Comprehensive Isomorphic Subtree Enumeration

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ABSTRACT

A fundamental problem in program analysis and optimization concerns the discovery of structural similarities between different sections of a given program and/or across different programs. Specifically, there is a need to find topologically identical segments within compiler intermediate representations (IRs).

Such topological isomorphism has many applications. For example, finding isomorphic sub-trees within different expression trees points to common computational resources that can be shared when targeting application-specific hardware. Isomorphism in the control-flow graph can be used to discovery of custom instructions for customizable processors. Discovering isomorphism in context call trees during program execution is invaluable to several JIT compiler optimizations. Thus, all these different applications rely on the fundamental ability to find topologically identical segments within a given tree or graph representation.

In this paper, we present a generic formulation of the subtree isomorphism problem that is more powerful than previous proposals. We prove that an optimal quadratic time solution exists for this problem. We employ a dynamic programming based algorithm to efficiently enumerate all isomorphic sub-trees within given reference trees and also demonstrate its efficacy in a production compiler.

Categories and Subject Descriptors

C.3 [**Special-purpose and Application-based Systems**]: Real-time and Embedded Systems

General Terms

Algorithms, Design

Keywords

Subtree Isomorphism, Subtree Matching Algorithm, Embedded Systems

1. INTRODUCTION

Two subgraphs of a given set of graphs can be said to be isomorphic when there is a one-to-one correspondence between their nodes and edges in terms of some chosen attributes. The problem of subgraph isomorphism is quite ubiquitous in the domain of compilers, hardware synthesis and embedded systems. However, this problem is known to be NP-complete [14]. Therefore, in practice, these graphs are transformed into trees by replicating nodes having multiple fanouts in order to obtain a reasonable solution [14, 3]. Thus, the problem of subgraph isomorphism is often translated into the simpler problem of subtree isomorphism.

In the domain of compilers and architectures, the subtree isomorphism problem is known to appear in instruction selection [9], where trees representing ISA instructions are matched against the compiler's intermediate representation (IR). Most IRs are directed acyclic graphs (DAGs) to begin with, but can be converted in to a tree representation. Furthermore, the subtree isomorphism problem can also be effectively applied to common subexpression elimination and code reuse optimizations.

In the hardware synthesis domain, technology mapping [10] is a well-known problem, where tree patterns from a given standard cell library are matched against a given abstract netlist of the hardware circuit. In the domain of behavioral synthesis, resource sharing is an important problem that aims to maximize the use of arithmetic and logic operators like adders or multipliers. However, a more sophisticated approach can be taken whereby an entire subtree pattern, instead of a single operation, is chosen for sharing resources. Finding isomorphic subtrees is useful for all these synthesis-related problems.

In the last few years, application-specific customizable processors of different flavors have been proposed as viable solutions for meeting the rapidly changing demands of applications in embedded systems. One of the key problems in such systems is automatic generation of instruction set extensions (ISEs) [5]. Increasing the effectiveness and reusability of the chosen ISEs requires the identification of isomorphic subtree patterns of instructions in the IR, such that a frequently occuring subtree isomorph can become a custom instruction in the ISE.

Thus, we can see that finding an optimal solution to the subtree isomorphism problem would have a great impact in several domains. In this paper, we propose a novel algorithm to enumerate all isomorphic subtrees occuring within two given trees. We formally prove that the proposed algorithm is optimal in that it is guaranteed to enumerate all subtree matches and that the algorithm has quadratic time and space complexity. This is the main contribution of the paper.

Consider two reference trees (shown in Fig. 1), labeled as T1 and T2. The shaded subtrees in T1 and T2 represent an example of isomorphic subtrees that can be matched. The enumeration process of the isomorphic subtrees must also take care of some key properties of a topological match. First, for some nodes, the children

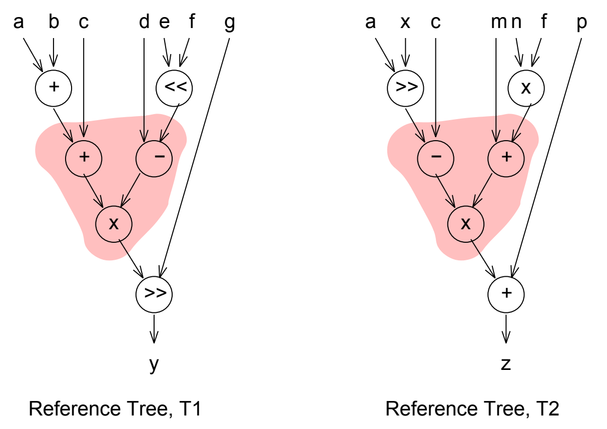


Figure 1: *Example to motivate the general subtree isomorphism problem. Given two reference trees, T1 and T2, the goal is to find all topologically identical subtrees in T1 and T2. The shaded subtrees represent an example of a match.*

are unordered; so a match may be formed by flipping the children, as is the case for the $\times$ operation in Fig. 1. Second, the common subtree match may exist anywhere in the two reference trees. Several existing subtree isomorphism problems define a match only if the matched subtrees share the same root with the reference trees or the matched subtrees share all their leaves with the reference trees [15, 14, 7, 2]. Thus, the general problem we address in this paper is a superset of the subtree isomorphism problems addressed previously.

The rest of the paper is organized as follows. In the next section, we compare our algorithm with the state of the art. Section 3 formally describes the problem statement. In Section 4, we present our isomorphic subtree enumeration algorithm and then prove its optimality and complexity. In Section 5, we explore its implications when applied on real-world applications and finally conclude in Section 6.

2. RELATED WORK

Subtree isomorphism is a general graph theory problem and has been employed in several domains like data mining, circuit synthesis, compiler code generation, etc. The most conventional form of the problem is the pattern matching variety—given a finite set of pattern tiles, it is the problem of finding all isomorphic subtrees that match one of the these tiles in a reference graph [7]. This is akin to technology mapping [10] and instruction selection [3]. There have been several advances made in the graph theory world that have looked at alternative algorithms to explore time-space complexity trade-offs of this problem [6, 7, 14, 2]. The data mining domain employs such a version of the problem to find frequencies of occurrences of each pattern tile within a database of forests [7, 16, 4]. There are also other variants of this problem, like the tree inclusion problem [11] that is similar yet different from the problem we are solving here.

We explore a different version of the graph isomorphism problem—given two reference trees, the goal is to enumerate all matching subtrees common to the two reference trees. Bottom-up search [2] is one of the oldest attempts at solving this problem. It simply traverses the trees from leaves up and at each node, records the subtree matches found leading to a natural dynamic programming formulation. However, this algorithm will always find subtrees that must share their leaves with the reference trees—such subtrees are sometimes referred to as maximal subtrees. Other advancements have been made on this algorithm; a common theme includes labeling nodes in the trees such that two nodes in a tree will have the same number if the subtrees under the nodes are isomorphic [15]. This is essentially similar to the value numbering algorithm used in traditional compilers [13, 1]. All these algorithms inherently find only those subtrees whose leaves are also the leaves of the reference trees. Thus, these algorithms cannot (by definition) find the subtree match shown in Fig. 1. There are related problems of finding similarity between two trees [8, 17], but their objective is similarity rather than isomorphism.

