STATISTICAL GENERALIZATION OF PERFORMANCE-RELATED HEURISTICS FOR KNOWLEDGE-LEAN APPLICATIONS

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ABSTRACT

In this paper, we present new results on the automated generalization of performance-related heuristics learned for knowledge-lean applications. By first applying genetics-based learning to learn new heuristics for some small subsets of test cases in a problem space, we study methods to generalize these heuristics to unlearned subdomains of test cases. Our method uses a new statistical metric called probability of win. By assessing the performance of heuristics in a range-independent and distribution-independent manner, we can compare heuristics across problem subdomains in a consistent manner. To illustrate our approach, we show experimental results on generalizing heuristics learned for sequential circuit testing, VLSI cell placement and routing, branch-and-bound search, and blind equalization. We show that generalization can lead to new and robust heuristics that perform better than the original heuristics across test cases of different characteristics.

Keywords: Generalization, genetics-based learning, heuristics, machine learning, probability of win.

1 Introduction

Heuristics or heuristic methods (HMs), in general terms, are "Strategies using readily accessible though loosely applicable information to control problem-solving processes in human beings and machines" [1]. They exist as problem solving procedures in problem solvers to find (usually) suboptimal solutions for many engineering ap-
lications. Since their design depends on user experience and is rather ad hoc, it is desirable to acquire them automatically by machine learning.

We make the following assumptions in this paper. First, we assume that the applications are knowledge-lean, implying that domain knowledge for credit assignment is missing. In this class of applications, we are interested to learn and generalize performance-related HMs whose goal is to find solutions with the best numerical performance. Examples of targeted HMs and applications include symbolic formulae for decision making in a branch-and-bound search and a set of numerical parameters used in a simulated annealing package for placement and routing of VLSI circuits. (See Section 4).

Second, we assume that performance of a HM is characterized by one or more statistical metrics and is obtained by evaluating multiple test cases (noisy evaluations). We further assume that a HM may have different performance distributions across different subsets of test cases in the problem space, thereby disallowing the use of performance metrics such as the average. For example, in testing two heuristic methods $H M_1$ and $H M_2$ on two subsets of test cases $T C_1$ and $T C_2$, we find the average performance for $H M_1$ to be $\{10, 100\}$ and for $H M_2$ to be $\{150, 5\}$. It will be difficult to say whether $H M_1$ is better than $H M_2$ and which HM should be used as a general HM for all test cases in the problem domain.

Third, we assume that heuristics used in generalization are learned by a genetics-based learning method [9, 10]. This is a form of learning by induction that involves applying genetic algorithms [11] to machine learning problems. There are two steps involved in this learning method:

- **Generation and selection** of HMs that can better solve test cases used in learning, as compared to the best existing (baseline) HMs;

- **Generalization** of the selected HMs to test cases not seen in learning with the same high level of performance as compared to that of the baseline HMs.

As illustrated in Figure 1, these two steps are generally separated in genetics-based learning.

In this paper, we study statistical generalization of HMs across test cases of an application with different performance distributions. Generalization is important because learning time is often limited, and only a small set of test cases can be evaluated during learning. Generalization in many existing genetics-based learning systems [10, 11, 13] is a post-learning verification phase that simply verifies the generalizability of the learned HMs by evaluating them on a new set of test cases. This approach is suitable when test cases used in learning are representatives of all the test cases targeted by the HM. When test cases used in generalization have different characteristics, the HMs learned cannot be generalized.

To compare HMs bearing different performance distributions across different subsets of test cases in an application, we need to develop a performance metric that is independent of the actual distributions. We propose in this paper a new metric called probability of win that measures the probability that a particular HM is better than another randomly chosen HM from a set of learned HMs for a given subset of test cases. Since probabilities are between 0 and 1, we eliminate the dependence of HMs on actual performance distributions. Using this metric, we

\[1\] Figure 1. Learning a heuristic method

can verify whether performance distributions are independent (i.i.d.).

- **Partitioning** of multiple test cases that do not meet certain conditions.

This paper focuses on partitioning in probability of win and results on four routing, branch and circuit problems are given in Section 5.

## 2 Problem Statement

Given an application in learning and development, a unique HM can be acquired, and is generally a combinatorial circuit.

For instance, circuits. Previous methods are different from the combinatorial circuit
can verify whether a HM is generalizable across test cases of different performance distributions. Our approach can be summarized as follows:

- Partition the domain of test cases into subdomains in such a way that performance values in a subdomain are independent and identically distributed (i.i.d.).
- Develop conditions under which a HM can be considered to perform well across multiple subdomains. In contrast to studies in artificial intelligence [12], we do not modify a HM in order to generalize it across subdomains. Rather, we test certain conditions to see if a HM is generalizable.

This paper is divided into five sections. Section 2 defines problem space and its partitioning into subdomains. We propose in Section 3 a new metric called probability of win and a new generalization strategy. Section 4 reports our experimental results on four real-world applications — circuit testing, VLSI cell placement and routing, branch-and-bound search and blind equalization. Conclusions are drawn in Section 5.

2 Problem Domains and Subdomains

Given an application problem consisting of a collection of test cases, the first task in learning and generalization is to classify the test cases into domains such that a unique HM can be designed for each [14]. This classification step is domain specific and is generally carried out by experts in the area.

For instance, consider the problem of generating test patterns to test VLSI circuits. Previous experience shows that sequential circuits require tests that are different from those of combinatorial circuits. Consequently, we can consider combinatorial circuits and sequential circuits as two different problem domains.
In comparing the performance of HMs in a problem domain, it is necessary to aggregate their performance values into a small number of performance metrics (such as average or maximum). Computing these aggregate metrics is not meaningful when performance values are of different ranges and distributions across different subsets of test cases in the domain. In this case, we need to decompose the domain into smaller partitions so that quantitative comparison of performance of HMs in a partition is possible. We define a problem subdomain as a partitioning of the domain of test cases such that performance values of a HM in a subdomain are i.i.d. Under this condition, it is meaningful to compute the average performance of test cases in a subdomain. It is important to point out that performance values may need to be normalized with respect to those of the baseline HM before aggregated.

