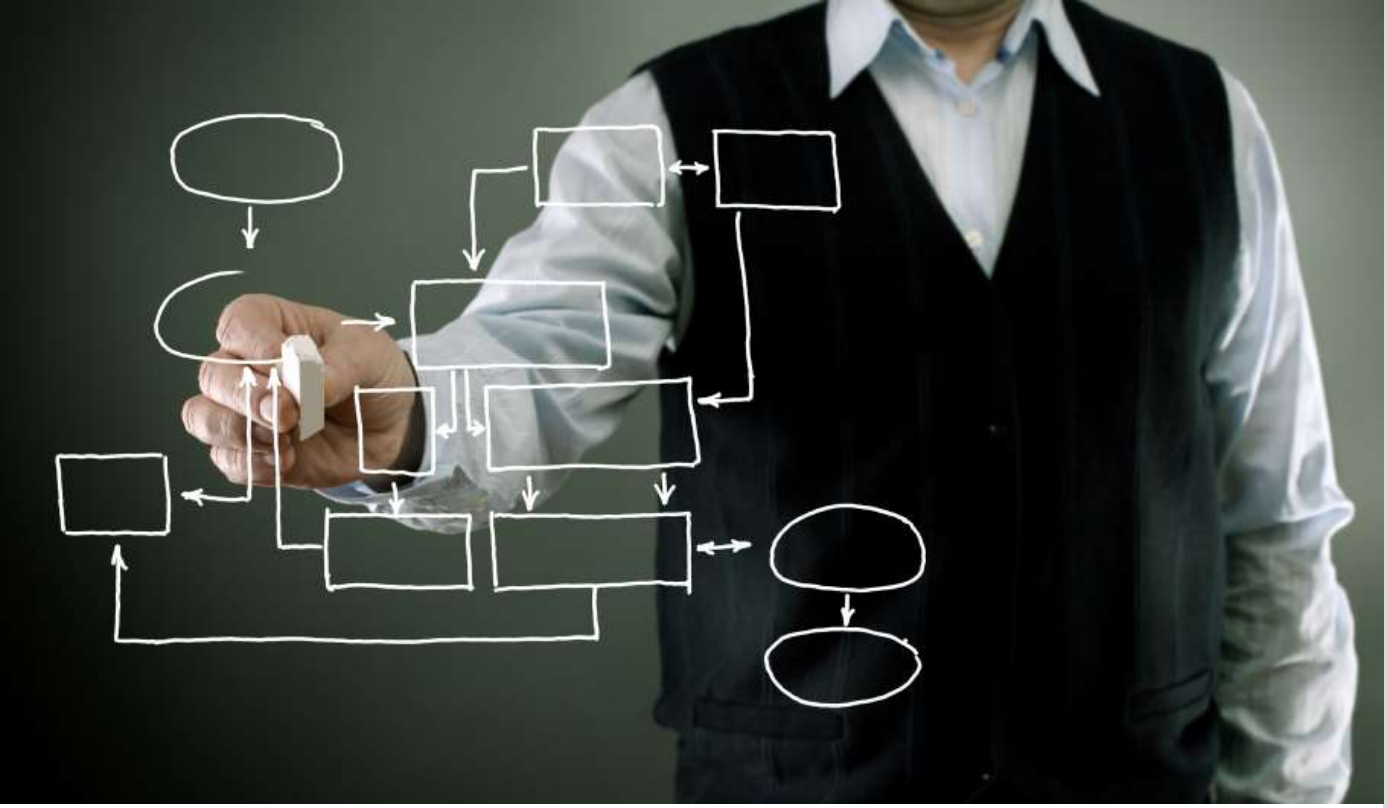

Hash-based Tree Similarity and Simplification in Genetic Programming for Symbolic Regression