In this paper, we solve a more general problem of finding all isomorphic subtrees, including those that are not maximal. On first glance, this problem may seem to have a potentially exponential search space. We show, however, that the problem is well structured and solvable in polynomial time. We present a dynamic programming algorithm to search the reference trees for subtree isomorphism. The algorithm enumerates all (maximal and non-maximal) isomorphic subtree matches. For two reference trees of sizes $G_1 = (V_1, E_1)$ and $G_2 = (V_2, E_2)$, it has a $O(|V_1||V_2|)$ time and space complexity. To the best of our knowledge, this is the first paper to solve this general problem, which is a superset of traditional subtree isomorphism problems where the isomorphic trees are maximal subtrees [15].

3. PROBLEM DESCRIPTION

This section provides a formal description of the subtree isomorphism problem. First, we define some terminologies and then present the problem statement.

3.1 Definitions

We define *tree* as a directed acyclic graph, $T = (V, E, r, type)$, with a set of nodes V, a set of edges $E \subseteq V \times V$, and a root node, $r \in V$, such that all nodes except the root have exactly one parent. Every node has a specific type given by the mapping, $type : V \mapsto \mu$. The direction of the edges is from leaves to root. The node sets, $In(v)$ and $Out(v)$, define the inputs and outputs of a given node. The tree invariants are given by: $\forall\ v, s.t., v \neq r$, $|Out(v)| = 1$ and for the root node, $|Out(r)| = 0$.

If the children of a node can be interchanged, then we say that the node is unordered. Conversely, an ordered node, v, imposes a left-to-right sequencing of its children, given by $Child(v) = \langle u_1, \ldots, u_n \rangle$, where $\forall\ 1 \leq i \leq n, u_i \in In(v)$. Whether or not a node is ordered is determined by its type and is given by the mapping $Order : \mu \mapsto \{0, 1\}$.

Putting these definitions in context, a tree in the compiler's intermediate representation is typically an expression tree with some functional operations as nodes and the root, r computing the final result. The set, μ, represents all the operations performed by the program. Thus, $type(v)$ specifies the operation encapsulated by v. Finally, an unordered node maps to commutative operations, while ordered nodes are non-commutative.

Without loss of generality, we also add pseudo leaf nodes to the trees we consider. This is especially designed to deal with expression trees where nodes are operations and are typically associated with some inputs. The pseudo leaf nodes represent a terminal input, e.g., a variable or constant, that is typically supplied as input to the expression tree. We assume that every leaf of a tree is a pseudo node, v_p, such that $In(v_p) = \emptyset$ and $type(v_p) = \$$, i.e., the type of a pseudo node is considered to be a special alphabet, \$. All non-pseudo nodes must have children (inputs) associated with them.

DEFINITION 1. *Two trees, $T_1 = (V_1, E_1, r_1, type_1)$ and $T_2 = (V_2, E_2, r_2, type_2)$, are isomorphic or topologically equivalent,* *if there exists a relation, $\tau : V_1 \mapsto V_2$, between T_1 and T_2, which satisfies the following conditions:*

1. *τ is bijective, i.e., for $\forall\ u,v \in V_1,\ u \neq v \implies \tau(u) \neq \tau(v)$, and $\forall\ v' \in V_2, \exists\, v \in V_1$, s.t., $\tau(v) = v'$.*

2. *τ preserves the edge relations, i.e., for $(u,v) \in E_1$, there exists $(\tau(u),\tau(v)) \in E_2$.*

3. *τ preserves the types, i.e., for $v \in V_1$, $type_1(v) = type_2(\tau(v))$.*

4. *For every ordered node, $v \in V_1$, the ordering relation is preserved, i.e., if $Child(v) = \langle u_1,\ldots,u_n\rangle$, then $Child(\tau(v)) = \langle \tau(u_1),\ldots,\tau(u_n)\rangle$.*

A *subtree*, $S = (V_s, E_s, r_s, type)$ of a tree, $T = (V, E, r, type)$, is a tree that contains a subset of the nodes of T and preserves the edge, type and ordering relations. In other words, $V_s \subseteq V$, both trees share the same *type* mapping, the edge relations in E are preserved in E_s and the ordering relations in T are preserved in S. Further, S is a *maximal subtree* iff $Leaves(S) \subseteq Leaves(T)$. It follows that for every node, u, in the tree, there exists a unique maximal subtree rooted at u. We refer to this mapping from a given tree node, u, in T to its maximal subtree by $MaxSubtree(u)$.

3.2 Problem Statement

Given two trees, $T_1 = (V_1, E_1, r_1, type_1)$ and $T_2 = (V_2, E_2, r_2, type_2)$, find the set of all isomorphic subtrees contained within these two trees. If T_1^* and T_2^* are the domains of all subtrees contained in T_1 and T_2 respectively, then the goal of the problem is to find the exhaustive set of subtree isomporphs, $STI \subseteq T_1^* \times T_2^*$, that satisfies the following conditions:

1. *Every member is a pair of isomorphs: $\forall\ (S_1,S_2) \in STI$, the subtrees $S_1 \in T_1^*$ and $S_2 \in T_2^*$ are isomorphic as per Definition 1.*

2. *If a subtree pair is not a member of STI, then they are not isomorphic, i.e., $\forall\ (S_1 \in T_1^*, S_2 \in T_2^*) \notin STI$, the subtrees S_1 and S_2 violate some condition in Definition 1 and are therefore not isomorphic.*

4. SUBTREE MATCHING ALGORITHM

A large body of previous work has focused on maximal subtree isomorphism. This has been shown to be a linear-time search complexity [2, 15]. The problem stated here is to find a set of subtree isomorphs that includes not only maximal subtree matches but also those subtree matches that are not maximal. If we were to naively use maximal subtree isomorphism algorithms, then we would have to enumerate all subtrees within the given reference trees and then use the maximal subtree isomorphism algorithm on each pair of subtrees in this space. Clearly, this has exponential complexity since we are enumerating all subtrees in the reference trees. The key insight to combating this complexity is recognizing that the problem in Section 3.2 has an optimal sub-structure that we can exploit. In particular, we use the concept of *maximal isomorphs* to identify this sub-structure.

