RBF-HS's direct usage

- *as a space-efficient alternative* to (exponential-space) best-first diagnosis search algorithms such as HS-Tree [2], HST tree [15], DynamicHS [49], GDE [3], or StaticHS [19], or
- *as a best-first alternative* to sound and complete linear-space *any-first* searches like Inv-HS-Tree [18], or
- *as a complete alternative* to best-first, but incomplete algorithms like CDA* [29] or STACCATO [23],

several uses of RBF-HS combined with existing ones can be conceived of. We briefly sketch some of them next, before we discuss a hybrid method combining HS-Tree [2] and RBF-HS in more detail in the next section:

(A) Informed HS-Tree: The idea is to run RBF-HS as a preprocessor in order to provide more informed node probabilities, and to subsequently adopt HS-Tree using these "learned" probabilities as f-values. To this end, e.g., RBF-HS could be executed with a fixed time limit and modified to store backed-up F-values of (a subset of) the visited nodes—not only of the ones that are kept in memory after backtracking steps. Like a heuristic for classic A*, this additional "lookahead" information might lead to the finding of the preferred diagnoses by expanding significantly fewer nodes.

(B) RBF-HS as a Decision Heuristic: The rationale is to run RBF-HS for a certain limited time and to afterwards take the "learned" F-value(s) as an estimate of the hardness or some other relevant property of the diagnosis problem. Depending on how the node costs are set (cf. Sec. 3.2.1), the backed-up F-value can provide an estimation of the least depth of the search tree, i.e., of the least size of minimum-cardinality diagnoses, or an upper bound estimate of the probability of the minimal diagnoses. Such an estimate can then be used, e.g.:

- *To decide which algorithm to use*, e.g., whether to drop some nice-to-have requirement(s) to the adopted diagnosis computation algorithm (such as completeness or the best-first property) in order to keep performance reasonable (cf., e.g., [18]).
- *For an informed selection of a limit for depth-limited or cost-limited search* [45] (cf. Example 8). When using a suitable limit, the latter can be powerful linear-space strategies to find the preferred diagnoses, and might be substantially faster than iterative deepening, IDA* (hitting set) searches and RBF-HS.

(C) RBF-HS as a Plug-In: Given a diagnosis search method that uses a hitting set generation routine as a black-box, such as SDE [50], RBF-HS can be used as a plug-in, e.g., in case memory issues are faced when using other best-first algorithms.

4. Hybrid Best-First Hitting Set Search (HBF-HS)

The goal of HBF-HS is to allow for an as fast as possible sound, complete and best-first diagnosis search also in cases where state-of-the-art searches boasting these three properties (e.g., HS-Tree) run out of memory. The principle is to normally execute standard HS-Tree (see Example 9) initially, but to equip it with a switch criterion (e.g., a maximal number of processed nodes, or a maximal amount or fraction of memory consumed) that, when triggered, prompts a switch to RBF-HS. The latter then continues the search while only consuming a linear amount of additional memory. In this vein, HS-Tree can utilize as much memory as it needs while executing (*focus on time*

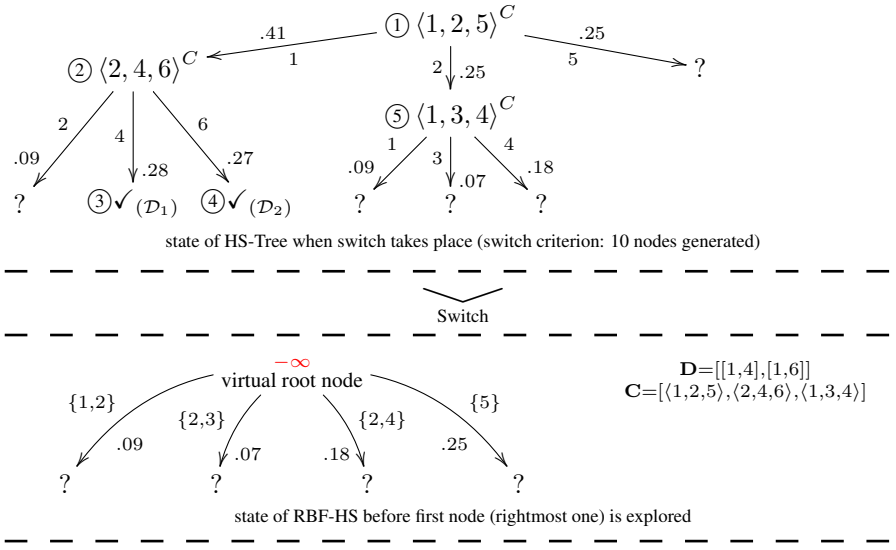


Figure 3: Sketch of the execution of HBF-HS on DPI from Example 10

optimization), and, before the available memory is depleted, RBF-HS takes over (*focus on space optimization*) such that the problem remains solvable.

The transfer of control between HS-Tree and RBF-HS is rather straightforward while guaranteeing the retention of soundness, completeness and best-first properties. Specifically, merely three steps are necessary to set up the execution of RBF-HS after the switch criterion stops HS-Tree:

(S1) View all current open nodes of HS-Tree as child nodes Child_Nodes of an imaginary root node; set the bound of this root node to $-\infty$.

(S2) Delete all duplicate nodes from Child_Nodes (e.g., if $\{1, 2\}$ and $\{2, 1\}$ is contained, delete one of these nodes). This prevents RBF-HS (which does not encompass duplicate checks) from performing redundant actions.

(S3) Copy all minimal diagnoses and minimal conflicts stored by HS-Tree to the collections $\mathbf{D}$ and $\mathbf{C}$ of RBF-HS, respectively.

Then, execute plain RBF-HS.[27]

Example 11 *(HBF-HS)* Let us reconsider the DPI introduced in Example 10 and have a look how HBF-HS would proceed for it. Assume the switch criterion is defined as "ten generated nodes". Specifically, this means: Execute HS-Tree until ten nodes are generated, then execute steps *(S1)–(S3)*, and finally run RBF-HS. Fig. 3 shows at the top the end state of HS-Tree before the switch is performed, and at the bottom the state of the transformed tree on which RBF-HS will begin its operations. Observe the following things:

[27] Our implementation of HBF-HS can be accessed at https://bit.ly/2Gp3XwX.

- At the time the switch takes place, ten node generations have taken place, and seven nodes are currently maintained by HS-Tree, encompassing two $valid$ nodes (✓) and five open nodes ("?"). Note that two of the open nodes, the leftmost and fourth-leftmost one, are equal (i.e., the path labels $\{1, 2\}$ and $\{2, 1\}$ coincide). Hence, one of them is a duplicate and does not need to be further considered (recall that diagnoses are *sets* of edge labels). Now, step *(S1)* of the switch process prompts the construction of a new tree through *(i)* the generation of a virtual root node with $bound$ (red color) set to $-\infty$ and *(ii)* the connection of this root node by one edge each to the four *non-duplicate* open nodes (cf. step *(S2)*), as shown at the bottom of Fig. 3. Note that the labels of the edges *emanating from the root node* are now *sets of* elements from $\mathcal{K}$. Nevertheless, all labels for other edges non-linked to the root node are singletons, just as in plain RBF-HS[28] (cf. Example 10).

- Two minimal diagnoses have already been located by HS-Tree (nodes ③ and ④), and three minimal conflicts have been computed (node labels ①, ② and ⑤). These are copied to the respective collections $\mathbf{D}$ and $\mathbf{C}$ maintained by RBF-HS in step *(S3)*, as depicted on the right in the bottom part of Fig. 3.

- The execution of RBF-HS works exactly as discussed in Example 10, with the difference that it starts with the partial hitting set tree displayed at the bottom of Fig. 3, where we have one root node and four elements among the Child_Nodes of the root. That is, the first explored node would be the rightmost one, $\{5\}$, with the maximal F-value 0.25 among Child_Nodes, and the $bound$ for the processing of $\{5\}$ would be 0.18, the second-best F-value (of node $\{2, 4\}$) among Child_Nodes. Intuitively, the RBF-HS execution in the course of HBF-HS can be regarded as a warm-start version of RBF-HS with some conflicts and open nodes, and potentially also some diagnoses, provided from the outset. □

5. Related Work

5.1. Classifying Diagnosis Computation Methods

Literature offers a wide variety of diagnosis computation algorithms, motivated by different diagnosis problems, domains and challenges. These algorithms can be compared along multiple dimensions, e.g.,[29]

- *best-first:* minimal diagnoses are output in order, most-preferred first, according to a given preference criterion [2, 3, 7, 17, 19, 25]
  vs.

[28] In RBF-HS, we simply do not use set notation as all the edge labels in RBF-HS are *single* elements from $\mathcal{K}$, cf. Figs. 1 and 2.

[29] The list of references quoted for each dimension (bullet point) is not intended to be exhaustive. We rather tried to give *some* representatives of each property and to give credit to (hopefully) most of the relevant works *over all the discussed dimensions*.

any-first: no particular order on output minimal diagnoses can be guaranteed [16, 18, 51],

- *complete:* given sufficient runtime and memory, all minimal diagnoses are computed [2, 3, 16, 17, 18, 19, 50, 52, 53]
  vs.
  incomplete: in general, not all minimal diagnoses are found [23, 29, 36, 54, 55, 56],

- *conflict-based:* minimal diagnoses are built as hitting sets of conflicts [2, 3, 7, 15, 16, 17, 19, 50, 53, 57]
  vs.
  direct: minimal diagnoses are built without reliance on conflicts, e.g., through divide-and-conquer or compilation techniques [18, 58, 59, 60, 61],

- *stateful:* the state of the search data structure, usually a tree or graph, is maintained and reused throughout a diagnosis session, i.e., even if the diagnosis problem changes through the acquisition of new information about the diagnosed system [3, 7, 19, 49, 62]
  vs.
  stateless: whenever the diagnosis computation algorithm is called, it computes diagnoses by means of a fresh search data structure [2, 15, 17, 53, 57],

- *black-box:* the theorem prover called throughout diagnosis search is used as it is, i.e., as a pure oracle, which makes the diagnosis search very general in that no dependency on any particular logic or reasoning mechanism is given [2, 7, 15, 17, 18, 19]
  vs.
  glass-box: the used theorem prover is internally optimized or modified for diagnostic purposes, which can bring performance gains, but makes the method reliant on one particular reasoning mechanism and on certain logics used to describe the diagnosed system [43, 44, 63, 64],

- *on-the-fly:* conflicts are computed on demand in the course of the diagnosis search [2, 3, 15, 17, 19]
  vs.
  preliminary: the set of minimal conflicts must be known in advance and given as an input to the diagnosis search [16, 23, 51, 53, 55, 57],

- *worst-case linear-space:* the algorithm requires an amount of memory that is linear in the problem size, even in the worst case [18, 59]
  vs.
  worst-case exponential-space: the algorithm requires an amount of memory that is generally exponential in the problem size [2, 3, 15, 16, 17, 19, 49, 58].