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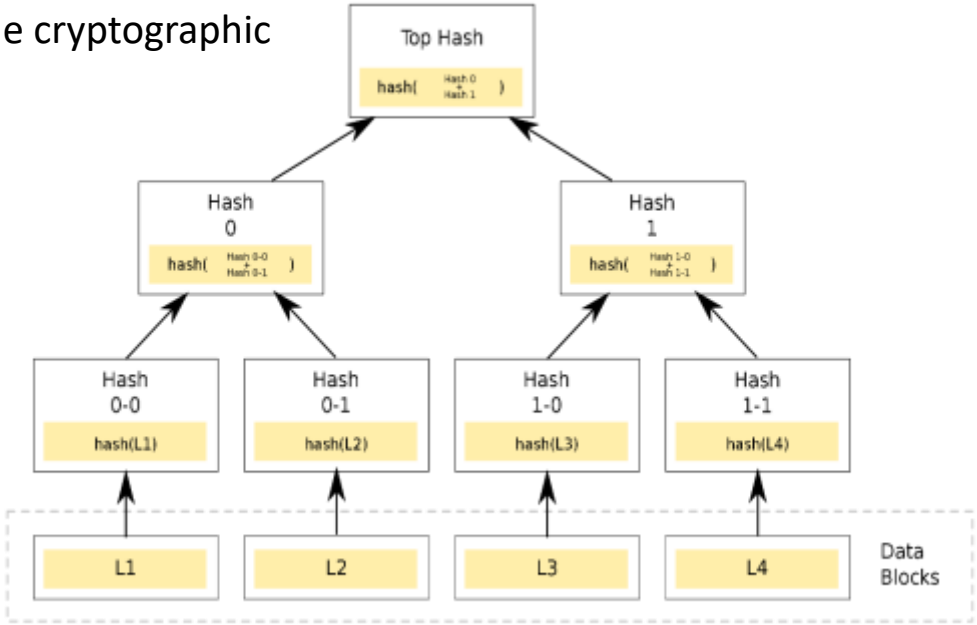
Hashing of Symbolic Expressions

Similar in concept to Merkle trees

- Every leaf node is labelled with the hash of a data block
- Every non-leaf node is labelled with the cryptographic hash of the labels of its child nodes



But different

- Initial node hash values
- Sorting of child nodes
- Non-cryptographic

Same hash → isomorphism

- Hash trees → postfix sequences
- Efficient comparison (=tree distance)

Hashing of Symbolic Expressions

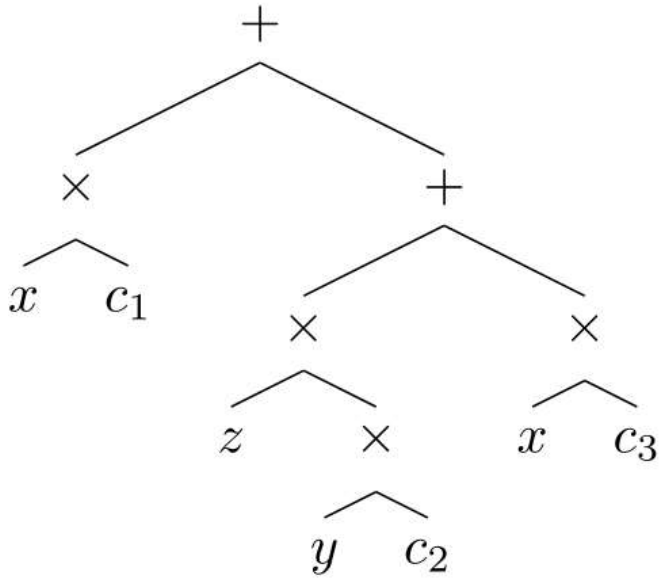
Algorithm 1: Tree hash algorithm

input : A symbolic expression tree T
output : A sequence of hash values for each node in T in postorder

```
1 nodes ← Postorder(T);
2 hashes ← empty hash value array;
3 foreach node n in nodes do
4     H(n) ← an initial hash value (for leaf nodes, it will remain unchanged);
5     if n is an internal node then
6         if n is commutative then
7             Sort the child nodes of n;
8         hashes ← Hash(Children(n), H(n));
9 return hashes;
```