DEFINITION 2. *Given two reference trees, T_1 and T_2, let the domains, T_1^* and T_2^*, represent all subtrees contained within these trees respectively. A **maximal isomorph** is a pair of subtrees, $(S_1 \in T_1^*, S_2 \in T_2^*)$, that satisfy the following conditions:*

1. *S_1 and S_2 are isomorphic as per Definition 1.*

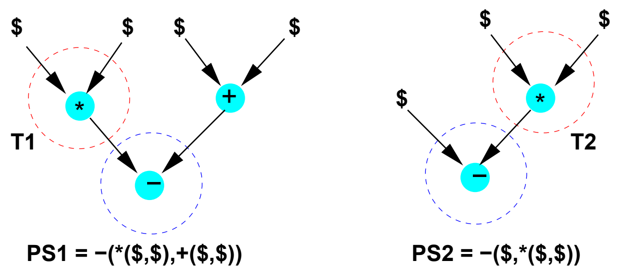


Figure 2: *Two sample reference trees, their corresponding prefix strings, and the maximal isomorphs*

2. *S_1 and S_2 are not subtrees of any other pair of isomorphic subtrees in the $T_1^* \times T_2^*$ space. This means that $\nexists\ (R_1 \in T_1^*, R_2 \in T_2^*)$, such that: (a) S_1 is a subtree of R_1, and (b) S_2 is a subtree of R_2, and (c) R_1 and R_2 are isomorphic.*

If we can identify all the maximal isomorphs within T_1 and T_2, then we have reduced the problem to smaller sub-problems. This is the key insight to our solution and is described in Section 4.2. First, however, we must deal with unordered nodes. Since there is no ordering in these nodes, a simple topological pattern match is not sufficient to detect isomorphism. To address this, we derive a canonical tree representation that forces an ordering on unordered nodes as well. This representation generates a canonical prefix string representation for a given tree. Next, a dynamic programming based algorithm is described for finding all maximal isomorphs that will form the basis for the solution.

4.1 Canonical Prefix String Representation

Determining if two trees, T_1 and T_2, are isomorphic is straightforward if all nodes in the trees are ordered. In this case, we would simply perform a bottom-up traversal checking if each of the conditions of the mapping (defined by τ in Definition 1) hold. The presence of unordered nodes, however, introduces additional complexity. Not only are the children nodes of an unordered node interchangeable, but the entire maximal subtrees beneath the children are also interchangeable.

To address this problem, we represent all trees using a canonical representation, in effect bringing order to unordered nodes. One approach to canonicalization is to order the children according to some order of their types. This is not sufficient, however, since ambiguity creeps in when two children of an unordered node have the same type. Taking this concept a step further, we use the prefix string representation of a given tree to canonicalize it. This representation is defined according to the following grammar:

$$\begin{array}{rcl} PS & \rightarrow & TYPE(CHILD[,CHILD]^*) \quad (1) \\ CHILD & \rightarrow & \$ \mid PS \\ TYPE & \rightarrow & \langle t \in \mu \rangle \end{array}$$

The prefix string for a subtree under a given node, v, is essentially, the node's $type(v)$ (we assume members of μ constitute a unique alphabet), followed by parenthesized, comma-separated list of its children. Each child, in turn, is either another prefix string or the terminal '$', if the child is a (pseudo) leaf node of the tree.

Constructing a prefix string for a given tree amounts to performing a pre-order traversal of the tree. At each node, v, we append $type(v)$ to the string. When the first child is accessed from a given node, a '(' is appended to the string; when accessing the next sibling, a ',' is appended and finally after accessing the last child of

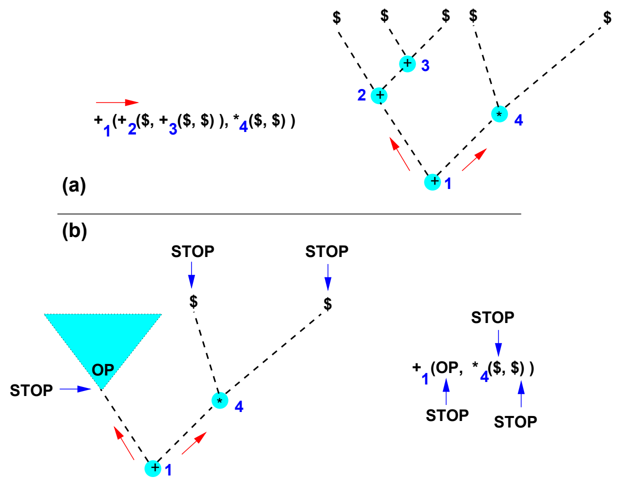


Figure 3: *An example to illustrate (a) the mapping between traversing an expression tree and performing a linear scan of the string, and (b) introducing OP at a point where the traversal or linear scan is stopped.*

a node, a ')' is appended to the string. Thus, there is a one-to-one mapping between a tree and its prefix string, given by Prefix(T). An example of the prefix string for a tree is shown in Fig. 3.

DEFINITION 3. *In **canonical form**, all nodes of a tree are ordered. The ordering of children, given by Child(v), for a node, v, is determined as follows:*

- *If Order$(type(v)) = 1$, then use the pre-defined child ordering, Child(v) (see Section 3.1).*
- *If Order$(type(v)) = 0$, then we construct Child(v) as follows: let the position in Child(v) of an input node, u, be $pos(u) \in \mathbb{N}$. Then, the ordering of Child(v) is given by the following implication:*

$$\forall\ u,w \in Child(v),$$
$$\begin{aligned} & strcmp(Prefix(MAX(u)), Prefix(MAX(w))) < 0 \\ \Longrightarrow\ & pos(u) < pos(w) \end{aligned}$$

Canonical form is achieved by enforcing a lexicographical ordering on unordered nodes. Specifically, the order of children of an unordered node is the same as the lexicographic order of the children's maximal subtrees' prefix strings. In the above definition, MAX(u) represents the maximal subtree under a given tree node, u and Prefix(MAX(u)) gives the prefix string encoding for this maximal subtree. Converting a given tree into its canonical form involves a post-order traversal; at each unordered node, we reorder its children to obey the conditions in Definition 3. Observe the importance of canonicalization—we use it primarily to prune the search space without sacrificing optimality. In other words, we do not have to flip the children of unordered trees in looking for a match because the canonical representation of two identical subtrees is guaranteed to be the same.

4.2 The Common Prefix Substring Matching (CPSM) Formulation

After obtaining the canonical prefix strings for two reference trees, one may think of running a simple maximal substring matching on the prefix strings to obtain the maximal isomorphs of the reference trees. Unfortunately, that is not a solution, as illustrated in Fig. 2. There are two maximal isomorphs, rooted at '$*$' and '$-$'. However, a naive substring matching algorithm can only yield the matching at $*$ by matching $*(\$,\$)$. In fact, it can be proved that simple substring matching will only yield isomorphs that are also maximal subtrees, i.e., those sharing their leaves with the reference trees. Internal (non-maximal) subtrees like the '$-$' in Fig. 2 will never be matched by substring matching. Therefore we need a more context-aware string scanning mechanism in order to find all maximal isomorphs.

Note that traversing an expression tree in the prefix order amounts to performing a linear scan of its prefix string. During the process of scanning a prefix string, skipping an entire operation string pattern starting at an operation effectively means stopping the traversal of the expression tree at the corresponding operation node. If we stop the traversal at an operation before reaching the terminal ('\$'), we represent that point in the string by *OP*. Fig. 3 illustrates this principle. The arrows in Fig. 3(a) show the directions of traversal and scan. After visiting node 1, pruning the subtree rooted at node 2 is tantamount to skipping the whole string pattern, $+_2(\$,+_3(\$,\$))$. The newly formed pattern (as shown in Fig. 3(b)) is thus represented as $+_1(OP,*_4(\$,\$))$, clearly indicating the places the traversal stopped by '\$' or OP depending on whether the stopping point is a terminal node or intermediate node respectively.