5.2. Towards Improving Existing Methods

Our study of these existing works suggests two different things. First, the best choice of algorithm, in general, depends largely on the particular tackled problem (domain and requirements). Consequently, there is little hope to find an algorithm that

comes anywhere near improving *all* of the existing ones. Second, performance improvements for algorithms are often achieved at the cost of losing desirable properties (e.g., completeness or the best-first guarantee). Hence, it is particularly noteworthy that RBF-HS as well as HBF-HS aim to improve existing sound, complete and best-first diagnosis search *while preserving all these favorable properties*. Moreover, to the best of our knowledge, RBF-HS is the *first* linear-space diagnosis computation method that ensures soundness, completeness and the best-first property.

5.3. Related Works in Diagnosis Domain

In terms of the above-mentioned dimensions, RBF-HS and HBF-HS are best-first, complete, stateless, conflict-based, black-box, and on-the-fly. Moreover, RBF-HS is worst-case linear-space whereas HBF-HS is not.[30] We now discuss diagnosis algorithms related to the ones proposed in this work and point out crucial differences wrt. the enumerated dimensions. Specifically, these related algorithms can be categorized into *compilation-based* (not black-box; can be polynomial-space or linear-space, but only under certain circumstances), *duality-based* (either not best-first or not linear-space) and *best-first search* (whenever sound and complete, then exponential-space) approaches:

5.3.1. Compilation-Based Approaches

These techniques compile the diagnosis problem into some target representation such as SAT [60], OBDD [61] or DNNF [58]. Often, the generation of (minimum-cardinality; but not maximal-probability) diagnoses can be accomplished in worst-case polynomial time in the size of the respective compilation. For a polynomial-sized compilation, this implies polynomial-time diagnosis generation. However, the size of the compilation might be exponential in the size of the diagnosis problem for all these approaches, which means that no guarantee for polynomial-space (or polynomial-time), let alone linear-space, diagnosis generation can be given. Second, for these compilation approaches to be applicable to a DPI, the diagnosed system must be amenable to a propositional-logic description, which is not always the case [32, 43, 44]. Beyond that, compilation approaches usually do not allow to take influence on the exact order in which diagnoses are output. In summary, these methods are in general not linear-space, not best-first, and not black-box.

A compilation-based approach that is based on abstraction techniques and especially suited for a sequential diagnosis scenario is SDA [62]. One difference between RBF-HS and SDA is that only a single best diagnosis (instead of a set of best diagnoses) is output by SDA at the end of the sequential diagnosis process. Second, it is questionable if similar abstraction-techniques as used in SDA are applicable to logics more expressive than propositional logic and to systems that are structurally different from typical circuit topologies.

[30] Although a linear-space guarantee in not given for HBF-HS, note that HBF-HS is nevertheless meant to be an improved variant of RBF-HS which "is allowed" to consume more than a linear amount of memory in order to reduce computation time.

[65] present an approach that translates a circuit diagnosis problem into a constraint optimization problem. When the dual constraint graph of this problem is a tree, then the minimum-cardinality diagnoses can be generated in linear time and space. However, it is unclear if and how non-circuit-problems and more expressive or other types of logics can be addressed.

5.3.2. Duality-Based Approaches

FastDiag [59] and its sequential diagnosis extension Inv-HS-Tree [18] perform a linear-space depth-first diagnosis search that is grounded on the relationship between diagnoses and conflicts according to the Duality Property (cf. Sec. 2.1.5). The soundness and completeness of the diagnosis computation despite the depth-first search is accomplished by interchanging the role of conflicts and diagnoses in the hitting set tree. That is, in these approaches the node labels correspond to minimal diagnoses and the tree paths represent conflicts. The computation of minimal diagnoses instead of minimal conflicts during the labeling process is achieved by a suitable adaptation [18] of the QuickXPlain algorithm [38, 39]. The main difference between these approaches and RBF-HS (and HBF-HS) is that the former cannot ensure that the diagnoses are computed in any particular (preference) order.

[50] present a sound and complete approach that interleaves conflict and diagnosis computation in a way that information from conflict computation aids the diagnosis computation and vice versa. However, unlike RBF-HS, this approach is not linear-space in general. In addition, it cannot compute most-probable, but only minimum-cardinality diagnoses.

5.3.3. Best-First-Search Approaches[31]

First and foremost, we have the seminal methods HS-Tree [2], along with its amended version HS-DAG proposed by [17], and GDE [3], which are sound, complete[32] and best-first.

[7, 44] describe sound and complete uniform-cost search variants of Reiter's HS-Tree which enumerate diagnoses in some order of preference. At this, [7] defines the preference order by means of a probability model over diagnoses (as characterized in Sec. 2.1.3) whereas [44] relies on a heuristic model that ranks single axioms based on their "importance". The sum over axioms included in a diagnosis is used to determine the rank of the diagnosis. [26] goes one step further and incorporates a heuristic function into the search, yielding a hitting set version of A*. Note that the specification of a useful heuristic function, as suggested in [26] for an additive cost function, is an open problem in uniform-cost hitting set search with non-additive costs (cf. *(VI)* in Sec. 2.2), as in the case of our proposed methods.[33]

[31] We restrict the discussion here to sound and complete methods. The consideration of all best-first algorithms would go beyond the scope of this work.

[32] Reiter's original HS-Tree is complete only if no non-minimal conflicts are generated during the construction of the HS-Tree (cf. Example 9).

[33] Multiplicative costs can be reframed as additive costs by applying the negative logarithm to each component probability $pr(ax)$ for $ax \in \mathcal{K}$ [66]. However, this does not solve problem of finding a useful heuristic.

[15] suggests a variant of HS-DAG which builds a hitting set tree based on a subset-enumeration strategy in order improve the diagnosis computation time. The same objective is pursued by [14], who propose parallelization techniques for Reiter's HS-Tree.

Further, there are sound, complete and best-first diagnosis searches that are particularly useful for fault isolation and sequential diagnosis, StaticHS [19] and DynamicHS [49]. These are stateful in that they exploit a persistently stored and incrementally adapted (search) data structure to make the diagnostic process more efficient. More specifically, StaticHS aims at the reduction of the number of interactions necessary from a user, e.g., to make system measurements or answer system-generated queries, and DynamicHS targets the minimization of the computation time.

In contrast to RBF-HS, all these best-first search approaches require exponential space in general.

5.4. Related Works in Heuristic Search Domain

Next, we discuss other memory-limited general search algorithms that are related to RBFS (and thus to RBF-HS), works that aim at improving RBFS, and methods related to HBF-HS.

5.4.1. Memory-Limited Search Algorithms

Beside RBFS, there is a range of alternative linear-space heuristic search techniques. Some examples are IDA* [67], MREC [68], MA* [69], DFS* [70], IDA*-CR [71], MIDA* [72], ITS [73], IE [74], and SMA* [74]. In contrast to RBFS, these algorithms generally do not expand nodes in best-first order if the given cost function is non-monotonic. This property, however, does not pose a problem in the hitting set computation scenario. The reason for this is that the cost function in hitting set search *has to be* anti-monotonic (cf. *(VI)* in Sec. 2.2) to find solutions in best-first order. Recall that anti-monotonicity (for maximal-cost solutions) in hitting set search is the equivalent to monotonicity (for minimal-cost solutions) in classic heuristic search. Hence, in principle, any of these algorithms could have been used as a basis for this work, i.e., for being "translated" to a hitting set version.

The causes for choosing RBFS as a foundation for our presented algorithms are twofold: First, RBFS is particularly well-understood and covered by a rich collection of literature including both theoretical and empirical analyses of the algorithm. Second, and more importantly, RBFS is asymptotically optimal[34], requiring $O(b^d)$ time[35] when being used for minimum-cardinality diagnosis computation [31], which is one of the most central and fundamental problems in model-based diagnosis.

Compared to IDA*,[36] which is the most prominent[37] linear best-first search algorithm and also asymptotically optimal for minimum-cardinality hitting set search,

[34] An algorithm algo is called *asymptotically optimal* for some problem class C iff it is (for the problem size n growing to infinity) not more than a constant factor worse than the best achievable running time best on problems of class C. Formally: $time(\mathsf{algo}, C) \in O(time(\mathsf{best}, C))$.

[35] At this, b is the branching factor, i.e., the maximal number of successors of any node, and d is the maximum search depth.

[36] Cf. Example 8, where we give a brief description of IDA*.

[37] When we judge "prominence" by the citation tally on Google Scholar (as of April 2020).

RBFS exhibits a better practical (empirical) time complexity[38] [76], which can be intuitively explained by the fact that RBFS, unlike IDA*, does not discard the entire search tree between any two iterations [31]. This runtime advantage of RBFS over IDA* holds especially when the cost for node expansion is high [75]. This is absolutely the case in diagnosis search where node expansion requires a conflict, which must either be sought in a maintained list of conflicts (reuse case) or must be newly generated using expensive theorem proving (computation case), see the LABEL function in Alg. 2. This is why RBFS appeared to be a more appropriate base for constructing a hitting set search than IDA*.

Finally, there is CDA* [29], a version of A*, originally proposed for solving optimal constraint satisfaction problems, which is also employable for diagnosis search. It incorporates an any-space algorithm that generates the most preferred diagnoses first. The two important differences to RBF-HS are that CDA* is not black-box, i.e., appears to be not as flexibly usable with arbitrary logics and reasoners as RBF-HS, and that CDA* is generally incomplete [50].

5.4.2. Works towards Improving RBFS

The price to pay for the guaranteed linearity of RBFS in terms of space consumption is that nodes have to be forgotten each time a backtracking step is made. Whenever an already explored subtree becomes attractive again (because all other better subtrees have been explored), it will be re-examined. This scheme results in a potentially large number of node re-explorations. In the worst case, when every node has a unique f-value and the node with next-best f-value is always located in a different subtree of the root, $O(n^2)$ nodes will be expanded where n is the number of nodes A* would expand [48]. Addressing this problem, [48] have proposed three techniques for controlling the overhead caused by excessive backtracking in RBFS, at the cost of generating suboptimal solutions in general. These techniques are called RBFS$_\epsilon$, RBFS$_{kthrt}$ and RBFS$_{\mathsf{CR}}$. The idea of RBFS$_\epsilon$ is to allow the algorithm to explore a little (as ruled by the choice of the parameter ϵ) further than suggested by $bound$, i.e., $bound$ in line 25 of Alg. 1 is replaced by $bound + \epsilon$. While this slight change yields good results in practice under an adequate setting of ϵ, it does not lower the quadratic worst-case time complexity. RBFS$_{kthrt}$ goes one step further by loosening both $bound$ and the f-function, thereby achieving fewer backtrackings *and* fewer node expansions, albeit still without theoretical time complexity savings. Finally, RBFS$_{\mathsf{CR}}$ adopts a concept originally introduced by [71] for IDA* in order to reduce re-expansions. The idea is to track the distribution of f-values under each node along the currently explored path, which allows to adapt the backed-up F-value in a way it can be guaranteed that, each time a node is re-explored, twice as many successor nodes will be investigated than when this node was last explored. In this vein, the number of explored nodes can be shown to be in $O(n)$, i.e., asymptotically maximally by a constant worse than for A*.