We need to know the attributes of an application in order to classify its test cases, and a set of decision rules to identify the subdomain to which a test case belongs. For example, in learning new decomposition HMs in a branch-and-bound search for solving a traveling-salesman problem (Section 4), we can treat graph connectivity as an attribute to classify graphs into subdomains.

In some applications, it may be difficult to determine the subdomain to which a test case belongs. This is true because the available attributes may not be well defined or may be too large to be useful. For instance, in test-pattern generation for sequential circuits, there are many attributes that can be used to characterize circuits (such as length of the longest path and maximum number of fan-in’s and fan-out’s). However, none of these attributes is a clear winner.

When we do not know the attributes to classify test cases into subdomains, we can treat each test case as a subdomain by itself. This works well when the HM to be learned has a random component: by using different random seeds in the HM, we can obtain statistically valid performance values of the HM on a test case. We have used this approach in the two circuit-related applications discussed in Section 4 and have chosen each circuit as an independent subdomain for learning.

After applying learning to find good HMs for each subdomain, we need to compare their performance across subdomains. This may be difficult because test cases in different subdomains of a domain may have different performance distributions, even though they can be evaluated by a common HM. As a result, the performance of test cases cannot be compared statistically. For instance, we cannot use the average metric when performance values are dependent or have multiple distributions.

As an example, Table 1 shows the average and maximum fault coverages of two HMs used in a test-pattern generator to test sequential circuits. The data indicate that we cannot average their fault coverages across the two circuits as the performance distribution of $HM_{101}$ across the two circuits is not the same as that of $HM_{535}$.

It should now be clear that there can be many subdomains in an application, and learning can only be performed on a small number of them. Consequently, it is important to generalize HMs learned for a small number of subdomains to unlearned subdomains. In some situations, multiple HMs may have to be identified and applied together at a higher cost to find a high quality solution.

### 3 Generalization

Since learning HMs to generalize HMs learned in learning a domain, we used in learning a new domain, as illustrated in Section 4. As a result, different performance across subdomains would be observed. Normalization helps to solve this problem, by normalizing the performance across subdomains.

The goal is to know which subdomain an HM performs best on, compared to the baseline HM.

- How to generalize a HM learned on an independent subdomain and get it to work on another independent subdomain?

- How to choose the best subdomain?

Our method of choice is a method that selects the subdomain with the highest probability of success. This method is more likely to pick a good subdomain. However, it is more likely to pick a subdomain with the highest probability of success.
Table 1. Maximum and average fault coverages of two HMs used in a test-pattern generator with different random seeds.

<table>
<thead>
<tr>
<th>Circuit</th>
<th>HM</th>
<th>Maximum FC</th>
<th>Average FC</th>
</tr>
</thead>
<tbody>
<tr>
<td>S444</td>
<td>101</td>
<td>60.3</td>
<td>28.5</td>
</tr>
<tr>
<td></td>
<td>535</td>
<td>86.3</td>
<td>84.8</td>
</tr>
<tr>
<td>S1196</td>
<td>101</td>
<td>94.9</td>
<td>94.2</td>
</tr>
<tr>
<td></td>
<td>535</td>
<td>93.6</td>
<td>93.1</td>
</tr>
</tbody>
</table>

3 Generalization of Heuristic Methods Learned

Since learning can only cover a small subset of a problem space, it is necessary to generalize HMs developed to test cases not studied in learning. When test cases used in learning have the same performance distribution as those used in generalization, generalization simply involves verifying the performance results. However, as illustrated in the last section, test cases used in generalization may have different performance distribution for two reasons: (a) A learned HM has different performance distributions across subdomains. (b) The baseline HM used in normalisation has different performance distributions across subdomains. In either case, performance values after normalisation will have different distributions across subdomains. This leads us to develop a generalization strategy that can compare HMs across different subdomains with different performance distributions.

The goal of generalisation is somewhat vague: we like to find one or more HMs that perform well most of the time across multiple subdomains as compared to the baseline HM (if it exists). To achieve this goal, two issues are apparent here:

- How to compare the performance of HMs within a subdomain in a range-independent and distribution-independent fashion? Here, we need to evaluate and generalise the performance of a HM in a single subdomain in a range-independent and distribution-independent way.

- How to define the notion that one HM performs well across multiple subdomains?

Our method to address these two issues involves a new metric called probability of win. Informally, probability of win is a range-independent metric that evaluates the probability that the true mean performance of a HM in one subdomain is better than the true mean performance of another randomly selected HM in the same subdomain. It is important to point out that the HMs used in computing the probability of win are found by learning; hence, they already perform well within a subdomain. Further, probabilities of win are in the range zero to one, independent of the number of HMs evaluated and the distribution of performance values.
3.1. Performance Evaluation within a Subdomain

There are many ways to address the first issue raised above, and solutions to the second issue depend on the solution to the first. For instance, scaling and normalization of performance values is a possible way to compare performance in a distribution-independent manner; however, this may lead to new inconsistencies [9]. Another way is to rank HMs by their performance values and use the average ranks of HMs for comparison. This does not work well because it does not account for actual differences in performance values, and two HMs with very close or very different performance may differ only by one in their ranks. Further, the maximum rank of HMs depends on the number of HMs evaluated, thereby biasing the average ranks of individual HMs. In this section, we propose a metric called probability of win to select good HMs within a subdomain.

\[ P_{\text{win}}(h_i, d_m) = \sum_{j \neq i} P \left[ \mu_i^m > \mu_j^m \mid \tilde{\mu}_i^m, \tilde{\sigma}_i^m, n_i^m, \tilde{\mu}_j^m, \tilde{\sigma}_j^m, n_j^m \right] / |s| - 1, \]

where \( |s| \) is the number of HMs under consideration, and \( n_i^m, \tilde{\sigma}_i^m, \tilde{\mu}_i^m, \) and \( \mu_i^m \) are, respectively, the number of tests, sample standard deviation, sample mean, and true mean of \( h_i \) in \( d_m \).