The following theorem formally brings out important properties of the prefix strings, which are used in formulating our dynamic programming algorithm.

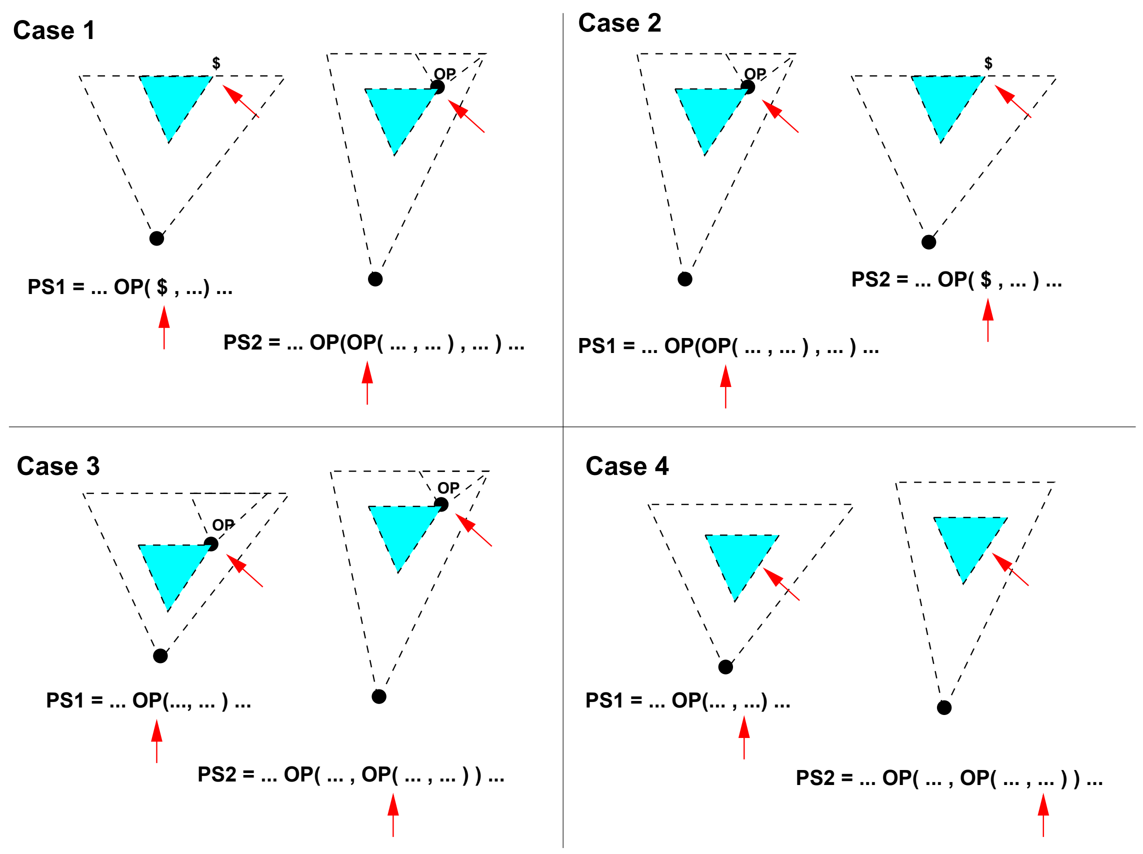
THEOREM 1. *Let $PS_1[1..m]$ and $PS_2[1..n]$ be the two prefix strings of length m and n respectively. Let k be the length of the longest common prefix substring and LCPS(k) be the set of all longest common prefix substring matches, each of length k, ending at positions $1 \le p_1, p_2, \ldots, p_t \le m$ in PS_1 and $1 \le q_1, q_2, \ldots, q_t \le n$ in PS_2, where $t = |LCPS(k)|$. Let L_k refer to a member of LCPS(k).*

if $PS_1[p] = PS_2[q]$, where $1 \le p \le m$, $1 \le q \le n$, then the following must hold true:

1. *If $PS_1[p-1] =$'\$' and $PS_2[q-j+1..q-1] = OP$, $(2 \le j \le q)$, then L_{k-1} is a longest common prefix string for $PS_1[1..p-2]$ and $PS_2[1..q-j]$ ending at the alphabet positions $p-2$ and $q-j$ of PS_1 and PS_2 respectively.*
2. *If $PS_1[p-i+1..p-1] = OP$ and $PS_2[q-1] =$'\$', $(2 \le i \le p)$, then L_{k-1} is a longest common prefix string for $PS_1[1..p-i]$ and $PS_2[1..q-2]$ ending at the alphabet positions $p-i$ and $q-2$ of PS_1 and PS_2 respectively.*
3. *If $PS_1[p-i+1..p-1] = OP$ and $PS_2[q-i+1..q-1] = OP$, $(2 \le i \le p,\ 2 \le j \le q)$, then L_{k-1} is a longest common prefix string for $PS_1[1..p-i]$ and $PS_2[1..q-j]$ ending at the alphabet positions $p-i$ and $q-j$ of PS_1 and PS_2 respectively.*
4. *Otherwise, L_{k-1} is a longest common prefix string for $PS_1[1..p-1]$ and $PS_2[1..q-1]$, ending at the alphabet positions $p-1$ and $q-1$ of PS_1 and PS_2 respectively.*

PROOF. We prove these assertions using contradiction.

1. $L_k \in LCPS(k) \Rightarrow L_{k-1} \in LCPS(k-1)$, where k^{th} alphabet is a '\$' or *OP*. In this case, $PS_1[p-1] =$'\$' and $PS_2[q-j+1..q-1] = OP$, $(2 \le j \le q)$. Let $L'_{k-1} \notin LCPS(k-1)$ be a longest common prefix string for $PS_1[1..p-2]$ and $PS_2[1..q-j]$ ending at the alphabet positions $p-2$ and $q-j$ of PS_1 and PS_2 respectively. Therefore, by skipping over '\$' at $PS_1[p-1]$ and *OP* in $PS_2[q-j+1..q-1]$, one can match



Case 1
$
OP
PS1 = ... OP($, ...) ...
PS2 = ... OP(OP(... , ...) , ...) ...
Case 2
OP
$
PS2 = ... OP($, ...) ...
PS1 = ... OP(OP(... , ...) , ...) ...
Case 3
OP
OP
PS1 = ... OP(..., ...) ...
PS2 = ... OP(... , OP(... , ...)) ...
Case 4
PS1 = ... OP(... , ...) ...
PS2 = ... OP(... , OP(... , ...)) ...

Figure 4: *The four cases presented in Theorem 1.*

$PS_1[p]$ and $PS_2[q]$, and thus come up with L'_k as another longest common prefix string. Now, $L'_{k-1} \notin LCPS(k-1) \Rightarrow L'_k \in LCPS(k)$. Since $L'_k \notin LCPS(k)$, this is a contradiction, as $LCPS(k)$ is the set of all largest common prefix string matches of length k. Therefore, L_{k-1} is a longest common prefix string for $PS_1[1..p-2]$ and $PS_2[1..q-j]$ ending at the alphabet positions $p-2$ and $q-j$ of PS_1 and PS_2 respectively. Now, if L'_{k-1} is a longest common prefix string that does not end at $PS_1[p-2]$ and $PS_2[q-j]$, it can only extend through the other three possibilities, because there is no other way to extend the common prefix string.