All of these three techniques are applicable to RBF-HS as well, and we expect the (positive) implications on practical performance in the hitting-set case to be in line with

[38] Note, the theoretical number of expanded nodes is $O(n^2)$ for both algorithms where n is the number of nodes expanded by A* [75].

what was observed in [48] for classic search problems. A clear shortcoming of such an approach, however, will be the potential non-minimality of the returned diagnoses (unsoundness) and the potential violation of the preference order on the output diagnoses (best-first property not given). Whereas the soundness problem can be taken care of by postprocessing the returned diagnoses, e.g., by means of Inv-QX [18], it is not straightforward how to handle the best-first violation, i.e., how to ensure that the returned collection $\mathbf{D}$ includes exactly the $|\mathbf{D}|$ best diagnoses. Both the implementation of these suboptimal RBF-HS variants as well as the study of this latter question will be part of our future work.

If only one solution is demanded, i.e., only the single most probable or single minimum-cardinality diagnosis is to be found, then techniques discussed in [77] can be applied to RBF-HS. However, this is useful only if a reasonable heuristic function (for non-additive, probabilistic costs) can be expressed for hitting set searches, which is to date still an open problem.

5.4.3. Works Related to HBF-HS

HBF-HS follows a similar principle for RBF-HS as MREC [68] does for IDA*. MREC trades off the time and space complexity by a single parameter that determines how much memory is available for use by the algorithm. In the same way that MREC behaves equally to IDA* for minimal available memory and similarly to A* for a large amount of conceded memory, HBF-HS resembles RBF-HS and HS-Tree in these two cases.

Two other strategies that attempt to optimally exploit and exhaust the available memory in order to increase search speed are MA* [69] and SMA* [74]. Their underlying principle is to store every node until the memory limit is reached, and to then purge the least promising node(s) in order to make room for the next node to be explored. Whenever the search problem is solvable within the given amount of memory, these algorithms will not run out of memory and return a best solution. Theoretically, this property cannot be proven for HBF-HS as it acts like RBF-HS from the point where the (memory-dependent) switch criterion is triggered. In other words, if the switch takes place too late (such that very little memory remains which cannot hold the linear number of nodes additionally explored after the switch), then HBF-HS can run out of memory. However, first, we observed in our experiments (cf. Sec. 6.4) that the number of additional nodes stored by HBF-HS after the switch was always minor (small single digit percentage) relative to those generated before the switch took place. Second, (S)MA*'s concept of on-demand node pruning can be integrated into HBF-HS as well in order to resolve this problem. Still, as a future work, we plan to carry over these algorithms to the diagnosis domain as well, and to study their hitting set versions.

Moreover, [74] suggested the IE algorithm, which however behaves the same as RBFS for a monotonic cost-function (and thus, a hitting set version of it would act identically to RBF-HS, cf. bullet *(VI)* on page 12).

6. Evaluation

6.1. Objective

The goals of our evaluation are

- to demonstrate the out-of-the-box general applicability of the proposed algorithms to diagnosis problems over different and highly complex[39] knowledge representation languages,
- to understand their practical runtime, memory efficiency, and scalability, and
- to compare the suggested methods against a state-of-the-art algorithm with the same properties in terms of the classification discussed in Sec. 5.1.

Importantly, the goal is *not* to show that the proposed algorithms are better than all or most algorithms in literature, which is pointless (cf. Sec. 5.2). Rather, we intend to show the advantage of using RBF-HS and HBF-HS in a scenario where the properties soundness, completeness, best-firstness and general applicability are of interest or even required.

One such domain is ontology and knowledge base[40] debugging, where practitioners and experts from the field usually[41], and especially in critical applications of ontologies such as medicine [21], want a debugger to output exactly the faulty axioms that really explain the observed faults in the ontology (*soundness* and *completeness*) at the end of a debugging session. In addition, experts often wish to perpetually monitor the most promising fault explanation throughout the debugging process (*best-first property*) with the intention to stop the session early if they recognize the fault. As was recently studied by [79], the use of best-first algorithms often also involves efficiency gains in debugging as opposed to other strategies. Apart from that, it is a big advantage for users of knowledge-based systems to have a debugging solution that works out of the box for different logical languages and with different logical reasoners (*general applicability*, cf. *black-box* property in Sec. 5.1). The reasons for this are that *(i)* ontologies are formulated in a myriad of different (Description) logics [80] with the aim to achieve the required expressivity for each ontology domain of interest at the least cost for inference, and *(ii)* highly specialized reasoners exist for different logics (cf., e.g., [81]), and being able to flexibly switch to the most efficient reasoner for a particular debugging problem can bring significant performance improvements.

For these reasons, we use

- HS-Tree [2, 7] (cf. Example 9), a state-of-the-art diagnosis search algorithm that is sound, complete, best-first, and generally applicable (in the sense that it is independent of both the used monotonic logic and of the adopted reasoner, just as the proposed strategies), to compare our methods against. Especially in the knowledge base debugging field, HS-Tree appears to be the most prevalent algorithm used for diagnosis computation [7, 26, 32, 43, 44, 64, 82].
- real-world knowledge base debugging problems (cf. Sec. 6.2) formulated over a range of different logics with hard reasoning complexities to test our approaches.

[39] By "complex" we refer to the expressivity and the related reasoning complexity of the logical language.

[40] We will use the terms *ontology* and *knowledge base* interchangeably throughout this section. For the purposes of this paper, we consider both to be finite sets of axioms expressed in some monotonic logic, cf. $\mathcal{K}$ in Sec. 2.

[41] The discussed requirements have been elicited in discussions with ontologists with whom we are collaborating to develop and customize our ontology debugging tool *OntoDebug* [35, 78] to match its users' needs.

Table 2: Dataset used in the experiments (sorted by the number of components/axioms of the diagnosis problem, 2nd column).

KB $\mathcal{K}$	$\lvert\mathcal{K}\rvert$	expressivity [1)]	#D/min/max [2)]
Koala (K)	42	$\mathcal{ALCON}^{(D)}$	10/1/3
University (U)	50	$\mathcal{SOIN}^{(D)}$	90/3/4
IT	140	$\mathcal{SROIQ}$	1045/3/7
UNI	142	$\mathcal{SROIQ}$	1296/5/6
Chemical (Ch)	144	$\mathcal{ALCHF}^{(D)}$	6/1/3
MiniTambis (M)	173	$\mathcal{ALCN}$	48/3/3
ctxmatch-cmt-conftool (ccc)	458	$\mathcal{SIN}^{(D)}$	934*/2/16*
ctxmatch-conftool-ekaw (cce)	491	$\mathcal{SHIN}^{(D)}$	953*/3/35*
Transportation (T)	1300	$\mathcal{ALCH}^{(D)}$	1782/6/9
Economy (E)	1781	$\mathcal{ALCH}^{(D)}$	864/4/8
DBpedia (D)	7228	$\mathcal{ALCHF}^{(D)}$	7/1/1
Opengalen (O)	9664	$\mathcal{ALEHIF}^{(D)}$	110/2/6
CigaretteSmokeExposure (Cig)	26548	$\mathcal{SI}^{(D)}$	1566*/4/7*
Cton (C)	33203	$\mathcal{SHF}$	15/1/5

1): Description Logic expressivity: each calligraphic letter stands for a (set of) logical constructs that are allowed in the respective language, e.g., $\mathcal{C}$ denotes negation ("complement") of concepts, for details see [80, 83]; intuitively, the more letters, the higher the expressivity of a logic and the complexity of reasoning for this logic tends to be.

2): #D/min/max denotes the number/the minimal size/the maximal size of minimal diagnoses for the DPI resulting from each input KB $\mathcal{K}$. If tagged with a *, a value signifies the number or size determined within 1200sec using HS-Tree (for problems where the finding of *all* minimal diagnoses was impossible within reasonable time).

6.2. Dataset

The benchmark of inconsistent real-world ontologies we used for our experiments is given in Tab. 2.[42] Subsets of this dataset have been investigated i.a. in [32, 42, 44, 84, 85, 86, 87]. As the table shows, the ontologies cover a spectrum of different problem sizes (number of axioms or components; column 2), logical expressivities (which determine the complexity of consistency checking; column 3), as well as diagnostic structures (number and size of minimal diagnoses; column 4). Note that the complexity of consistency checks[43] over the logics in Tab. 2 ranges from EXPTIME-complete to 2-NEXPTIME-complete [46, 83]. Hence, from the point of view of model-based diagnosis, ontology debugging problems represent a particularly challenging domain as they usually deal with harder logics than more traditional diagnosis problems (which often use propositional knowledge representation languages that are not beyond NP-complete).

6.3. Experiment Settings

6.3.1. Different Diagnosis Scenarios

To study the performance and robustness of our approaches under varying circumstances, we considered a range of different *diagnosis scenarios* in our experiments. A diagnosis scenario is defined by the set of inputs given to Alg. 2, i.e., by a DPI dpi, a number ld of minimal diagnoses to be computed, as well as a (cost-adjusted) setting of the component fault probabilities pr. The DPIs for our tests were defined as

[42] The benchmark problems can be downloaded from http://isbi.aau.at/ontodebug/evaluation.

[43] Recall, consistency checks are used by the presented search algorithms within the FINDMINCONFLICT procedure, cf. Alg. 2 and Sec. 3.4.

$\langle \mathcal{K}, \emptyset, \emptyset, \emptyset \rangle$, one for each $\mathcal{K}$ in Tab. 2. That is, the task was to find a minimal set of axioms (faulty components) responsible for the inconsistency of $\mathcal{K}$, without any background knowledge or measurements initially given (cf. Example 10). For the parameter ld we used the values $\{2, 6, 10, 20\}$. The fault probability $pr(ax)$ of each axiom (component) $ax \in \mathcal{K}$ was either chosen uniformly at random from $(0, 1)$ (*maxProb*), or specified in a way (cf. Sec. 3.2.1) the diagnosis search returns minimum-cardinality diagnoses first (*minCard*). As a Description Logic reasoner, we adopted Pellet [88].