Hashing Example (1)

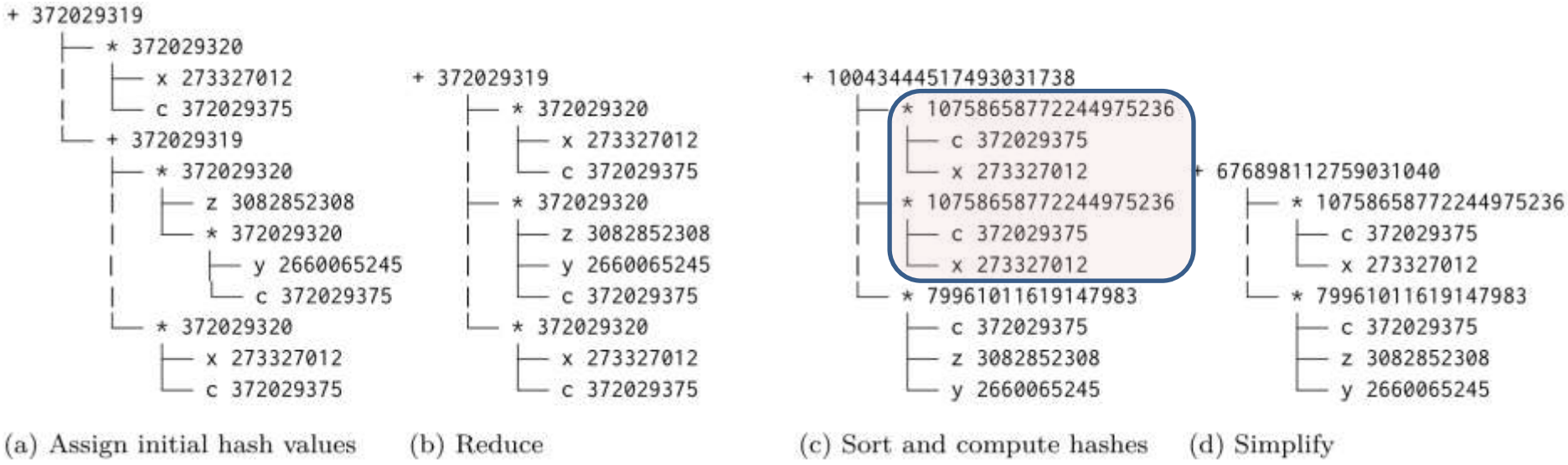
- $F(x, y, z) = c_1 x + c_2 yz + c_3 x$
  - Postfix representation: `c3 x * c2 y * z * + c1 x * +`
  - Tree representation




```
+ 372029319
    ├── * 372029320
    │   ├── x 273327012
    │   └── c 372029375
    └── + 372029319
        ├── * 372029320
        │   ├── z 3082852308
        │   └── * 372029320
        │       ├── y 2660065245
        │       └── c 372029375
        └── * 372029320
            ├── x 273327012
            └── c 372029375
```

Hashing Example (2)

- $F(x, y, z) = c_1 x + c_2 yz + c_3 x$
  - Steps (b) and (d) only required for simplification



- Tree hash value: `676898112759031040`
- Terms with the same hash value can be simplified according to arithmetic rules
- $F_{simplified}(x, y, z) = c_4 x + c_5 yz$ (original constants folded)

Fast Distance Matrix Calculation

Algorithm

1. Hash all trees into sequences of hash values
$$\{T_1, \dots, T_n\} \rightarrow \{H_1, \dots, H_n$$
2. Sort all hash sequences
3. Simple merge-count to calculate tree distance

Validation

- Identical results to bottom-up tree distance [Valiente, 2001]
- Improved performance
- Performance test: 5000 random trees