2. $PS_1[p-i+1..p-1] = OP$ and $PS_2[q-1] =$'\$', $(2 \le i \le p)$. The proof of this assertion is symmetric to the above reasoning.

3. $PS_1[p-i+1..p-1] = OP$ and $PS_2[q-i+1..q-1] = OP$, $(2 \le i \le p,\ 2 \le j \le q)$. The proof of this assertion is also symmetric to the above reasoning.

4. When none of the above conditions are true, but only $PS_1[p] = PS_2[q]$, the previous match has to be a direct match.

The above four cases are depicted in Fig. 4. The arrows pinpoint to the cases clearly using two sample reference trees and prefix strings ($PS1$ and $PS2$). The cases 1 through 3 involve skipping over an entire operation substring or a terminal, while case 4 is an exact match of a non-leaf alphabet and therefore does not involve any skipping transforms. □

This shows that the problem of canonical prefix substring matching (CPSM) has an optimal substructure, i.e., an optimal solution to this problem contains within it optimal solutions to its subproblems. For $1 \le p \le m$ and $1 \le q \le n$, let $LCPSL(p,q)$ be the length of a longest common prefix substring for $PS_1[1..p]$ and $PS_2[1..q]$. We express the three conditions presented by the first three cases in Theorem 1 as follows:

$$\begin{aligned} \text{condition1} \quad &= PS_1[p-1] = \text{`\$'} \\ &\ \&\&\ PS_2[q-j+1..q-1] = OP \\ \text{condition2} \quad &= PS_1[p-i+1..p-1] = OP \\ &\ \&\&\ PS_2[q-1] = \text{`\$'} \\ \text{condition3} \quad &= PS_1[p-i+1..p-1] = OP \\ &\ \&\&\ PS_2[q-i+1..q-1] = OP \end{aligned}$$

The optimal substructure of CPSM gives the following recursive formula:

If $PS_1[p] = PS_2[q]$, where $1 \le p \le m$, $1 \le q \le n$, for $2 \le i \le p$ and $2 \le j \le q$, the following holds true:

$$LCPSL(p,q) = \begin{cases} LCPSL(p-2,q-j)+1 & \text{if condition1} \\ LCPSL(p-i,q-2)+1 & \text{if condition2} \\ LCPSL(p-i,q-j)+1 & \text{if condition3} \\ LCPSL(p-1,q-1)+1 & \text{otherwise} \end{cases}$$

Based on the above equation, one could easily write an exponential-time recursive algorithm to compute the matching prefix substrings. However, because there are only $O(m \cdot n)$ distinct subproblems as per Theorem 1, we can use dynamic programming to obtain the solutions bottom up.

The dynamic programming implementation employs an $m \times n$ *LCPSL* matrix to store the intermediate lengths of the matching substrings. In addition, it encodes the substring enumeration solution with the help of $P\_PREV(p,q)$ and $Q\_PREV(p,q)$, which are respectively defined as the last positions in the prefix strings PS_1 and PS_2 that were matched by the algorithm, prior to matching the current positions p and q in the two strings (i.e., $PS_1[p] = PS_2[q]$, where $1 \leq p \leq m$, $1 \leq q \leq n$). This encoding alleviates the exponential space overhead that would be otherwise required to enumerate all solutions.

$$P\_PREV(p,q) = \begin{cases} p-2 & \text{if condition1} \\ p-i & \text{if condition2} \\ p-i & \text{if condition3} \\ p-1 & \text{otherwise} \end{cases}$$

$$Q\_PREV(p,q) = \begin{cases} q-j & \text{if condition1} \\ q-2 & \text{if condition2} \\ q-j & \text{if condition3} \\ q-1 & \text{otherwise} \end{cases}$$

Using *LCPSL*, *P_PREV*, and *Q_PREV*, we can generate all the common prefix strings enumerating PS_1 (using *P_PREV*) and PS_2 (using *Q_PREV*). This in turn corresponds to all the maximal isomorphs in the original expression tree. In order to walk the generated substring positions in *LCPSL* in the forward direction, we define *P_NEXT* and *Q_NEXT* as follows: $P\_NEXT(P\_PREV(p), Q\_PREV(q)) = p$ and $Q\_NEXT(P\_PREV(p), Q\_PREV(q)) = q$, where $0 \leq p \leq m$, $0 \leq q \leq n$. To enumerate all the matching prefix strings, we need to simply start with positions having *LCPSL* set to 1 and then walk the *PS_1* or *PS_2* strings using *P_NEXT* and *Q_NEXT* respectively. These matched prefix strings in turn enumerate all the maximal isomorphs in the reference trees.

In practice, in order to enumerate the longest common prefix string or the maximal isomorphs (instead of capturing all the internal ones as well), we check before setting $LCPSL(p,q)$ whether the newly computed value is greater than the stored value of $LCPSL(p,q)$. This is because any one of the above 4 cases can be the reason for finding a match at location (p,q).

4.3 The CPSM Algorithm

We present the CPSM algorithm in Figure 5, which uses the above formulation. The algorithm takes the prefix strings PS_1 and PS_2 as inputs, and populates the solution in terms of matrices *LCPSL*, $\triangle P\_NEXT$ and $\triangle Q\_NEXT$, where *LCPSL* tracks the lengths of substrings at various positions in PS_1 and PS_2, $P\_NEXT(p,q) = p + \triangle P\_NEXT(p,q)$ points to the next matching position for PS_1, and $Q\_NEXT(p,q) = q + \triangle Q\_NEXT(p,q)$ points to the next matching position for PS_2.

The algorithm begins by building operation position tables for strings *PS_1* and *PS_2*, which mark the beginning and ending of each valid operation in the prefix strings. The dynamic computation of the solution matrices based on the above formulation is shown between lines 21 and 57. Note that in order to favor the growth of the largest valid substring, we explicitly check whether the new substring length is greater than any existing substring length evaluated so far, at a particular matching point (p,q). This is done in lines 36, 44, and 52. The dynamic updates of *LCPSL*, $\triangle P\_NEXT$, and $\triangle Q\_NEXT$ can be tracked in lines 28-30, 37-39, 45-47, and 53-55.