6.3.2. Goal to Find Actual Diagnosis

To simulate as realistic as possible diagnosis circumstances, where the *actual diagnosis* (i.e., the de-facto faulty axioms) is of interest and needs to be isolated from a set of initial minimal diagnoses (cf. column 4 of Tab. 2), we ran five sequential diagnosis [3, 32] sessions for each diagnosis scenario defined above. At this, a different randomly chosen actual diagnosis was set as the target solution in each session.

A *sequential diagnosis session* can be conceived of having the following two alternating phases that are iterated until a single diagnosis remains:

- diagnosis search, and
- measurement conduction.

The former involves the determination of ld minimal diagnoses $\mathbf{D}$ for a given DPI. The latter subsumes the selection of an optimal system measurement [89, 90] based on $\mathbf{D}$ (to rule out as many spurious diagnoses as possible), as well as the incorporation of the new system knowledge resulting from the measurement outcome into the DPI.

Measurement selection requires a *measurement selection function* [3, 91, 92] which gets a set of minimal diagnoses $\mathbf{D}$ as input, and outputs one system measurement such that any measurement outcome eliminates at least one spurious diagnosis in $\mathbf{D}$. As measurement selection functions we adopted *split-in-half (SPL)* [32], which suggests a measurement with the lowest worst-case number of spurious diagnoses in $\mathbf{D}$ eliminated[44], and *entropy (ENT)* [3], which selects a measurement with highest information gain. These functions appear to be the most commonly adopted ones in model-based diagnosis, cf., e.g., [18, 32, 92, 93, 94, 95, 96, 97, 98].

In our experiments, a measurement was defined as a true-false question to an oracle [7, 32, 42, 99], e.g., for a biological knowledge base one such query could be $Q := \mathsf{Bird} \sqsubseteq \exists \mathsf{hasCapability}.\mathsf{Flying}$ ("is every bird capable of flying?"). Given a positive (negative) answer, Q is moved to the positive (negative) measurements of the DPI (cf. Sec. 2.1.1). The new DPI is then used in the next iteration of the sequential diagnosis session. That is, a new set of diagnoses $\mathbf{D}$ is determined for this updated DPI, an optimal measurement is calculated for $\mathbf{D}$, and so on. Once there is only a single minimal diagnosis for a current DPI, the session stops and outputs the remaining diagnosis. To determine measurement outcomes (i.e., to answer the generated questions), we used the predefined actual diagnosis, i.e., each question was automatically answered in a way the actual diagnosis was not ruled out.

[44] If such a measurement exists, SPL will select one which eliminates half of the diagnoses in $\mathbf{D}$ regardless of the outcome; therefore the name "split-in-half".

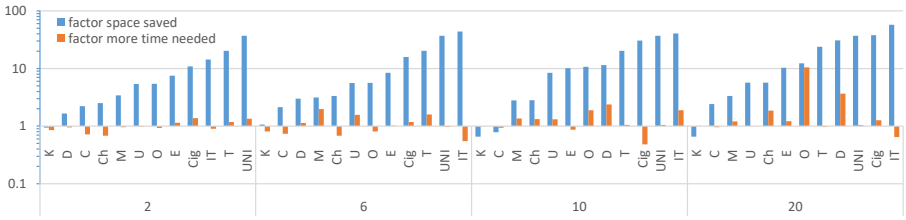


Figure 4: Experiment results (RBF-HS vs. HS-Tree) for SPL: x-axis shows ontologies from Table 2 and parameter $ld \in \{2, 6, 10, 20\}$.

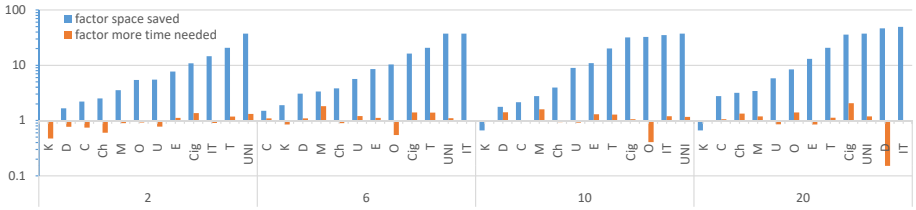


Figure 5: Experiment results (RBF-HS vs. HS-Tree) for ENT: x-axis shows ontologies from Table 2 and parameter $ld \in \{2, 6, 10, 20\}$.

The advantages of using sequential diagnosis sessions in our evaluations (instead of just applying a single diagnosis search execution to the DPIs listed in Tab. 2) are:

- Multiple diagnosis searches, each for a different (updated) DPI, are executed during one sequential session and flow into the experiment results, which gives us a more representative picture of the algorithms' real performance.
- The potential impact of measurement selection functions on algorithms' performances can be assessed.
- Sequential diagnosis is one of the main applications of diagnosis searches.
- Without the information acquisition through sequential diagnosis it is in many cases practically infeasible to find the actual fault (cf. the large numbers of diagnoses in the fourth column of Tab. 2).

6.3.3. Settings in a Nutshell

In summary, we ran five diagnosis sessions, each searching for a randomly specified minimal diagnosis, for each algorithm among RBF-HS and HS-Tree, for each measurement selection function among ENT and SPL, for each DPI from Tab. 2, for each probability setting among maxProb and minCard, and for each number of diagnoses $ld \in \{2, 6, 10, 20\}$ to be computed (in each iteration of the session, i.e., at each call of a diagnosis search algorithm).

6.4. Experiment Results[45]

The results for the minCard experiments are shown by Figures 4–6. Each figure compares the runtime and memory consumption we measured for RBF-HS and HS-Tree averaged over the five performed sessions (note the logarithmic scale). More

specifically, the figures depict the factor of less memory consumed by RBF-HS (blue bars), as well as the factor of more time needed by RBF-HS (orange bars), in relation to HS-Tree. That is, blue bars tending upwards (downwards) mean a better (worse) memory behavior of RBF-HS, whereas upwards (downwards) orange bars signify worse (better) runtime of RBF-HS. For instance, a blue bar of height 10 means that HS-Tree required 10 times as much memory as RBF-HS did in the same experiment; or a downwards orange bar representing the value 0.5 indicates that RBF-HS finished the diagnosis search task in half of HS-Tree's runtime. Regarding the absolute runtime and memory expenditure (not displayed in the figures) in the experiments, we measured a min / avg / max runtime of 0.04 / 24 / 744sec and 0.05 / 17 / 1085sec for ENT and SPL, respectively, as well as a min / avg / max space consumption of 9 / 17.5K / 1.3M and 9 / 4.4K / 183K tree nodes for ENT and SPL, respectively.

We make the following observations:[46]

(1) Favorable space-time tradeoff: Whenever the diagnosis problem was non-trivial to solve, i.e., required a runtime of more than one second (which was the case in 94 % of the tested cases), RBF-HS trades space favorably for time. In other words, compared to HS-Tree, the factor of memory saved by RBF-HS is higher than the factor of incurred time overhead in all interesting cases (blue bar is higher than orange one).

(2) Substantial space savings: Space savings of RBF-HS range from significant to tremendous, and often reach values larger than 10 (in 45 % of the cases) and up to 50 (ENT) and 57 (SPL). In other words, HS-Tree required up to 57 times as much memory for the same tasks as RBF-HS did. On average, the factor of memory saved amounted to 14.1 for ENT and to 13.8 for SPL, i.e., RBF-HS required an average of less than 8 % of the memory HS-Tree consumed.

(3) Often even runtime improvements: In 35 % (ENT) and 38 % (SPL) of the cases RBF-HS exhibited *both* a lower or equal runtime compared with HS-Tree *and* saved significant portions of memory (blue bar goes up, orange one goes down). This observation may appear surprising at first sight, since RBF-HS relies on forgetting and re-exploring, whereas HS-Tree keeps all relevant information in memory. However, also studies comparing classic (non-hitting-set) best-first searches have observed that linear-space approaches can outperform exponential-space ones in terms of runtime [76]. One reason for this is that, at the processing of each node, the management (node insertion and removal) of an exponential-sized priority queue of open nodes requires time linear in the current tree depth. Hence, when the queue management time of HS-Tree outweighs the time for redundant node regenerations expended by RBF-HS, then the latter will outperform the former.

(4) Whenever it takes RBF-HS long, use HBF-HS: In those cases (for ENT) where RBF-HS manifested a 20 % or higher time overhead, the use of HBF-HS (with a mere allowance of 400 nodes in memory before the switch is triggered) could *always* reduce

[45] Please see http://isbi.aau.at/ontodebug/evaluation for the raw data.

[46] Note that all tested algorithms *always* return exactly the same minimal diagnoses as output because they provenly have the same features soundness, completeness and best-firstness. Hence, any savings observed do *not* arise at the cost of losing any theoretical guarantees.

the runtime to equally as much or even less that of HS-Tree. At the same time, remarkably, memory consumption of HBF-HS *never* exceeded 416 nodes, whereas HS-Tree required memory for up to more than half a million nodes, which amounts to a deterioration factor of over 1000 compared to HBF-HS. Similar observations can be made in case of SPL, where, e.g., a runtime overhead factor of 10.4 (the worst value for RBF-HS we measured in all our experiments, see SPL20, case O, Fig. 4) could be reduced to a factor of 0.98 (i.e., to even a 2 % *better* runtime than HS-Tree's) by means of HBF-HS.

This suggests that, whenever RBF-HS gets caught in redundant re-explorations of subtrees and thus requires notably more time than HS-Tree, the allowance of a relatively short run of HS-Tree (until it creates 400 nodes) before switching to RBF-HS can already yield to a runtime comparable to HS-Tree. One reason for this phenomenon is that RBF-HS can save a significant number of re-explorations through the information gained by the initial breadth-first exploration of the top of the search tree. A potential second reason might be the above-mentioned high expense of managing an increasingly large queue of open nodes required by HS-Tree, as opposed to a set of open nodes of smaller and almost fixed size in case of HBF-HS.

(5) HBF-HS allows to almost "cap" the used memory: The number of nodes in memory additionally consumed by HBF-HS after the switch (at 400 nodes) to RBF-HS was less than 2 % on average, and never more than 4 %, compared to the number of nodes where the switch takes place. Similar and only slightly higher values could be observed for HBF-HS performing the switch at 200 (3 % exceedence on average) and 100 (7 %) generated nodes. This suggests that the consumed amount of memory can practically often be more or less arbitrarily limited by the definition of a suitable switch condition[47]—of course, only as long as the specified limit is not lower than the (very low) memory requirement of standalone RBF-HS.