Since we are using the average performance metric, it is a good approximation to use the normal distribution as a distribution of the sample average. The probability that \( h_i \) is better than \( h_j \) in \( d_m \) can now be computed as follows.

\[ P \left[ \mu_i^m > \mu_j^m \mid \tilde{\mu}_i^m, \tilde{\sigma}_i^m, n_i^m, \tilde{\mu}_j^m, \tilde{\sigma}_j^m, n_j^m \right] \approx \Phi \left( \frac{\tilde{\mu}_i^m - \tilde{\mu}_j^m}{\sqrt{\tilde{\sigma}_{i^m}^2/n_i^m + \tilde{\sigma}_{j^m}^2/n_j^m}} \right), \]

where \( \Phi(z) \) is the cumulative distribution function for the \( N(0, 1) \) distribution.

To illustrate the concept, we show in Table 2 the probabilities of win of four HMs tested to various degrees. Note that \( P_{\text{win}} \) is not only related to the sample mean but also depends on the sample variance and number of tests performed. Further, the probability that \( h_i \) is better than \( h_j \) and the probability that \( h_j \) is better than \( h_i \) are both counted in the evaluation. Hence, the average of \( P_{\text{win}} \) over all HMs in a subdomain (\( = \sum_i P_{\text{win}}(h_i, d_m) / |s| \)) will be 0.5.

\( P_{\text{win}} \) defined in (3.1) is range-independent and distribution-independent because all performance values are transformed into probabilities between 0 and 1 independent of the number of HMs evaluated and the distribution of performance values. It assumes that all HMs are i.i.d. and takes into account uncertainty in their sample averages (by using their variances); hence, it is better than simple scaling that only compresses performance averages into a range between 0 and 1. It is also important

\[ \text{Table 2:} \]

<table>
<thead>
<tr>
<th>HM</th>
<th>Probability of Win</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>0.5</td>
</tr>
<tr>
<td>B</td>
<td>0.5</td>
</tr>
<tr>
<td>C</td>
<td>0.5</td>
</tr>
<tr>
<td>D</td>
<td>0.5</td>
</tr>
</tbody>
</table>

Note: Table 2 shows the probabilities of win for four HMs (A, B, C, and D) when evaluated within a subdomain.

3.2. Summary

One of the difficulties of the method is that it is not possible to easily find a subdomain. In the future, we plan to extend the method to a partial database, where subdomains from two or more databases may be used. In the last subsection, we will discuss the implementation of this method.

Second, the selection of HMs for each subdomain is not done in a consistent way. One way to select HMs is to use a probabilistic method, but this may lead to the selection of suboptimal HMs. Another way is to use a statistical method, which is not feasible for large databases.

Here, \( \delta \) is a constraint on the number of HMs included in each subdomain. 

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Due to space limitation, we do not consider issues dealing with multiple performance measures in this paper.
Table 2. Probabilities of win of four HMs in \(d_m\).

<table>
<thead>
<tr>
<th>(h_i)</th>
<th>(\bar{\mu}_i)</th>
<th>(\bar{\sigma}_i)</th>
<th>(n_i)</th>
<th>(P_{\text{win}}(h_i, d_m))</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>43.2</td>
<td>13.5</td>
<td>10</td>
<td>0.4787</td>
</tr>
<tr>
<td>2</td>
<td>46.2</td>
<td>6.4</td>
<td>12</td>
<td>0.7976</td>
</tr>
<tr>
<td>3</td>
<td>44.9</td>
<td>2.5</td>
<td>10</td>
<td>0.6006</td>
</tr>
<tr>
<td>4</td>
<td>33.6</td>
<td>25.9</td>
<td>8</td>
<td>0.1231</td>
</tr>
</tbody>
</table>

to point out that the HMs used in computing \(P_{\text{win}}\) are found by learning; hence, they already perform well within a subdomain.

3.2. Performance Evaluation across Subdomains

One of the major difficulties in handling multiple subdomains is that it may be difficult to aggregate performance values statistically from different subdomains, and to define the notion that one HM performs better than another across multiple subdomains. For instance, it is not meaningful to find an average of random numbers from two different distributions. We address this problem using \(P_{\text{win}}\) defined in the last subsection.

First, we assume that when HM \(h\) is applied over multiple subdomains in partition \(\Pi_p\) of subdomains, all subdomain are equally likely. Here, we compute \(P_{\text{win}}\) of \(h\) over subdomains in \(\Pi_p\) as the average \(P_{\text{win}}\) of \(h\) over all subdomains in \(\Pi_p\).

\[
P_{\text{win}}(h, \Pi_p) = \frac{\sum_{d \in \Pi_p} P_{\text{win}}(h, d)}{|\Pi_p|},
\]

where \(\Pi_p\) is the \(p\)'th partition of subdomains in the problem domain. The HM picked is the one that maximizes (3.2). When subdomains are not equally likely but with known relative weights, we can compute \(P_{\text{win}}\) as a weighted average instead of (3.2). HMs picked using 3.2 generally wins with a high probability across most of the subdomains in \(\Pi_p\) but occasionally may not perform well in a few subdomains.