THEOREM 2. *The running time of the dynamic programming (CPSM) algorithm as well as its space complexity is $O(m \cdot n)$.*

PROOF. Each of the computations presented in the formulation is $O(1)$, which is run within two nested loops of size m and n.

```
CPSM($PS_1$, $PS_2$)
00: Create $op\_pos\_table(PS_1)$
01: Create $op\_pos\_table(PS_2)$
02: Reset $LCPSL$, $\triangle P\_NEXT$ and $\triangle Q\_NEXT$
03: $len_1 \Leftarrow length(PS_1)$
04: $len_2 \Leftarrow length(PS_2)$
05: for ($p = 0$ to $len_1 - 1$)
06:     for ($q = 0$ to $len_2 - 1$)
07:         $cond_1 \Leftarrow (PS_1[p] == PS_2[q])$
08:         $cond_2 \Leftarrow (PS_1[p-1] == \text{`\$'})$
09:         $cond_3 \Leftarrow (PS_1[p-1] == \text{`)'})$
10:         $cond_4 \Leftarrow (PS_2[q-1] == \text{`\$'})$
11:         $cond_5 \Leftarrow (PS_2[q-1] == \text{`)'})$
12:         $valid_1 \Leftarrow is\_valid\_op(PS_1)$
13:         $valid_2 \Leftarrow is\_valid\_op(PS_2)$
14:         $is\_valid \Leftarrow valid_1 \&\& valid_2$
15:         if ($cond_3$)
16:             $pos_1 \Leftarrow get\_op\_pos(PS_1, p-1, op\_pos\_table)$
17:         endif
18:         if ($cond_5$)
19:             $pos_2 \Leftarrow get\_op\_pos(PS_2, q-1, op\_pos\_table)$
20:         endif
21:         /* Populate solution matrices */
22:         if($cond_1$)
23:             if($p == 0 \ || \ q == 0$)
24:                 $LCPSL(p,q) \Leftarrow 1$
25:             else
26:                 $newLCPSL \Leftarrow LCPSL(p-1, q-1) + 1$
27:                 if($newLCPSL > 1 \ || \ is\_valid$)
28:                     $LCPSL(p,q) \Leftarrow newLCPSL$
29:                     $\triangle P\_NEXT(p-1, q-1) \Leftarrow 1$
30:                     $\triangle Q\_NEXT(p-1, q-1) \Leftarrow 1$
31:                 endif
32:             endif
33:         endif
34:         if($cond_1$ && $cond_3$ && $cond_4$ && $(pos_1 > 0)$)
35:             $newLCPSL \Leftarrow LCPSL(pos_1 - 1, q-2) + 1)$
36:             if($newLCPSL > LCPSL(p,q)$)
37:                 $LCPSL(p,q) \Leftarrow newLCPSL$
38:                 $\triangle P\_NEXT(pos_1 - 1, q-2) \Leftarrow p - pos_1 + 1$
39:                 $\triangle Q\_NEXT(pos_1 - 1, q-2) \Leftarrow 2$
40:             endif
41:         endif
42:         if($cond_1$ && $cond_2$ && $cond_5$ && $(pos_2 > 0)$)
43:             $newLCPSL \Leftarrow LCPSL(p-2, pos_2 - 1) + 1)$
44:             if($newLCPSL > LCPSL(p,q)$)
45:                 $LCPSL(p,q) \Leftarrow newLCPSL$
46:                 $\triangle P\_NEXT(p-2, pos_2 - 1) \Leftarrow 2$
47:                 $\triangle Q\_NEXT(p-2, pos_2 - 1) \Leftarrow q - pos_2 + 1$
48:             endif
49:         endif
50:         if($cond_1$ && $cond_3$ && $cond_5$ && $(pos_1 \& pos_2 > 0)$)
51:             $newLCPSL \Leftarrow LCPSL(pos_1 - 1, pos_2 - 1) + 1)$
52:             if($newLCPSL > LCPSL(p,q)$)
53:                 $LCPSL(p,q) \Leftarrow newLCPSL$
54:                 $\triangle P\_NEXT(pos_1 - 1, pos_2 - 1) \Leftarrow p - pos_1 + 1$
55:                 $\triangle Q\_NEXT(pos_1 - 1, pos_2 - 1) \Leftarrow q - pos_2 + 1$
56:             endif
57:         endif
58:     endfor
59: endfor
```

Figure 5: *The CPSM Algorithm*

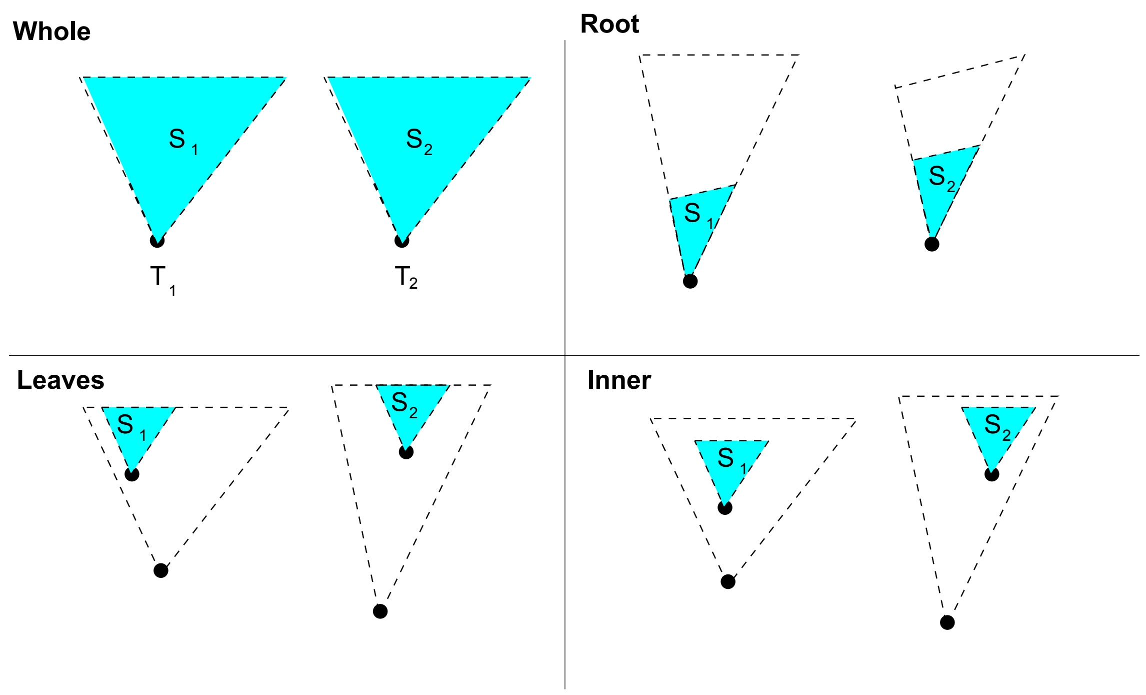


Figure 6: *The four different types of isomorphic subtrees, S_1 and S_2, that can be found in two reference trees, T_1 and T_2.*

Therefore the time complexity is $O(m \cdot n)$. Since, we are employing three $m \times n$ matrices to capture the results, the space complexity is also $O(m \cdot n)$. $\square$

4.4 A Running Example

In order to illustrate the working of the CPSM algorithm, let us consider again the reference trees shown in Fig. 2 and their corresponding prefix string representations:

$$\begin{aligned} PS1 &= -(*(\$,\$),+(\$,\$)) \\ PS2 &= -(\$,*(\$,\$)) \end{aligned}$$

The solution matrices *LCPSL*, *P_NEXT* and *Q_NEXT*, built according the CPSM algorithm are shown together in Table 1a and Table 1b. There are two maximal substring matches encoded within the solution matrices. To enumerate each matching substring, we find the starting position by the entry 1 in the *LCPSL* matrix and with the assistance of (P_NEXT, Q_NEXT), we find the full matching substring. The first match is $(-(OP, OP)$ in $PS1$, $-(\$, OP)$ in $PS2)$, which starts at (0,0) (as indicated by *LCPSL*) and then walking down string positions as guided by the (P_NEXT, Q_NEXT) entries (1,1), (8,3), and (15,10). When the jump of *P_NEXT* or *Q_NEXT* is greater than 2, it indicates stopping at an operation subtree, and we show that by putting the symbol 'OP'. The second match is $(*(\$,\$)$ in $PS1$, $*(\$,\$)$ in $PS2)$, corresponding to the entries (2,4), (3,5), (4,6), (5,7), (6,8), and (7,9). The second match is a straight-forward match as there is no jump in *P_NEXT* or *Q_NEXT* greater than 2.