(6) Performance independent of number of computed diagnoses and measurement selection function: The relative performance of RBF-HS versus HS-Tree appears to be largely independent of the number ld of computed minimal diagnoses as well as of the used measurement selection function (cf. Figs. 4 and 5).

(7) Performance improves for harder diagnosis problems: The gain of using RBF-HS instead of HS-Tree gets the larger, the harder the considered diagnosis problem is. This tendency can be clearly seen in Figs. 4 and 5, where the ontologies on the x-axis are sorted in ascending order of RBF-HS's memory reduction achieved, for each value of ld. Note that roughly the same group of (more difficult / easy to solve) diagnosis problems ranks high / low for all values of ld.

(8) Performance dependent on diagnosis preference criterion: The discussion of the results so far concentrated on the consistently good results attained by RBF-HS for the

[47] In fact, there is theoretical evidence supporting that. That is, HBF-HS will never exceed the number of nodes already in memory when the switch takes place by more than a number of nodes linear in the problem size. Stated in terms of Sec. 3.4, the memory overhead beyond the memory consumption at the time of the switch is bounded by $|\mathcal{C}_{\max}| * |\mathbf{mC}|$. This follows directly from the linear space complexity of RBF-HS (cf. Theorem 1).

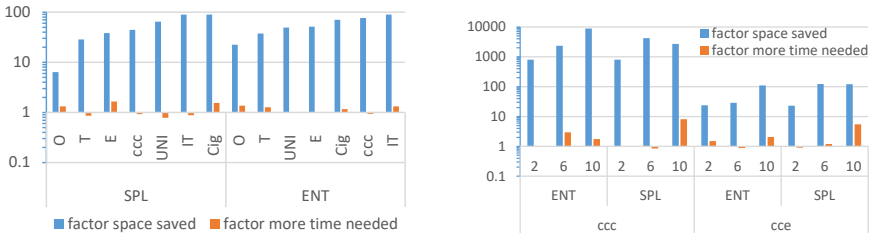


Figure 6: *(left)* Scalability results (RBF-HS vs. HS-Tree) for $ld = 100$ and SPL+ENT: x-axis shows ontologies from Tab. 2. *(right)* Results (RBF-HS vs. HS-Tree) for hardest cases ccc, cce from Tab. 2 for SPL+ENT and $ld \in \{2, 6, 10\}$.

minCard probability setting. In case of the maxProb setting, we see a pretty different picture, where time is more or less traded one-to-one for space, i.e., k orders of magnitude savings in space against HS-Tree require approximately k orders of magnitude more runtime of RBF-HS (blue and orange bars roughly equal). The reason for this performance degradation in case of maxProb is a known property of Korf's RBFS algorithm to perform relatively poorly when original f-values (in our case: probabilities) of nodes vary only slightly [48] (cf. Sec. 3.4.1). As a result, RBF-HS suffers from too many "mind shifts" and spends most of the time doing backtracking and re-exploration steps while making very little progress in the search tree.

However, like in the case of minCard, when we allow for the utilization of a small amount of more memory than RBF-HS does, this problem is remedied to a great extent. In fact, adopting HBF-HS with a switch at 400 generated nodes, led to a comparable—in 43 % of scenarios even lower—runtime as opposed to HS-Tree. Only in a single scenario, i.e., SPL20 with ontology O, HBF-HS (with switch at 400 nodes) still required substantially more time than HS-Tree did. Obviously, this exact combination represents a particularly demanding case for HBF-HS and RBF-HS (cf. bullet *(4)*).

As additional tests turned out, the answer to this problem is the employment of HBF-HS equipped with a *relative switch criterion* (instead of an absolute one). Concretely, we allowed HS-Tree to consume 60 % of the available memory before handing over to RBF-HS. Runtimes as for HS-Tree could be achieved in this way (while making use of only marginally more than 60 % of the disposable memory, cf. bullet *(5)*).

(9) Scalability tests: The observations discussed so far have brought to light that DPIs with thousands of axioms and diagnoses (cf. columns 2 and 4 in Tab. 2) could be well handled by RBF-HS in our tests (Figs. 4 and 5), and even led to a better relative performance in comparison to HS-Tree than problems with fewer components and possible faults. In order to evaluate the scalability of RBF-HS wrt. ld, i.e., the number of diagnoses to be computed, we conducted an additional scalability experiment. To this end, we first selected the most demanding DPIs based on their absolute runtime and memory cost in the normal experiments, and then ran the same experiments on these DPIs as described in Sec. 6.3, but with $ld := 100$.

The results we obtained for the minCard setting are presented by Fig. 6(left). It displays that enormous space savings (in all cases) oppose

- minor runtime overheads (7 cases; RBF-HS's runtime overhead always lower than factor 1.65),
- roundly equal runtimes (2 cases), and
- even time savings (5 cases; runtime savings of RBF-HS between 7 % and 22 %).

Space savings achieved by RBF-HS ranged from 83 % (case O, SPL) to 99 % (case Cig, SPL; case IT, SPL+ENT) and exceeded 90 % in all but a single case. Note, even the combination of function SPL and ontology O, which proved to be a particularly unfavorable case as regards runtime in the normal experiments (cf. bullets *(4)* and *(8)*), turned out to be unproblematic in the scalability tests. This shows that RBF-HS scales very well when minimum-cardinality diagnoses are of interest.

For the maxProb setting, the insight was that RBF-HS, in general, does not scale to large numbers of computed diagnoses like $ld = 100$, as it required up to several hours computation time per executed sequential session. HS-Tree as well as HBF-HS (with a relative switch criterion of 60 % consumption of the available memory, cf. bullet *(8)*), on the other hand, could finish the same tasks in the range of few minutes. The conclusion is that, for the computation of most probable diagnoses, HBF-HS with a relative switch criterion should be used rather than RBF-HS.

(10) Results for the hardest cases: For the purpose of clarity of Figs. 4 and 5, we excluded the results for the two DPIs ccc and cce. These two DPIs result from the integration (*alignment* [100]) of two ontologies describing a common domain (in this case: a conference management system) in a different way. As a consequence of the automatized alignment process, a multitude of independent issues in terms of (minimal) conflicts emerge at once in the resulting ontology. This leads to large sizes of minimal diagnoses (cf. Tab. 2, column 4), which causes a high depth and thus enormous size of the hitting set tree. The runtime and memory measurements for these hard cases are demonstrated by Fig. 6(right). We detect gigantic space savings up to four orders of magnitude while runtime still remains in most cases comparable with HS-Tree (in 25 % of the cases RBF-HS's runtime is even better). For instance, for the case ccc, ENT, 2 we observed that HS-Tree required more than 800 times the memory used by RBF-HS, while RBF-HS exhibited also a 3 % lower runtime. Even more impressingly, RBF-HS reduced the memory consumption by a factor of more than 4200 while at the same time decreasing the computation time by 15 % in the case ccc, SPL, 6. Again, as discussed above, the use of HBF-HS allows to level any significant time overheads of RBF-HS while consuming a limited amount of memory.

7. Conclusions and Future Work

In this work, we introduced two new diagnostic search techniques, RBF-HS and HBF-HS, which borrow ideas from Korf's seminal RBFS algorithm [31]. The unique characteristic of RBF-HS is that it requires only linear space for the computation of an arbitrary fixed finite number of minimal diagnoses (fault explanations) while preserving the desired features soundness (*only* actual fault explanations are computed), completeness (*all* fault explanations can be computed), and the best-first property (fault explanations are computed *in order* based on a given preference criterion). HBF-HS is

a hybrid strategy that aims at leveraging synergies between Reiter's HS-Tree [2] and RBF-HS in a way that problems can be solved in reasonable time without depleting the required memory. Both suggested algorithms are generally applicable to any diagnosis problem according to Reiter's theory of model-based diagnosis [2]; in particular, they are independent of the (monotonic) knowledge representation language used to describe the diagnosed system and of the adopted inference engine.

In comprehensive experiments on a corpus of real-world knowledge-based diagnosis problems of various size, diagnostic structure and reasoning complexities beyond NP-complete, we compared our approaches against HS-Tree, a state-of-the-art diagnosis computation algorithm with the same properties (soundness, completeness, best-firstness, general applicability) as the proposed methods. The results testify that RBF-HS, when computing minimum-cardinality diagnoses, scales to large numbers of computed leading diagnoses and leads to a significant memory reduction up to several orders of magnitude for all non-easy problem instances while in addition reducing also the runtime by up to 90 % in more than a third of the cases. When used to determine the most probable diagnoses, RBF-HS trades space for time more or less one-to-one compared to HS-Tree. Moreover, for both minimum-cardinality and most-probable diagnoses, whenever the runtime of RBF-HS was significantly higher than that of HS-Tree, the use of HBF-HS could level this overhead while still reasonably limiting the used memory. Overall, this demonstrates that the suggested techniques allow for *memory-aware model-based diagnosis*, which can contribute, e.g., to the successful diagnosis of memory-restricted devices or memory-intensive problem instances.

Since our methods are not restricted to diagnosis problems, but applicable to best-first hitting set computation in general, and since a multitude of real-world problems can be formulated as hitting set problems, this work has the potential to impact research and application domains beyond the frontiers of model-based diagnosis.

Future work topics include the integration of RBF-HS and HBF-HS into our ontology debugging plug-in *OntoDebug*[48] [78] for *Protégé*[49] [101], closer investigations of applications of RBF-HS discussed in Sec. 3.6, as well as further research on hitting set variants of other heuristic search approaches outlined in Sec. 5.4.

Acknowledgments

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Appendix A. RBF-HS: Proof of Correctness

We next show the validity of the theorem below, which is stated in Sec. 3.5:

Theorem 2. *Let* FINDMINCONFLICT *be a sound and complete method for conflict*

[48] See http://isbi.aau.at/ontodebug.
[49] See https://protege.stanford.edu/.

computation, i.e., given a DPI, it outputs a minimal conflict for this DPI if a minimal conflict exists, and 'no conflict' otherwise. Then RBF-HS is sound, complete and best-first, i.e., it computes all *and* only *minimal diagnoses* in descending order of probability *as per the cost-adjusted probability measure* pr.

Before we are able to state the proof of Theorem 2, we formulate some useful definitions and lemmas that will help us keep the proof relatively concise.

Appendix A.1. Preparation for the Proof

Definition 1. *We say that a* node n is processed *by RBF-HS iff a call of RBF-HS'*$(\mathsf{n}, \_, \_)$ *(line 9 or 32) is executed.*[50]

Lemma 1. *In RBF-HS, only diagnoses can be added to the collection* $\mathbf{D}$.