Second, we consider the problem of finding a good HM across multiple subdomains in \(\Pi_p\) as a multi-objective optimization problem. In this case, evaluating HMs based on a combined objective function (such as the average \(P_{\text{win}}\) in (3.2) may lead to inconsistent conclusions. To alleviate such inconsistencies, we should treat each subdomain independently and find a common HM across all subdomains in \(\Pi_p\) satisfying some common constraints. For example, let \(\delta\) be the allowable deviation of \(P_{\text{win}}\) of any chosen HM from \(q_{\text{win}}^m\), the maximum \(P_{\text{win}}\) in subdomain \(m\). Generalization, therefore, amounts to finding \(h\) that satisfies the following constraints for every subdomain \(m \in \Pi_p\).

\[
P_{\text{win}}(h, m) \geq (q_{\text{win}}^m - \delta) \quad \forall m \in \Pi_p
\]

Here, \(\delta\) may need to refined if there are too many or too few HMs satisfying the constraints.
Figure 2. $P_{\text{win}}$ of six HMs across five subdomains in the test-pattern generation problem.

To illustrate the generalization procedure, consider the test-pattern generation problem discussed in Section 2. Assume that learning had been performed on five circuits (subdomains), and that the six best HMs from each subdomain were reported. After full evaluation of the 30 HMs (initialised by ten random seeds) across all five subdomains, we computed $P_{\text{win}}$ of each HM in every subdomain. Figure 2 shows the probabilities of win of six of these HMs. If we generalise HMs based on (3.2), then $HM_{15}$ will be picked since it has the highest average $P_{\text{win}}$. Likewise, if we generalise using (3.3), we will also select $HM_{15}$. Note that in this example, no one HM is the best across all subdomains.

4 Experimental Results

To illustrate the generalization procedure described in Section 3, we present in this section results on generalization for two applications in VLSI design and branch-and-bound search. These results were obtained using TEACHER [9], a genetics-based learning system that implements our proposed generalization strategy. The parameters used during learning are shown in Table 3.

4.1. HM for Sequential Circuit Testing

The first application is based on CRIS [15], a genetic-algorithm software package for generating patterns to test sequential VLSI circuits. CRIS mutates an input test sequence continuously and analyses the mutated vectors in selecting a test set. Since many copies of a circuit may be manufactured, it is desirable to obtain as high a fault coverage as possible, and computational cost is of secondary importance.
Table 3. Genetic-algorithm parameters used in our learning system. (# HMs Verified at Termination is the number of HMs selected for verification at the end of the last generation)

<table>
<thead>
<tr>
<th>Application</th>
<th>CRIS</th>
<th>Timber-Wolf</th>
<th>Branch-and-Bound</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Generations</td>
<td>10</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>Duration of a Generation</td>
<td>100</td>
<td>100</td>
<td>160</td>
</tr>
<tr>
<td># Active HMs in each Gen.</td>
<td>30</td>
<td>30</td>
<td>40</td>
</tr>
<tr>
<td>New HMs Generated in each Gen.</td>
<td>20</td>
<td>20</td>
<td>30</td>
</tr>
<tr>
<td>Crossover Rate</td>
<td>0.45</td>
<td>0.45</td>
<td>0.5</td>
</tr>
<tr>
<td>Mutation Rate</td>
<td>0.35</td>
<td>0.35</td>
<td>0.17</td>
</tr>
<tr>
<td>Random Generation Rate</td>
<td>0.20</td>
<td>0.20</td>
<td>0.33</td>
</tr>
<tr>
<td># HMs Verified at Termination</td>
<td>20</td>
<td>20</td>
<td>20</td>
</tr>
</tbody>
</table>

In our experiments, we used sequential circuits from the ISCAS89 benchmarks [16] plus several other larger circuits. We treat each circuit as an individual subdomain. Since we want one common HM for all circuits, we assume that all circuits are from one domain.

CRIS in our experiments is treated as a black-box problem solver, as we have minimal knowledge in its design. A HM targeted for improvement is a set of eight parameters used in CRIS (Table 4). Note that parameter $P_8$ is a random seed, implying that CRIS can be run multiple times using different random seeds in order to obtain better fault coverages. (In our experiments, we used a fixed sequence of ten random seeds.) Our goal is to develop one common HM that can be applied across all the benchmark circuits and that has similar or better fault coverages as compared to those of the original CRIS. Note that in the original CRIS, the HM used for each circuit is unique and was tuned manually. The advantage of having one HM is that it can be applied to new circuits without further manual tuning.

In our experiments on CRIS, we chose five circuits as our learning subdomains. In each of these subdomains, we used TEACHER [9] to test CRIS 1000 times (divided into 10 generations) with different HMs. A HM in learning is represented as a tuple of the first seven parameters in Table 4. At the end of learning, we picked the top twenty HMs in each subdomain and evaluated them fully by initializing CRIS using ten different random seeds ($P_8$ in Table 4). We then selected the top five HMs from each subdomain, resulting in a total of 25 HMs supplied to the generalization phase. We evaluated the 25 HMs fully (each with 10 random seeds) on the five subdomains used in learning and five new subdomains. We then selected one generalized HM to be used across all the ten circuits (based on (3.2)). The HM found is shown in the last column in Table 4.

Table 5 summarizes the improvements of our learned and generalized HMs as compared to the published results of CRIS [15] and HITEC [17]. Each entry of the table shows the number of times our HM wins and ties in terms of fault coverage with respect to the method(s) in the first column. Note that the maximum fault coverages reported in Table 5 were based on ten runs of the underlying problem solver, implying that the computational cost is ten times of the average cost. Recall
Table 4. Parameters in CRIS treated as a HM in learning and in generalisation. (The type, range, and step of each parameter were given to us by the designer of CRIS. The default parameters were not given to us as they are circuit-dependent.)