5. CASE STUDY: COMBINATIONAL RESOURCE SHARING

Thus far in the paper, we have described the theoretical rigor behind subtree isomorphism mining. In this section, we test the practical usefulness of the algorithm. Although there are many applications of this algorithm, we explore its effectiveness in the combinational resource sharing problem [12].

This is a well known problem in high-level synthesis, where the goal is to share commonly used resources in mutually exclusive control paths in the given source program. For example, if a multiplier is used within the `true` and `false` branches of an `if-else` statement, then we know that the result of only one multiplier is needed. Thus, it is possible to share this multiplier across both conditional branches and muxing its inputs.

Of course, we need not stop at just a single operation. We can imagine sharing entire expression trees between mutually exclusive code regions, which necessitates finding common code segments between these regions that can form the resource (or expression tree) to be shared.

To enumerate all opportunities for such resource sharing, we create expression forests for each control-flow region—one forest for each mutually exclusive control branch. Next, we can use the proposed subtree isomorphism algorithm to scan the forests to find common structural expression tree patterns that form potential sharable resources. The inputs to the algorithm are two trees from two different forests. A quadratic complexity search will enumerate all subtree matches that are present in these forests and each of these matches will form a candidate for combinational resource sharing.

This scan algorithm was applied on a variety of representative input programs that are used to test and benchmark the Simulink® HDL Coder^{TM} product. Due to proprietary issues, we cannot reveal the names of these tests but mention here that they are various applications from the signal processing and control systems domains. A total of about 50 different test programs were used. We categorized the subtree matches found into four groups. If S_1 and S_2 are the matched subtrees within reference trees, T_1 and T_2, then the four categories are illustrated in Fig. 6 and can be described as:

- *Whole*: If $S_1 = T_1 = T_2 = S_2$, then the two reference trees were themselves isomorphic.
- *Root*: Here, the subtrees shared the roots with the reference trees, i.e., $root(S_1) = root(T_1)$ and $root(S_2) = root(T_2)$.

		0	1	2	3	4	5	6	7	8	9	10
		-	(	$	,	*	(	$	,	$	)	)
0	-	1	0	0	0	0	0	0	0	0	0	0
1	(	0	2	0	0	0	0	0	0	0	0	0
2	*	0	0	0	0	1	0	0	0	0	0	0
3	(	0	0	0	0	0	2	0	0	0	0	0
4	$	0	0	0	0	0	0	3	0	0	0	0
5	,	0	0	0	0	0	0	0	4	0	0	0
6	$	0	0	0	0	0	0	0	0	5	0	0
7	)	0	0	0	0	0	0	0	0	0	6	0
8	,	0	0	0	3	0	0	0	0	0	0	0
9	+	0	0	0	0	0	0	0	0	0	0	0
10	(	0	0	0	0	0	0	0	0	0	0	0
11	$	0	0	0	0	0	0	0	0	0	0	0
12	,	0	0	0	0	0	0	0	0	0	0	0
13	$	0	0	0	0	0	0	0	0	0	0	0
14	)	0	0	0	0	0	0	0	0	0	0	0
15	)	0	0	0	0	0	0	0	0	0	0	4

(a)

		0	1	2	3	4	5	6	7	8	9	10
		-	(	$	,	*	(	$	,	$	)	)
0	-	1,1	-	-	-	-	-	-	-	-	-	-
1	(	-	8,3	-	-	-	-	-	-	-	-	-
2	*	-	-	-	-	3,5	-	-	-	-	-	-
3	(	-	-	-	-	-	4,6	-	-	-	-	-
4	$	-	-	-	-	-	-	5,7	-	-	-	-
5	,	-	-	-	-	-	-	-	6,8	-	-	-
6	$	-	-	-	-	-	-	-	-	7,9	-	-
7	)	-	-	-	-	-	-	-	-	-	-	-
8	,	-	-	-	15,10	-	-	-	-	-	-	-
9	+	-	-	-	-	-	-	-	-	-	-	-
10	(	-	-	-	-	-	-	-	-	-	-	-
11	$	-	-	-	-	-	-	-	-	-	-	-
12	,	-	-	-	-	-	-	-	-	-	-	-
13	$	-	-	-	-	-	-	-	-	-	-	-
14	)	-	-	-	-	-	-	-	-	-	-	-
15	)	-	-	-	-	-	-	-	-	-	-	-

(b)

Table 1: *A running example of the algorithm for finding common substrings between* $-(*(\$,\$),+(\$,\$))$ *and* $-(\$,*(\$,\$))$*: (a) the* (P_NEXT, Q_NEXT) *pairs, where* $P\_NEXT(p,q) = p + \triangle P\_NEXT(p,q)$ *and* $Q\_NEXT(p,q) = q + \triangle P\_NEXT(p,q)$*, and (b) the LCPSL matrix.*

- *Leaves*: These are maximal subtree matches, i.e., $Leaves(S_1) \subseteq Leaves(T_1)$ and $Leaves(S_2) \subseteq Leaves(T_2)$.
- *Inner*: Here, at least one of S_1 or S_2 does not share its root with its respective reference tree and there exists at least one leaf for each subtree that is not a leaf in the reference tree.

Previous techniques proposed for subtree isomorphism primarily finds matches in the *Leaves* category [15, 1, 2]. Typically, approaches similar to value numbering (used in common subexpression elimination) [13] are used to provide unique ids to nodes such that two nodes with the same id will be isomorphic all the way down to the leaves.

Finding matches in the *Root* category will involve a lock-step, pre-order traversal down the reference trees. The traversal ends when a difference is found in the nodes and portions of the trees matched to that point form the match. Although this is a straightforward linear search, it involves a different algorithm than the one used to find *Leaves* matches [15].

To our knowledge, no solutions have been proposed to efficiently find all matches belonging to the *Inner* category. The proposed CPSM algorithm can find all four different types of matches in a single sweep. The primary strength of our algorithm is its efficiency. Without explicitly enumerating all matches, it simply encodes all matches within the solution matrices as described in Section 4.3.