Proof. Let us start backwards from line 16, which is the only place in RBF-HS where elements are added to $\mathbf{D}$. The condition that must be fulfilled for this line to be reached is that $L = valid$ must be returned for the currently processed node n that is added to $\mathbf{D}$. Considering the LABEL function, we find that it must return in line 46 which in turn requires that FINDMINCONFLICT$(\langle \mathcal{K} \setminus \mathsf{n}, \mathcal{B}, P, N \rangle)$ before must have returned 'no conflict'. This means that $\mathcal{K} \setminus \mathsf{n}$ does not contain a minimal conflict, or, equivalently, is not a conflict. By the Duality Property (cf. Sec. 2.1), we obtain that n is a diagnosis. □

Lemma 2. *If line 9 is executed, then a non-empty minimal diagnosis exists.*

Proof. The statement of this lemma follows from the algorithm's the analysis (lines 4 and 6) of the output of the FINDMINCONFLICT call in line 3 along with the Duality Property (cf. Sec. 2.1). See paragraph "Trivial Cases" in Sec. 3.2 for a more detailed argumentation. □

Lemma 3. *If a node* n *corresponding to a minimal diagnosis* $\mathcal{D}$ *is processed for the first time by RBF-HS, then* n *will be (directly) added to* $\mathbf{D}$ *in line 16.*
(Equivalently: After any call of RBF-HS' which processes a node n *corresponding to* $\mathcal{D}$ *returns,* $\mathcal{D}$ *is an element of* $\mathbf{D}$*.)*

Proof. Assume that, for the first time throughout the execution of RBF-HS, a node n equal to $\mathcal{D}$ is processed, where $\mathcal{D}$ is a minimal diagnosis. Initially, in line 12, a label L is computed for n. Within the LABEL function, the first thing executed is the non-minimality check in lines 38–40, where a node n_i is sought in $\mathbf{D}$ which is a subset of n. Since *(1)* only diagnoses can be in $\mathbf{D}$ as per Lemma 1, *(2)* $\mathsf{n} = \mathcal{D}$ is a minimal diagnosis, and *(3)* it is the first time that a node equal to $\mathcal{D}$ is processed, there cannot be any subset n_i of n in $\mathbf{D}$. Hence, line 41 is reached. Due to the Hitting Set Property (cf. Sec. 2.1) and the fact that n is a (minimal) diagnosis, there cannot be any (minimal) conflict $\mathcal{C}$ such that $\mathcal{C} \cap \mathsf{n} = \emptyset$. Consequently, line 44 is reached. The FINDMINCONFLICT call in line 44 will return 'no conflict' due to the Duality Property and because n is a diagnosis. As a result, LABEL will return in line 46, which means that n will be added to $\mathbf{D}$ in line 16.

[50] The "_" signifies that the other input arguments to RBF-HS' do not matter.

(The equivalent statement of the lemma holds since no element once added to $\mathbf{D}$ can ever be removed from it, for the simple reason that there is no statement in RBF-HS that modifies $\mathbf{D}$ except for the one that adds elements to $\mathbf{D}$ in line 16.) □

Lemma 4. *For any call RBF-HS'*$(\mathsf{n}, F(\mathsf{n}), bound)$*, a value* $X < F(\mathsf{n})$ *is returned (unless the RBF-HS'-procedure is exited in line 18 before a return takes place).*

Proof. Assume an execution of some call of RBF-HS'$(\mathsf{n}, F(\mathsf{n}), bound)$ throughout which no exit of the RBF-HS'-procedure takes place in line 18. Observe that there are three spots where RBF-HS'might return, i.e., in any of the lines 14, 19 or 36. For the returns in lines 14 and 19, first two cases, $-\infty$ is returned. However, $F(\mathsf{n}) > -\infty$ must hold. To prove this, let us consider the two places where the RBF-HS'-call can have been issued, i.e., lines 9 or 32. In the former case, $F(n)$ is equal to $f(\emptyset)$, which can only attain values in $(0, 1)$ (cf. Sec. 2.1). In the latter case, n is equal to a child node n_1 of some node and $F(\mathsf{n}) = F(\mathsf{n}_1) > -\infty$ due to the while-condition in line 31. Therefore, the statement of the lemma holds for the returns in lines 14 and 19.

For the return in line 36, we first point out that, for any call RBF-HS'$(\mathsf{n}, F(\mathsf{n}),$ $bound)$, $F(\mathsf{n}) \geq bound$ must hold. To see this, consider again lines 9 and 32, where RBF-HS' can be invoked. In the former case, $bound = -\infty$ and $F(\mathsf{n}) > bound$ follows from the argumentation in the previous paragraph. In the second case, as explained above, n is equal to a child node n_1 of some node. Through the while-condition, we thus know that $F(\mathsf{n}) = F(\mathsf{n}_1)$ is larger than or equal to the old value of the bound. Moreover, we know by the sorting of Child_Nodes and the fact that n_1 is the node in Child_Nodes with the largest F-value (due to lines 28, 29, 33 and 34), that $F(\mathsf{n}) = F(\mathsf{n}_1) \geq F(\mathsf{n}_2)$ for the node n_2 with second-largest F-value in Child_Nodes (cf. lines 30 and 35). Since $bound$ is defined as the maximum among the old value of bound and $F(\mathsf{n}_2)$, $F(\mathsf{n}) \geq bound$ must be true.

Finally, note that a return in line 36, which is our current assumption, can only take place if the condition of the while-loop is violated. This implies that the returned value $(F(\mathsf{n}_1))$ is either equal to $-\infty$ or strictly less than $bound$. As $F(\mathsf{n})$ must be greater than $-\infty$, as demonstrated in the first paragraph of this proof, we deduce that the statement of the lemma also holds for the return in lines 36. □

Lemma 5. *Throughout the entire execution of RBF-HS and for any node* n*, the following invariant holds:* $F(\mathsf{n}) \leq f(\mathsf{n})$.

Proof. First, note that the each node's f-value remains constant throughout the entire execution of RBF-HS. We now prove that *(1)* when set, each node's F-value is smaller than or equal to its f-value, and that *(2)* as long as a node (and thus its F-value) remains in memory, its F-value can never increase.

Proof of (1): Here, we consider the root node and all other nodes separately. First, the root node's F-value is set to its f-value in line 9, i.e., $F(\mathsf{n}) = f(\mathsf{n})$ holds. Second, each other node's F-value is set in line 23 or 25 after it is (re)constructed in line 20. At this stage, the new node is refereed to as n_i in the Alg. 2. If line 23 applies, then clearly $F(\mathsf{n}_i) = \min(F(\mathsf{n}), f(\mathsf{n}_i)) \leq f(\mathsf{n}_i)$. If n_i's F-value is defined in line 25, then obviously $F(\mathsf{n}_i) = f(\mathsf{n}_i)$. This completes the proof of (1).

Proof of (2): Here, we need to demonstrate that the F-value of any node n constructed in line 20 is never increased until n is discarded by a backtracking step. The relevant backtracking step is issued by the execution of line 36 of the *same* RBF-HS'-call where n was constructed. Therefore, we only need to show that $F(\mathsf{n})$ cannot increase between lines 26 and 36. The only place where F-values of nodes are modified in this part of the algorithm is line 32, where the F-value of a node n_1 is adapted by processing n_1. By means of Lemma 4, we infer that n_1's new F-value must be strictly lower than its old F-value, for arbitrary nodes n_1. □

Lemma 6. *RBF-HS labels a node $valid$ or $closed$ iff it corresponds to a diagnosis.*

Proof. To show the bi-implication, we show both implications $\Rightarrow$ and $\Leftarrow$.

$\Rightarrow$: Assume a node n that is labeled $valid$ or $closed$ by RBF-HS. This implies that n is processed and that the call LABEL(n) returns either in line 40 or 46. In the former case, due to Lemma 1, we have that there is some diagnosis n_i such that $\mathsf{n} \supseteq \mathsf{n}_i$, which entails that n is a diagnosis.

$\Leftarrow$: Assume a node n equal to a diagnosis is labeled, i.e., LABEL(n) is executed. First, due to the Hitting Set Property (cf. Sec. 2.1) and the fact that n is a diagnosis, there cannot be any (minimal) conflict $\mathcal{C}$ such that $\mathcal{C} \cap \mathsf{n} = \emptyset$. Moreover, all elements (if any) in the collection $\mathbf{C}$ must be minimal conflicts due to the soundness and completeness (wrt. the computation of minimal conflicts) of the FINDMINCONFLICT function. Hence, LABEL cannot return in line 43. Second, if FINDMINCONFLICT is called for the DPI $\langle \mathcal{K} \setminus \mathsf{n}, \mathcal{B}, P, N \rangle$, then it must return 'no conflict'. This holds due to the soundness of FINDMINCONFLICT, the Duality Property (cf. Sec. 2.1), and the fact that n is a diagnosis. As a conclusion, LABEL cannot return in line 49. Overall, since there are exactly four possible lines where LABEL(n) might return, and lines 43 as well as 49 are impossible, we obtain that a return must take place in either line 40 or 46. □

Lemma 7. *Let n be an arbitrary node. Before n is processed for the very first time throughout the execution of RBF-HS, $F(\mathsf{n}) = f(\mathsf{n})$ holds whenever n is generated.*
(Note: By contraposition of this statement, along with Lemma 5, we obtain: If $F(\mathsf{n}) < f(\mathsf{n})$, then n was already processed at least once.)

Proof. We prove this lemma by induction based on the tree depth $d = |\mathsf{n}|$ of n.

Induction Base: Let $d = 1$. First, observe that the F-value of the root node $\emptyset$ is equal to its f-value due to lines 9 and 11 (cf. the second argument of RBF-HS' in both lines). Therefore, at the (very first) RBF-HS'-call that processes the root node n, the if-condition in line 22 is false for all child nodes n_i of n. Hence, line 25 is executed for all n_i, which is why $F(\mathsf{n}_i) = f(\mathsf{n}_i)$ for all n_i. However, the nodes n_i are exactly the nodes at depth $d = 1$ because $|\mathsf{n}_i| = 1$. Consequently, the proposition of the lemma holds for $d = 1$.

Induction Assumption: Assume the proposition of the lemma holds for $d = k$.

Induction Step: Let n be a node at depth $d = k+1$, and let n be generated (line 20). Let us denote the parent node of n by n_p. That is, n_p is the node that is currently being processed when line 20, at which n is generated, is executed. There are now two cases: either *(a)* n_p is currently being processed for the very first time during the execution of RBF-HS, or *(b)* n_p has already been processed before.