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Range</th>
<th>Step</th>
<th>Definition</th>
<th>New Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>$P_1$</td>
<td>1-10</td>
<td>1</td>
<td>related to the number of stages in a flip flop</td>
<td>1</td>
</tr>
<tr>
<td>$P_2$</td>
<td>1-40</td>
<td>1</td>
<td>sensitivity of state change of a flip flop</td>
<td>12</td>
</tr>
<tr>
<td>$P_3$</td>
<td>1-40</td>
<td>1</td>
<td>survival rate of a test sequence in next generation</td>
<td>38</td>
</tr>
<tr>
<td>$P_4$</td>
<td>0.1-10.0</td>
<td>0.1</td>
<td>number of test vec. concat. to form a new vec.</td>
<td>7.06</td>
</tr>
<tr>
<td>$P_5$</td>
<td>50-800</td>
<td>10</td>
<td>number of useless trials before quitting</td>
<td>623</td>
</tr>
<tr>
<td>$P_6$</td>
<td>1-20</td>
<td>1</td>
<td>number of generations</td>
<td>1</td>
</tr>
<tr>
<td>$P_7$</td>
<td>0.1-1.0</td>
<td>0.1</td>
<td>how genes are spliced in GA</td>
<td>0.1</td>
</tr>
<tr>
<td>$P_8$</td>
<td>Integer</td>
<td>1</td>
<td>seed for random number generator</td>
<td>-</td>
</tr>
</tbody>
</table>

Table 5. Summary of results comparing the performance of our generalised HMs with respect to those of HITEC and CRIS. (The first number in each entry shows the number of wins out of 21 circuits, and the second, the number of ties.)

<table>
<thead>
<tr>
<th>Our HM wins/ties with respect to the following</th>
<th>CRIS Generalised HM</th>
</tr>
</thead>
<tbody>
<tr>
<td>HITEC</td>
<td>Max. FC 4,</td>
</tr>
<tr>
<td>CRIS</td>
<td>Avg. FC 11,</td>
</tr>
<tr>
<td>Both HITEC and CRIS</td>
<td></td>
</tr>
</tbody>
</table>

that we like to obtain the maximum coverage of a circuit, and that computational cost is a secondary issue in circuit testing.

Our results show that our generalisation procedure can discover new HMs that are better than the original HMs in 16 out of 21 circuits in terms of the maximum fault coverage, and in 11 out of 21 circuits in terms of the average fault coverage. Our results are significant in the following aspects:

- new faults detected by our generalised HMs were not discovered by previous methods;
- only one HM (rather than many circuit-dependent HMs in the original CRIS) was found for all circuits.

Table 5 also indicates that HITEC is still better than our new generalised HM for CRIS in most of the circuits (in 14 out of 21 in term of the maximal fault coverage, and in 17 out of 21 in term of the average fault coverage). This happens because our generalisation procedure treats CRIS as a HM, whereas HITEC HMs in our baseline test were not.

4.2. Temperature
In our study, we used a software tool called HITEC circuit tester. While some HITEC settings were ideal for our purposes, and they have a limited ability to tolerate a software bug, we used a different approach for our experiments. Although the probability of using a software bug is quite low, we found that it would be better to use an approach that is more likely to cover all possible settings.

Although the probability of using a software bug is quite low, we found that it would be better to use an approach that is more likely to cover all possible settings.

Time and temperature
Many parameters are settings for the software tools. Our goal was to illustrate that we could improve the performance of the circuit tester despite the software bug.

In our experiments, we used a primary circuit that was provided by the University of California, Berkeley. We used the same tools, but we set the temperature to a different value for each experiment.

We used a set of 11 parameters, $P_1$ to $P_{11}$, for each experiment. Each parameter was set to a different value, and the software bug (or temperature) was set to be different for each experiment. We also used a set of 11 parameters, $P_1$ to $P_{11}$, for each experiment. Each parameter was set to a different value, and the software bug (or temperature) was set to be different for each experiment.
our generalized HM is bounded by the limitations in CRIS and our HM generator for CRIS. Such limitations cannot be overcome without generating more powerful HMs in our HM generator or using better test-pattern generators like HITEC as our baseline problem solver.

4.2. HM for VLSI Placement and Routing

In our second application, we use TimberWolf [18] as our problem solver. This is a software package based on simulated annealing (SA) [19] to place and route various circuit components on a piece of silicon. Its goal is to minimize the chip area needed while satisfying constraints such as the number of layers of poly-silicon for routing and the maximum signal delay through any path. Its operations can be divided into three steps: placement, global routing, and detailed routing.

The placement and routing problem is NP-hard; hence, heuristics are generally used. SA used in TimberWolf is an efficient method to randomly search the space of possible placements.

Although in theory SA converges asymptotically to the global optimum with probability one, the results generated in finite time are usually suboptimal. Consequently, there is a trade-off between the quality of a result and the cost (or computational time) of obtaining it. In TimberWolf version 6.0, the version we have studied, there are two parameters to control the running time (which indirectly control the quality of the result): fast-n and slow-n. The larger the fast-n is, the shorter time SA will run. In contrast, the larger the slow-n is, the longer time SA will run. Of course, only one of these parameters can be used at any time.

TimberWolf has six major components: cost function, generate function, initial temperature, temperature decrement, equilibrium condition, and stopping criterion. Many parameters in these components have been tuned manually. However, their settings are generally heuristic because we lack domain knowledge to set them optimally. In Table 6, we list the parameters we have focused in this study. Our goal is to illustrate the power of our learning and generalization procedures and to show improved quality and reduced cost for the placement and routing of large circuits, despite the fact that only small circuits were used in learning.

In our experiments, we used seven benchmark circuits [20] (s298, s420, fract, primary1, struct, primary2, industrial2) that were mostly from ftp.mncn.org in /pub/benchmark. We studied only the standard-cell placement problem, noting that other kinds of placement can be studied in a similar fashion. We used fast-n values of 1, 5, and 10, respectively.