The results of the subtree matches found in mutually exclusive expression forests in our benchmarks are reported in Fig. 7. We have categorized the matches according to the four groups described above. All these matches were found with a single sweep of our algorithm through the source code. The results indicate that most of the matches fall in to the *Whole* and *Root* categories. However, there are a significant number of matches that also fall in the other two categories. The results are promising in that we have been able to efficiently generate new opportunities for performing combinational resource sharing within the system design tool. The next logical step for effective combinational resource sharing is to prune these matches according to some objective cost function.

This case study is only one example of the possible applications of the algorithm. Naturally, it can also be used for sequential resource sharing, which is the traditional approach where resources across different control steps in a given pipeline schedule are shared. Again, instead of sharing just a single node, we can explore the possibilities of sharing expression trees across control steps. Other applications include code re-use optimizations, custom instruction creation in ISE architectures [5], JIT optimizations that seek out frequently executed code from the context call trees [17], amongst many others.

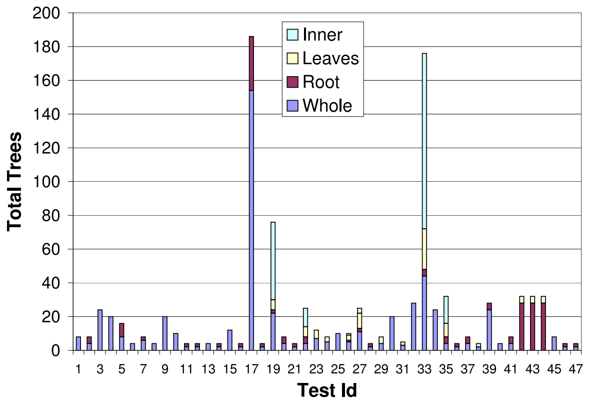
6. CONCLUSIONS

In this paper, we formally described a general version of the subtree isomorphism problem. It is the first formulation to enumerate all possible matches in two reference trees irrespective of whether the isomorphism exists at the root, leaves, or internal sections of the trees. In this respect, it is a superset of all subtree isomorphism problems addressed so far. Although, it is a seemingly exponential search space, we show that the problem is structured and thus an optimal, quadratic-time solution exists for this generic subtree isomorphism problem. We have also performed an experimental case study by applying the algorithm to find opportunities for combinational resource sharing in a set of signal processing and control system benchmarks—our results indicate that the proposed algorithm can rapidly, optimally and efficiently mine common tree patterns vital to compiler analysis and optimizations. We believe that our algorithm will find significant uses in the embedded computing domain where tree-based pattern matching problems are abundant.

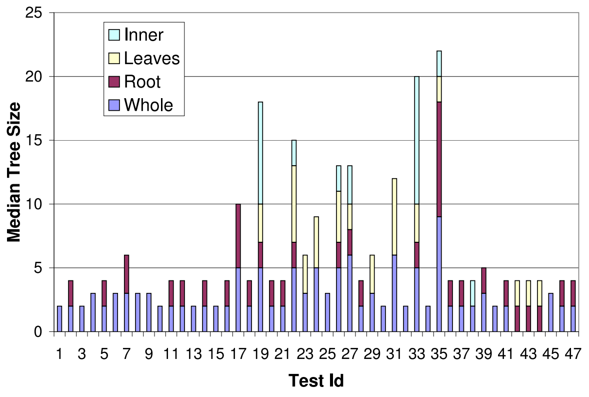
7. REFERENCES

[1] A. V. Aho, S. C. Johnson, and J. D. Ullman. Code generation for expressions with common subexpressions. In *POPL*, pages 19–31, New York, NY, USA, 1976. ACM.

[2] Alfred V. Aho and John E. Hopcroft. *The Design and Analysis of Computer Algorithms*. Addison-Wesley, Boston, MA, USA, 1974.



(a)



(b)

Figure 7: *(a) The number of subtree matches found (by category) in each test and (b) the median size (in terms of $|V|$) amongst all matches found in each test.*

[3] Alfred V. Aho, Ravi Sethi, and Jeffrey D. Ullman. *Compilers: principles, techniques, and tools*. Addison-Wesley Longman Publishing Co., Inc., Boston, MA, USA, 1986.

[4] T. Asai, K. Abe, S. Kawasoe, H. Arimura, H. Satamoto, and S. Arikawa. Efficient substructure discovery from large semi-structured data. In *SIAM Int. Conf. on Data Mining*, Arlington, VA, 2002.

[5] Kubilay Atasu, Laura Pozzi, and Paolo Ienne. Automatic application-specific instruction-set extensions under microarchitectural constraints. In *DAC '03: Proceedings of the 40th conference on Design automation*, pages 256–261, New York, NY, USA, 2003. ACM.

[6] Samuel R. Buss. Alogtime algorithms for tree isomorphism, comparison, and canonization. In *KGC '97: Proc. of the 5th Kurt Gödel Colloquium on Computational Logic and Proof Theory*, pages 18–33, London, UK, 1997. Springer-Verlag.

[7] Yun Chi, Richard R. Muntz, Siegfried Nijssen, and Joost N. Kok. Frequent subtree mining - an overview. *Fundamenta Informaticae*, 66(1-2):161–198, 2005.

[8] Jason Cong and Wei Jiang. Pattern-based behavior synthesis for fpga resource reduction. In *FPGA*, pages 107–116, New York, NY, USA, 2008. ACM.

[9] Christopher W. Fraser, David R. Hanson, and Todd A. Proebsting. Engineering a simple, efficient code-generator generator. *ACM Lett. Program. Lang. Syst.*, 1(3):213–226, 1992.

[10] K. Keutzer. Dagon: Technology binding and local optimization by dag matching. In *25 years of DAC*, pages 617–624, New York, NY, USA, 1988. ACM.

[11] Pekka Kilpelainen and Heikki Mannila. Ordered and unordered tree inclusion. *SIAM J. Comput.*, 24(2):340–356, 1995.

[12] T. Kim, N. Yonezawa, J.W.S. Liu, and C.L. Liu. A scheduling algorithm for conditional resource sharing - a hierarchical reduction approach. *IEEE TCAD*, 13(4):425–438, 1994.

[13] Steven S. Muchnick. *Advanced Compiler Design and Implementation*. Morgan Kaufmann, 1997.

[14] Ron Shamir and Dekel Tsur. Faster subtree isomorphism. In *5th Israeli Symposium on Theory of Computing and Systems*, pages 126–131, Bar-Ilan, Israel, 1997.

[15] Gabriel Valiente. *Algorithms on Trees and Graphs*. Springer-Verlag New York, Inc., Secaucus, NJ, USA, 2002.

[16] Yi Xia and Yirong Yang. Mining closed and maximal frequent subtrees from databases of labeled rooted trees. *IEEE Trans. on Knowl. and Data Eng.*, 17(2):190–202, 2005. Student Member-Yun Chi and Fellow-Richard R. Muntz.

[17] Xiaotong Zhuang, Suhyun Kim, Mauri io Serrano, and Jong-Deok Choi. Perfdiff: a framework for performance difference analysis in a virtual machine environment. In *CGO '08: Proceedings of the sixth annual IEEE/ACM international symposium on Code generation and optimization*, pages 4–13, New York, NY, USA, 2008. ACM.