Assume (a): Since n_p is a node at depth k, we obtain by the Induction Assumption that $F(\mathsf{n}_p) = f(\mathsf{n}_p)$. This implies that the if-condition in line 22 is false. Thus, line 25 is executed for n and $F(\mathsf{n}) = f(\mathsf{n})$.

Now suppose (b): Here, we know that n must have already been generated and subsequently discarded in the past since its parent n_p was already processed. By the argumentation for case (a), we know that $F(\mathsf{n}) = f(\mathsf{n})$ was true at the very first processing of n_p. When the execution of this respective RBF-HS'-call (the one that processed n_p for the very first time) ended, the backed-up F-value X returned and set as the new F-value of n_p was the maximal F-value of any child node of n_p at this time (lines 28, 29, 33 and 34). Since n was never processed so far by assumption, and since $F(\mathsf{n}) = f(\mathsf{n})$ was true when n was first generated, this must still have been true when X was returned. Hence, $X \geq F(\mathsf{n}) = f(\mathsf{n})$ was true after the termination of the said RBF-HS'-call. Since the maximal F-value over all child nodes is returned whenever the processing of a node for which children were generated terminates, a value greater than or equal to X is backed-up if the processing of n_p's parent node ends. The same holds recursively for any other ancestor of n_p until ancestors of depth 1. Note, all nodes at depth 1 remain in memory throughout the entire execution of RBF-HS and RBF-HS cannot terminate since n is generated again by assumption.

Since n is generated again by assumption, each of these ancestors must be processed again. Whenever child nodes for any of these ancestors n_a are (re)generated, $F(\mathsf{n}_a) \geq X$ and each child node's F-value is either set to its f-value or to $F(\mathsf{n}_a)$, due to lines 23 and 25. Hence, $F(\mathsf{n}_p) \geq X$ or $F(\mathsf{n}_p) = f(\mathsf{n}_p)$ when n_p is (re)generated. Now ,when n is (re)generated, either line 23 or 25 is executed to set n's F-value. If line 25 applies, we have that $F(\mathsf{n}) = f(\mathsf{n})$. Therefore, suppose line 23 is the one executed. As we have shown that $F(\mathsf{n}_p) \geq X \geq f(\mathsf{n})$, we can deduce $F(\mathsf{n}) = \min(F(\mathsf{n}_p), f(\mathsf{n})) = f(\mathsf{n})$ also in this case.

Regardless of how often the parent n_p is processed, the same argumentation can be applied to derive that $F(\mathsf{n}) = f(\mathsf{n})$ will hold whenever n is (re)generated. This completes the inductive proof. □

Appendix A.2. Proof of Theorem 2

We demonstrate the correctness of RBF-HS in the following order: termination, completeness, best-first property, and finally soundness.

Appendix A.2.1. Termination

Assume the RBF-HS does not terminate. The only possibilities for non-termination are that *(i)* one of the for-loops (lines 21, 38, 41, and 52) is iterated forever, *(ii)* the recursion is iterated forever (i.e., infinitely many calls of RBF-HS' are made), or *(iii)* the while-loop during some RBF-HS'-call is iterated forever.

Assume (i): Let us consider the four for-loops in turn in chronological order by the point in time at which they are executed by one call of RBF-HS'.
(Line 38): Since $\mathcal{D} \subseteq \mathcal{K}$ holds for any diagnosis $\mathcal{D}$ and $|\mathcal{K}|$ is finite (cf. Sec. 2.1), the for-loop must terminate.
(Line 41): Since $\mathcal{C} \subseteq \mathcal{K}$ holds for any conflict $\mathcal{C}$ and $|\mathcal{K}|$ is finite (cf. Sec. 2.1), the for-loop must terminate.

(Line 52): Each label L other than $closed$ or $valid$ output by the LABEL function must have been computed (either freshly or at an earlier stage) by the FINDMINCONFLICT function. By the soundness of FINDMINCONFLICT, L must be a conflict in this case. Hence, the argument L forwarded to the EXPAND function must be a conflict. Since $\mathcal{C} \subseteq \mathcal{K}$ holds for any conflict $\mathcal{C}$, $|\mathcal{K}|$ is finite (cf. Sec. 2.1), and the for-loop iterated by the EXPAND function processes each element of L once, this for-loop must terminate.
(Line 21): This for-loop iterates once through the set of child nodes output by the EXPAND function, which must be finite by the argumentation above. Hence, this for-loop must terminate as well.

Assume (ii): For each recursive call in line 32, the node n_1, for which the call is made, is one of the child nodes of the old node n_1, for which the call in line 32 was made one recursion level higher. Due to the construction of child nodes (line 53), and because lines 42 and 44 guarantee that the conflict used to label parent is disjoint with the parent node, it follows that each child node has exactly one more element than its parent. Moreover, each element e added to a node, and thus each element e of any node, is an element of some conflict $\mathcal{C} \subseteq \mathcal{K}$, which entails that $e \in \mathcal{K}$. This holds due to line 53 and the fact that the argument L passed to EXPAND must be a conflict, as argued above. So far, we have shown that each node along any tree branch is a subset of $\mathcal{K}$ and each recursive downward step along the branch adds exactly one element to a node.

Additionally, due to Lemma 2 and since line 32 was executed by assumption, we know that a diagnosis exists. By definition, each (minimal) diagnosis is a subset of $\mathcal{K}$. In particular, this means that $\mathcal{K}$ is necessarily a diagnosis. By Lemma 6, any processed node corresponding to a diagnosis will be labeled $valid$ or $closed$, which prompts a return in either line 14 or 19 and thus prevents any further recursive RBF-HS'-calls along this tree branch. Now, our assumption of an infinite sequence of recursive RBF-HS'-calls means that no node along this branch can be labeled $closed$ or $valid$. Due to $|\mathcal{K}| < \infty$ (cf. Sec. 2.1), this yields a contradiction since any such infinite branch must at some stage process the node $\mathsf{n} = \mathcal{K}$ which is a diagnosis.

Assume (iii): First, note that $bound$ occurring in the while-condition is fixed throughout the execution of one and the same while-loop. Second, by Lemma 4, each (of the infinitely many calls) of RBF-HS' executed during the while-loop execution decreases the F-value of the processed node. Third, each F-value returned by RBF-HS' in line 32 is equal to either $-\infty$ or to some original f-value of some node (see all return-statements throughout RBF-HS' and lines 23 and 25). Because there are only finitely many possible nodes (each node is a subset of $\mathcal{K}$ where $|\mathcal{K}| < \infty$), there can also be only finitely many different f-values $\{f_1, \ldots, f_q\}$ of nodes, which is why we can find a fixed $\epsilon > 0$ such that for all $f_i \neq f_j$ we have $|f_i - f_j| > \epsilon$. Hence, for any node n, the reduction of the F-value by means of one RBF-HS'-call must be greater than ϵ. Fourth, once its F-value is below $bound$, a node cannot be processed again during this while-loop execution (while-condition). Fifth, there are always finitely many child nodes which are processed by the while-loop (see above). From these five points, we conclude that, after a finite number of iterations, the while-condition must be violated. Contradiction.

Appendix A.2.2. Completeness

Let $ld := \infty$ (all existing minimal diagnoses should be found) and let there be a minimal diagnosis $\mathcal{D}'$ such that $\mathcal{D}' \notin \mathbf{D}$ for the collection $\mathbf{D}$ returned by RBF-HS. The return can take place in lines 5, 7 or 10. Line 5 cannot apply since, in this case, the FINDMINCONFLICT call in line 3 returns $\emptyset$, which means that there cannot be any diagnosis by the Duality Property—this is a contradiction to our assumption that $\mathcal{D}'$ is a diagnosis. If line 7 applies, then 'no conflict' was output by FINDMINCONFLICT in line 3, which implies that $\emptyset$ is the only diagnosis, again by the Duality Property. Hence, $\mathcal{D}' = \emptyset$ must hold. Since $\mathbf{D} = [\emptyset]$ is returned, we have a contradiction to the assumption that $\mathcal{D}'$ is not returned.

Finally, let the return of $\mathbf{D}$ be in line 10. This means that RBF-HS' must have been called in line 9. By Lemma 3, our assumption from above can be stated as: No node corresponding to $\mathcal{D}'$ is processed throughout the execution of RBF-HS'. First, note that, for each minimal diagnosis, there is a possible path from the root to that diagnosis, due to the Hitting Set Property (i.e., each diagnosis, in particular $\mathcal{D}'$, includes some element of every minimal conflict) and the fact that RBF-HS' can generate a node equal to $\mathcal{D}'$ by starting with the empty (root) node (cf. line 9), labeling it with a minimal conflict $\mathcal{C}_1$ (see LABEL function, line 43 or 49), and by selecting a child node equal to $\{x\}$ for some element $x \in \mathcal{C}_1 \cap \mathcal{D}'$, and labeling this child again with a conflict $\mathcal{C}_2 \cap \{x\} = \emptyset$, and so on. We next show that each node $\mathsf{n} \subseteq \mathcal{D}'$ along some path from the root to $\mathcal{D}'$ will be processed.

First, let us assume that some node $\mathsf{n}' \subseteq \mathcal{D}'$ of cardinality $k \geq 1$ is generated, but never processed. By Lemma 7, it follows that $F(\mathsf{n}') = f(\mathsf{n}') > 0 > -\infty$ will hold throughout the entire execution of RBF-HS'. Since RBF-HS terminates, any RBF-HS'-call for the parent node n'_p of n' must return, and since n' (i.e., a child node) was generated it must return exactly in line 36. (Note that $\mathsf{n}'_p (\subset \mathcal{D}')$ can be processed multiple times; however, each time the respective RBF-HS'-call that processes n'_p will return in line 36 since *(1)* $\mathcal{D}'$ is a *minimal* diagnosis by assumption, *(2)* only diagnoses can be labeled $valid$ or $closed$ by Lemma 6, and *(3)* $ld = \infty$ ensures that line 18 can never be executed.) Thus, for any call that processes n'_p, the returned value $F(\mathsf{n}'_p) \geq F(\mathsf{n}') > -\infty$ (due to the sorting of Child_Nodes, see lines 28 and 33, and due to the fact that the child node with maximal F-value is always returned, see lines 29 and 34). The same argumentation can be applied along the branch from n'_p to the root node, until the new n'_p is equal to the root. Finally, we can derive that $F(\mathsf{n}_1) \geq F(\mathsf{n}') > -\infty$ will hold throughout the entire execution of the first call of RBF-HS' made in line 9, which means that the condition of the while-loop is satisfied forever (recall that $bound = -\infty$ at the first RBF-HS'-call in line 9). This is a contradiction to the fact that RBF-HS always terminates. Thus, we have demonstrated that, for $k \in \{1, \ldots, |\mathcal{D}'|\}$, if some $\mathsf{n}' \subseteq \mathcal{D}'$ with $|\mathsf{n}'| = k$ is generated, it will also be processed. In particular, this implies that $\mathcal{D}'$ will be processed, given that it is generated.