We first applied TEACHER to learn good HMs for circuits s298 with fast-n of 1, s420 with fast-n of 5, and primary1 with fast-n of 10, each of which was taken as a learning subdomain. We used a fixed sequence of ten random seeds (P11 in Table 6) in each subdomain to find the statistical performance of a HM. Each learning experiment involved 1000 applications of TimberWolf divided into ten generations. Based on the best 30 HMs (10 from each subdomain), we applied our generalization procedure to obtain one generalized HM. This generalized HM as well as the default HM are shown in Table 6.

Figure 3 plots the quality (higher quality in the y-axis means reduced chip area
averaged over 10 runs using the defined random seeds) and cost (average execution
time of TimberWolf) between the generalised HM and the default HM on all seven
circuits with fast-n of 1, 5, and 10, respectively. Note that all performance values
in Figure 3 are normalised with respect to those of fast-n of 10, and that the
positive (resp., negative) portion of the z-axes shows the fractional improvement
(resp., degradation) in computational cost with respect to the baseline HM using
fast-n of 10 for the same circuit. Each arrow in this figure points from the average
performance of the default HM to the average performance of the generalised HM.

The equation for computing the normalised symmetric cost is as follows. Let
$C_{new}$, $C_{base}$ and $C_{norm}$ be, respectively, the costs of the new HM, the cost of
the baseline HM, and the normalised symmetric cost.

$$C_{norm}^{sym} = \begin{cases} 
\frac{C_{base}}{C_{new}} - 1 & \text{if } C_{new} \geq C_{base} \\
1 - \frac{C_{base}}{C_{new}} & \text{if } C_{new} < C_{base}
\end{cases} \quad (4.4)$$

The reason for using the above equation is to avoid uneven compression of the ratio

---

Table 6. Parameters in TimberWolf (Version 6) used in the original HM and after learning
and generalisation.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Range</th>
<th>Step</th>
<th>Meaning</th>
<th>Original</th>
<th>New</th>
</tr>
</thead>
<tbody>
<tr>
<td>$P_1$</td>
<td>0.1 - 2.5</td>
<td>0.1</td>
<td>vertical path weight for estimating the cost function</td>
<td>1.0</td>
<td>0.958</td>
</tr>
<tr>
<td>$P_2$</td>
<td>0.1 - 2.5</td>
<td>0.1</td>
<td>vertical wire weight for estimating the cost function</td>
<td>1.0</td>
<td>0.232</td>
</tr>
<tr>
<td>$P_3$</td>
<td>3 - 10</td>
<td>1</td>
<td>orientation ratio</td>
<td>6</td>
<td>10</td>
</tr>
<tr>
<td>$P_4$</td>
<td>0.33 - 2.0</td>
<td>0.1</td>
<td>range limiter window change ratio</td>
<td>1.0</td>
<td>1.30</td>
</tr>
<tr>
<td>$P_5$</td>
<td>10.0 - 35.0</td>
<td>1.0</td>
<td>high temperature finishing point</td>
<td>23.0</td>
<td>10.04</td>
</tr>
<tr>
<td>$P_6$</td>
<td>50.0 - 99.0</td>
<td>1.0</td>
<td>intermediate temperature finishing point</td>
<td>81.0</td>
<td>63.70</td>
</tr>
<tr>
<td>$P_7$</td>
<td>100.0 - 150.0</td>
<td>1.0</td>
<td>low temperature finishing point</td>
<td>125.0</td>
<td>125.55</td>
</tr>
<tr>
<td>$P_8$</td>
<td>130.0 - 180.0</td>
<td>1.0</td>
<td>final iteration temperature</td>
<td>155.0</td>
<td>147.99</td>
</tr>
<tr>
<td>$P_9$</td>
<td>0.29 - 0.59</td>
<td>0.01</td>
<td>critical ratio that determines acceptance probability</td>
<td>0.44</td>
<td>0.333</td>
</tr>
<tr>
<td>$P_{10}$</td>
<td>0.01 - 0.12</td>
<td>0.01</td>
<td>temperature for controller turn off</td>
<td>0.06</td>
<td>0.112</td>
</tr>
<tr>
<td>$P_{11}$</td>
<td>integer</td>
<td>1</td>
<td>seed for the random number generator</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>
Figure 3. Comparison of normalized average performance between the default and the generalized HMs. The plots are normalized with respect to the performance of applying the baseline HM on each circuit using fast-n = 10. (See (4.4)).

$C_{new}/C_{base}$. This ratio is between 0 and 1 when $C_{new} < C_{base}$, but is between 1 and $\infty$ when $C_{new} > C_{base}$. (4.4) allows increases in cost to be normalized in the range between 0 and $\infty$, and decreases to be normalized in the range between 0 and $-\infty$. The normalized symmetric quality in the y-axis is computed in a similar way.

Among the 21 test cases, the generalized HM has worse quality than that of the default in only two instances, and has worse cost in 4 out of 21 cases. We see in Figure 3 that most of the arrows point in a left-upward direction, implying improved quality and reduced cost. Note that these experiments are meant to illustrate the power of our generalization procedure. We expect to see more improvement as we learn other functions and parameters in TimberWolf. Further, improvements in TimberWolf are important as the system is actually used in industry.

4.3. Branch-and-Bound Search

A branch-and-bound search algorithm is a systematic method for traversing a search tree or search graph in order to find a solution that optimizes a given objective while satisfying the given constraints. It decomposes a problem into smaller subproblems and repeatedly decomposes them until a solution is found or infeasibility is proved. Each subproblem is represented by a node in the search tree/graph.

The algorithm has four sets of HMs: (a) Selection HM for selecting a search node for expansion based on a sequence of selection keys for ordering search nodes; (b) Decomposition HM (or branching mechanism) for expanding a search node into
Table 7. Generation of test cases for learning and generalization of decomposition HMs in a branch-and-bound search (each has 12 subdomains).