It remains to be shown that $\mathcal{D}'$ will be generated. To this end, observe that the root $\emptyset$ is trivially processed (see line 9) and must be labeled with a non-empty minimal conflict (as line 9 was reached, see above), which entails by line 20 (EXPAND function) that all tree nodes of cardinality $k = 1$ are generated, among them one subset n' of $\mathcal{D}'$. Since n' must be processed (note: maybe not immediately, but definitely at some

stage of the algorithm's execution), as proven, some $\mathsf{n}' \cup \{x\} \subseteq \mathcal{D}'$ of cardinality $k+1$ is generated. The same inductive argument can be applied to all nodes $\mathsf{n}' \subset \mathcal{D}'$. Consequently, $\mathcal{D}'$ will be eventually generated—and processed, as argued above. This is a contradiction to the assumption that $\mathcal{D}'$ is never processed, which finalizes the completeness proof.

Appendix A.2.3. Best-First Property

We already know that RBF-HS is complete, i.e., that all minimal diagnoses for the given DPI will be in the returned list $\mathbf{D}$. We now have to show that this list is sorted in descending order by f-value. Since any node corresponding to a minimal diagnosis that is processed by RBF-HS will be (directly) added to $\mathbf{D}$ by Lemma 3, it suffices to demonstrate that, for any two minimal diagnoses $\mathcal{D}', \mathcal{D}''$ with $f(\mathcal{D}') < f(\mathcal{D}'')$, some node equal to $\mathcal{D}''$ is processed prior to all nodes equal to $\mathcal{D}'$.

To this end, let $ld = \infty$ (the algorithm does not terminate before all minimal diagnoses have been found) and assume the opposite, i.e., some node corresponding to $\mathcal{D}'$ is processed earlier than all nodes equal to $\mathcal{D}''$. Take the (first ever) call RBF-HS'$(\mathsf{n}, F(\mathsf{n}), bound)$ with $\mathsf{n} = \mathcal{D}'$ (i.e., the first call that processes $\mathcal{D}'$). Then we have that $F(\mathsf{n}) \geq bound$ (while-condition) and $bound = \max\{F(\mathsf{n}^1_{2bst}), F(\mathsf{n}^2_{2bst}), \ldots, F(\mathsf{n}^k_{2bst})\}$ with $k = |\mathcal{D}'| - 1$ where n^r_{2bst} denotes the best alternative node (according to F-value) at tree depth r. (Note that, at any time during its execution, RBF-HS' involves only one expanded node at each tree level; amongst the generated nodes at one level r, the best one is expanded and the second best one is precisely n^r_{2bst}. To see that $bound$ is equal to the maximum of the stated set of best alternative nodes, observe that $bound = -\infty$ at the very first call of RBF-HS' in line 9, and for each node that is expanded, the new $bound$ is the maximum of the current $bound$ and the current best alternative node, cf. line 32).

Now, let n^* be the deepest common ancestor node of $\mathcal{D}'$ and $\mathcal{D}''$ in the tree, i.e., $\mathsf{n}^* = \mathcal{D}' \cap \mathcal{D}''$. Since both $\mathcal{D}'$ and $\mathcal{D}''$ are *minimal* diagnoses, $\mathsf{n}^* \subset \mathcal{D}'$ and $\mathsf{n}^* \subset \mathcal{D}''$. Moreover, let $\mathsf{n}^*_{r,\mathcal{D}''}$ denote the r-th successor node of n^* along a path to a node equal to $\mathcal{D}''$. E.g., $\mathsf{n}^*_{1,\mathcal{D}''}$ describes the child node of n^* along the path to $\mathcal{D}''$; note that $\mathsf{n}^*_{r,\mathcal{D}''} = \mathcal{D}''$ for $r = |\mathcal{D}''| - |\mathsf{n}^*|$ and that $\mathsf{n}^*_{r,\mathcal{D}''}$ is a node at tree depth $|\mathsf{n}^*| + r$.

For $s = |\mathsf{n}^*| + 1$, we know from above ($F(n) \geq bound$) that $F(\mathsf{n}) \geq F(\mathsf{n}^s_{2bst})$ and, since n^s_{2bst} is the best alternative node at level s, that $F(\mathsf{n}^s_{2bst}) \geq F(\mathsf{n}^*_{1,\mathcal{D}''})$. Furthermore, by Lemma 5, $f(\mathsf{n}) \geq F(\mathsf{n})$ must hold. Overall, since $\mathsf{n} = \mathcal{D}'$, we so far have $f(\mathcal{D}') \geq F(\mathsf{n}^*_{1,\mathcal{D}''})$. If $|\mathcal{D}''| - |\mathsf{n}^*| = 1$, i.e., $\mathsf{n}^*_{1,\mathcal{D}''} = \mathcal{D}''$, then (*) $F(\mathsf{n}^*_{1,\mathcal{D}''}) = f(\mathsf{n}^*_{1,\mathcal{D}''}) = f(\mathcal{D}'')$ must be true. The reason for this is Lemma 7 and that no node corresponding to $\mathcal{D}''$ can have been processed yet, as this would be a contradiction to our assumption that we are considering the *first* call that processes a node equal to $\mathcal{D}'$ and that this one is processed earlier than any node equal to $\mathcal{D}''$. Thus, we have deduced that $f(\mathcal{D}') \geq f(\mathcal{D}'')$, which gives a contradiction to our assumption.

So, let $|\mathcal{D}''| - |\mathsf{n}^*| \geq 2$, i.e., $\mathsf{n}^*_{1,\mathcal{D}''} \subset \mathcal{D}''$. By Lemma 5, there are now two cases: *(a)* $F(\mathsf{n}^*_{1,\mathcal{D}''}) = f(\mathsf{n}^*_{1,\mathcal{D}''})$, or *(b)* $F(\mathsf{n}^*_{1,\mathcal{D}''}) < f(\mathsf{n}^*_{1,\mathcal{D}''})$.

Assume (a) first. Since $f(X) > f(Y)$ whenever $X \subset Y$ due to the fact that f is cost-adjusted, we can derive that $f(\mathcal{D}') \geq F(\mathsf{n}^*_{1,\mathcal{D}''}) = f(\mathsf{n}^*_{1,\mathcal{D}''}) > f(\mathsf{n}^*_{j,\mathcal{D}''})$ for $j = 2, \ldots, |\mathcal{D}''| - |\mathsf{n}^*|$. Hence, $f(\mathcal{D}') \geq f(\mathcal{D}'')$, a contradiction to our assumption.

Finally, assume (b). From Lemma 7, we know that $\mathsf{n}^*_{1,\mathcal{D}''}$ must already have been processed. In addition, since $\mathcal{D}''$ is a minimal diagnosis and $\mathsf{n}^*_{1,\mathcal{D}''} \subset \mathcal{D}''$, we have that $\mathsf{n}^*_{1,\mathcal{D}''}$ can never be labeled *valid* or *closed* when it is processed, due to Lemma 6. Therefore, and because $ld = \infty$, every (and, in particular, the last) call of RBF-HS' that processed $\mathsf{n}^*_{1,\mathcal{D}''}$ must have returned in line 36. From this, we infer that $F(\mathsf{n}^*_{1,\mathcal{D}''}) = \max_{\mathsf{n}\in\mathsf{Child\_Nodes}}(F(\mathsf{n}))$ where Child_Nodes refers to the child nodes of $\mathsf{n}^*_{1,\mathcal{D}''}$. Since $\mathsf{n}^*_{2,\mathcal{D}''} \subseteq \mathcal{D}''$ is one node among Child_Nodes, we obtain that $F(\mathsf{n}^*_{1,\mathcal{D}''}) \geq F(\mathsf{n}^*_{2,\mathcal{D}''})$. If $|\mathcal{D}''| - |\mathsf{n}^*| = 2$, i.e., $\mathsf{n}^*_{2,\mathcal{D}''} = \mathcal{D}''$, then the same argumentation as in (*) above can be applied to show that $f(\mathcal{D}') \geq f(\mathcal{D}'')$, a contradiction.

Otherwise, we consider $|\mathcal{D}''| - |\mathsf{n}^*| \geq 3$, i.e., $\mathsf{n}^*_{2,\mathcal{D}''} \subset \mathcal{D}''$, and can again discern two analogous cases (a) and (b) for $\mathsf{n}^*_{2,\mathcal{D}''}$. In this vein, we can consecutively derive $f(\mathcal{D}') \geq F(\mathsf{n}^*_{j,\mathcal{D}''})$ for $j = 3, \ldots, |\mathcal{D}''| - |\mathsf{n}^*|$ and use (*) to obtain the contradiction. This completes the proof of the best-first property.

Appendix A.2.4. Soundness

We have to prove that every node that is added to $\mathbf{D}$ is a minimal diagnosis. To this end, assume that some $\mathcal{D}' \in \mathbf{D}$ is not a minimal diagnosis. That is, $\mathcal{D}'$ is *(a)* not a diagnosis or *(b)* a diagnosis, but not minimal. Suppose (a). Here we immediately get a contradiction to Lemma 1.

Now, suppose (b). That is, $\mathcal{D}'$ is a non-minimal diagnosis, or, in other words, there is a minimal diagnosis $\mathcal{D}'' \subset \mathcal{D}'$. By the fact that f is cost-adjusted, $f(\mathcal{D}'') > f(\mathcal{D}')$ must hold. Further, $\mathcal{D}'$ must have been added to $\mathbf{D}$ in line 16 as node n because this is the only place in RBF-HS where $\mathbf{D}$ is extended. Thus, the LABEL function must have been executed for n, in particular lines 38–40. However, no return can have taken place in line 40 due to the fact that n was assigned the label *valid* which implies that line 46 must have been reached. As a consequence, the test $\mathsf{n} \supseteq \mathsf{n}_i$ in line 39 must have been negative for all $\mathsf{n}_i \in \mathbf{D}$. Hence, no node in $\mathbf{D}$ is a subset of $\mathsf{n} = \mathcal{D}'$, which means that, in particular, $\mathcal{D}'' \notin \mathbf{D}$ at the time $\mathcal{D}'$ is processed. Now, since $\mathcal{D}''$ is a minimal diagnosis and has a higher f-value than $\mathcal{D}'$, we obtain a contradiction to the completeness and best-first properties shown above. This completes the soundness proof. □

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