<table>
<thead>
<tr>
<th>Application</th>
<th>Subdomain Attributes</th>
</tr>
</thead>
</table>
| VC          | • Connectivity of vertices is \((0.05 - 0.6)\) with step size 0.05  
             | • Number of vertices is between 16 and 45 |
| TSP         | • Distributions of 8-18 cities \((U(0,100)\) on both X and Y axes,  
             | \(N(50,12.5)\) on both axes, or \(U(0,100)\) and \(N(50,12.5)\) on different axes)  
             | • Graph connectivity of cities is \((0.1, 0.2, 0.3, \text{or} 1.0)\) |
| KS          | • Range of both profits and weights is \{(100-1000), (100-200), (100-105)\}  
             | • \(\sigma^2\) of profit/weight ratio is \(1.05, 1.5, 10, 100\)  
             | • 13-60 objects in the knapsack |

descendants using operators to expand (or transform) a search node into child nodes;  
(c) \textit{Pruning HM} for pruning inferior nodes in order to trim potentially poor subtrees;  
and (d) \textit{Termination HM} for determining when to stop. In this subsection, we apply learning to find new decomposition HMs for expanding a search node into descendants.

We illustrate our method on three applications: traveling salesman problem (TSP) on incompletely connected graphs mapped on a two-dimensional plane, vertex-cover problem (VC), and knapsack problem (KS). The second problem can be solved by a polynomial-time approximation algorithm with guaranteed performance deviations from optimal solutions, and the last can be solved by a pseudo polynomial-time approximation algorithm. Hence, we expect that improvements due to learning are likely for the first two problems and not likely for the last. Table 7 shows the parameters used in generating a test case in each application. We assume that each problem constitutes one domain.

The problem solver here is a branch-and-bound algorithm, and a test case is considered solved when its optimal solution is found. Note that the decomposition HM studied is only a component of the branch-and-bound algorithm.

We have used well-known decomposition HMs developed for these applications as our baseline HMs (see Table 8). The normalized cost of a candidate decomposition HM is defined in terms of its average symmetric speedup (see (4.4)), which is related to the number of nodes expanded by a branch-and-bound search using the baseline HM and that using the new HM. Note that we do not need to measure quality as both the new and existing HMs when applied in a branch-and-bound search look for the optimal solution.

In our experiments, we selected six subdomains in each application for learning. We performed learning in each subdomain using 1,600 tests, selected the top five HMs in each subdomain, fully verified them on all the learned subdomains, and selected one final HM to be used across all the subdomains. (See (3.2).) Table 9 summarizes the generalization and validation results.

We show in our results the average symmetric speedup of the top HM learned in each subdomain as the ratio of the average speedup times required to find the best solution that a new HM found in its average of all subdomains.

Table 8. On-line decomposition HMs.  
\((l:\) number of neighbors; \((U, N)\): current parameter used; \(\sigma^2: \) weight of optimal solution in each subdomain.

Table 8. Original and generalised decomposition HMs used in a branch-and-bound search

\( (l): \) number of uncovered edges or live degree of a vertex; \( n \): average live degree of all

neighbors; \( \Delta l \): difference between \( l \) of parent node and \( l \) of current node; \( c \): length of
current partial tour; \( m \): minimum length to complete current tour; \( p \): profit of object; \( w \):
weight of object).

<table>
<thead>
<tr>
<th>Application</th>
<th>Original HM</th>
<th>Generalized HM</th>
</tr>
</thead>
<tbody>
<tr>
<td>VC</td>
<td>( l )</td>
<td>( 1000 l + n - \Delta l )</td>
</tr>
<tr>
<td>TSP</td>
<td>( c )</td>
<td>( m c )</td>
</tr>
<tr>
<td>KS</td>
<td>( p/w )</td>
<td>( p/w )</td>
</tr>
</tbody>
</table>

Each subdomain and the normalized cost of learning, where the latter was computed as the ratio of the total CPU time for learning and the harmonic mean of the CPU
times required by the baseline HM on test cases used in learning. The results show that a new HM learned specifically for a subdomain has around 1-35% improvement
in its average symmetric speedups and 3,000-16,000 times in learning costs.

Table 9 also shows the average symmetric speedups of the generalised HMs. We
picked six subdomains randomly for learning. After learning and fully verifying the
five top HMs in each subdomain, we applied (3.2) to identify one top HM to be
used across all the twelve subdomains. Our results show that we have between 0-8% improvement in average symmetric speedups using the generalised HMs. Note that
these results are worse than those obtained by learning. Moreover, the baseline HM
is the best HM for solving the knapsack problem.

The second part of Table 9 shows the average symmetric speedups when we
validate the generalised HMs on larger test cases. These test cases generally require
10-50 times more nodes expanded than those used earlier. Surprisingly, our results show better improvement (9.23%). It is interesting to point out that six of the
twelve subdomains with high degree of connectivity in the vertex-cover problem have slowdowns. This is a clear indication that these subdomains should be grouped
in a different domain and learned separately.

Table 8 shows the new decomposition HMs learned for the three applications that
lists the variables used in the HMs. Note that we have included constants in our HMs in learning; an example of which is shown in the HM learned for the
vertex-cover problem. This formula can be interpreted as using \( l \) as the primary key
for deciding which node to include in the covered set. If the \( l \)'s of two alternatives are different, then the remaining terms in the formula \( (n - \Delta l) \) are insignificant. On
the other hand, when the \( l \)'s are the same, then we use \( (n - \Delta l) \) as a tie breaker.

In short, our results show that reasonable improvements can be obtained by
generalization of learned HMs. We anticipate further improvements by

- learning and generalizing new pruning HMs in a depth-first search,
- partitioning the problem space into a number of domains and learning a new
  HM for each, and
- identifying attributes that help explain why one HM performs well in one
  subdomain but not in others.
Table 9. Results of generalization for VC, TSP, and KS. (In the results on generalization, numbers with "*" are the ones learned; only one common HM is generalized to all 12 subdomains.)

<table>
<thead>
<tr>
<th>Subdomain</th>
<th>Subdomain Performance (Sym-SU)</th>
<th>Learning</th>
<th>Generalization</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>VC</td>
<td>TSP</td>
<td>KS</td>
</tr>
<tr>
<td>1</td>
<td>0.218</td>
<td>0.072*</td>
<td>0.000*</td>
</tr>
<tr>
<td>2</td>
<td>0.283*</td>
<td>0.004</td>
<td>0.000*</td>
</tr>
<tr>
<td>3</td>
<td>0.031</td>
<td>0.082*</td>
<td>0.000</td>
</tr>
<tr>
<td>4</td>
<td>0.068*</td>
<td>0.225</td>
<td>0.000</td>
</tr>
<tr>
<td>5</td>
<td>0.054</td>
<td>0.005*</td>
<td>0.000</td>
</tr>
<tr>
<td>6</td>
<td>0.060*</td>
<td>0.061*</td>
<td>0.000*</td>
</tr>
<tr>
<td>7</td>
<td>0.017</td>
<td>0.139</td>
<td>0.000*</td>
</tr>
<tr>
<td>8</td>
<td>0.049*</td>
<td>0.155</td>
<td>0.000</td>
</tr>
<tr>
<td>9</td>
<td>0.016</td>
<td>-0.010</td>
<td>0.000*</td>
</tr>
<tr>
<td>10</td>
<td>-0.000*</td>
<td>0.054</td>
<td>0.000</td>
</tr>
<tr>
<td>11</td>
<td>-0.011</td>
<td>0.090*</td>
<td>0.000</td>
</tr>
<tr>
<td>12</td>
<td>0.028*</td>
<td>0.083*</td>
<td>0.000*</td>
</tr>
<tr>
<td><strong>Average</strong></td>
<td><strong>0.068</strong></td>
<td><strong>0.080</strong></td>
<td><strong>0.000</strong></td>
</tr>
</tbody>
</table>

Table 10. Summary of average symmetric improvements in terms of number of accumulated errors for the learned cost function over ten subdomains. ($b_i$ in Figure 4 is the instantaneous value of $b$.)

<table>
<thead>
<tr>
<th>Average Symmetric Improvement</th>
<th>Original HM</th>
<th>New HM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Average</td>
<td>Std.Dev.</td>
<td>Maximum</td>
</tr>
<tr>
<td>0.153</td>
<td>0.395</td>
<td>0.694</td>
</tr>
</tbody>
</table>

4.4. Blind Equalization

Our last application is on applying genetic algorithms to learn a cost function in blind equalization. Our goal is to minimize the number of accumulated errors for a sequence of input data corrupted in transmission (Figure 4). The process is equivalent to adjusting the weights of an FIR filter using gradient descent in order to minimize the value of a cost function, which is defined in terms of the weights of the filter and its current output.

In this application, we define a test case as multiple random sequences of data of fixed length passing through a fixed channel and a blind equalizer with given random initial weights. We further define a subdomain to be all test cases with the same channel specification. In our experiments, we attempt to cover all possible third-order channels: from relatively easy ones ($|a_i| > \sum_{i \neq j} |a_j|$ where $a_i$ is the $i$-th weight of the channel) to the hardest one ($a_i = a_j$ for all $i$ and $j$).

5 Conclusion

In this paper, we have presented a new heuristic algorithm that may have potential applications in statistical analysis and knowledge discovery. Our experimental results show that the algorithm is effective and efficient.

One of the possible applications may have to do with the study of the effect of the number of subdomains on the performance of the algorithm.

We hope that this paper will stimulate further research in this area and contribute to the development of a new generation of learning algorithms.
Table 10 shows the average symmetric improvements in terms of number of accumulated errors for $H M_{base}$ (CMA 2-2) [21] and the new HM found after learning and generalization.

5 Conclusions

In this paper, we have presented a method for generalizing performance-related heuristics learned by genetics-based learning for knowledge-lean applications. We have focused on a class of heuristic methods (HMs) whose performance is evaluated statistically by applying them on multiple test cases. Due to a lack of domain-knowledge for improving such heuristics, we have used a genetics-based learning paradigm (a generate-and-test method) to learn new HMs.

One of the major problems in performance evaluation of heuristics is that a HM may have different performance distributions across different sets of test cases in an application. This renders it impossible to use statistical metrics, such as average, to compare their performance.

We have proposed in this paper a new metric $c_{H}$ to characterize the performance of heuristics. This metric evaluates the probability that the mean performance of a HM is better than the mean performance of another randomly chosen HM in a set of learned HMs on a common set of test cases. The only requirement on the choice of test cases in evaluating probabilities of win is that each HM, when evaluated on the test cases, produces a set of independent and identically distributed performance results. We define such a set of test cases as a subdomain. Since probabilities of win are between 0 and 1, we can compare them across subdomains in generalizing HMs.

We have developed TEACHER [22], an integrated system that incorporates the learning and generalization method presented in this paper. The system is relatively easy to use: the design of an interface between an application program

\[
y_i = \sum_{j=0}^{n-1} x_{i-j} a_j
\]

Figure 4. Blind equalization process for recovering input data stream for $n$-th order channel and $m$-th order filter.
and TEACHER usually takes less than two weeks to complete.

We have applied TEACHER [9], a genetics-based learning system that incorporates our generalization method, on four engineering applications and found very good improvements over existing HMs. These applications are hard to improve because they have been studied and tuned extensively by many others before. In each case, we have found very good improvements over existing HMs for these applications. These demonstrate that learning and generalization is important in refining heuristics used in many application problem solvers.

Acknowledgments

The authors would like to thank Mr. Yong-Cheng Li for interfacing TEACHER to TimberWolf and for collecting some preliminary results in Section 4.

References