Algorithm 3: Merge-count hash values

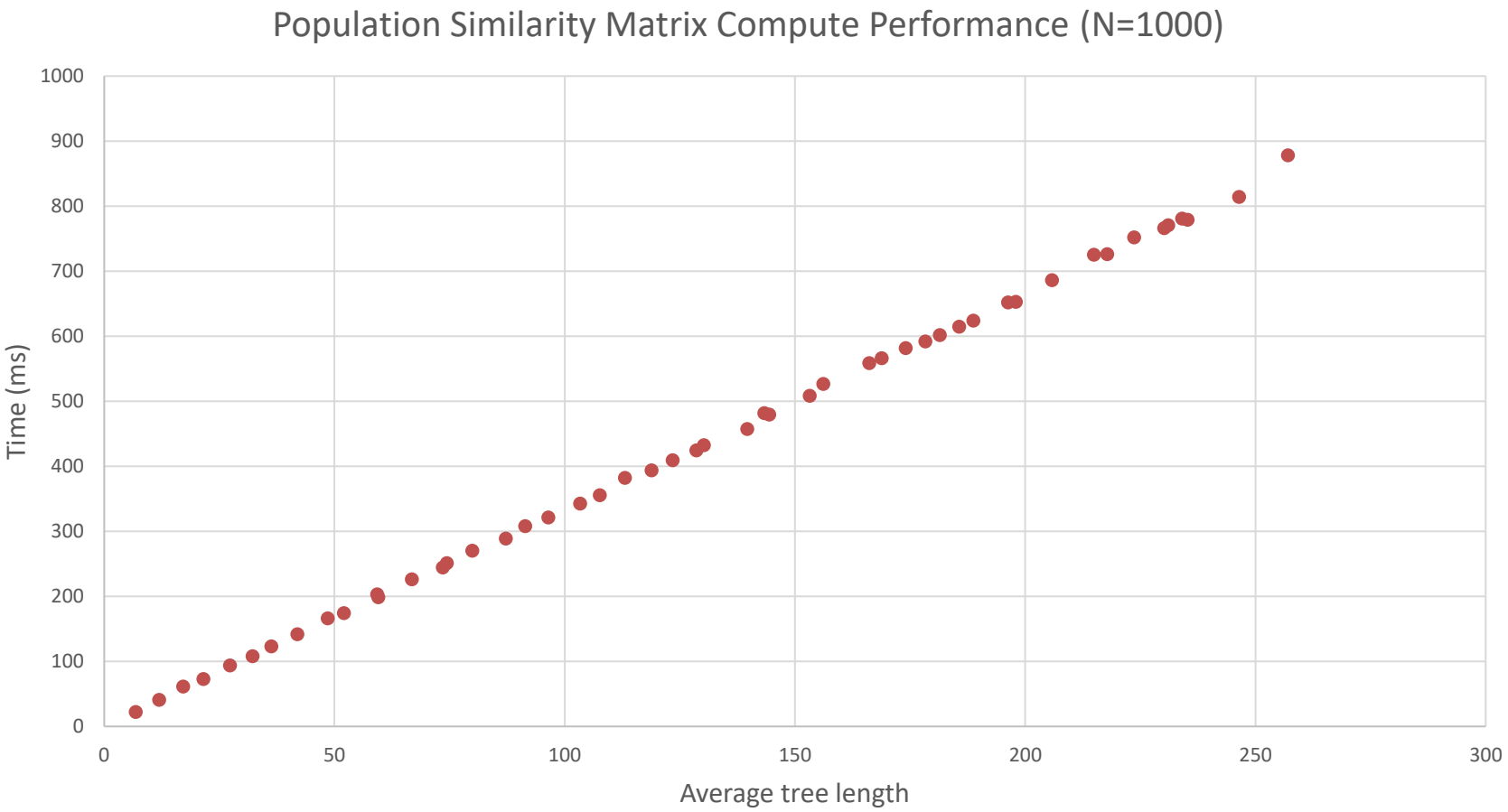
input : Two sorted hash arrays H_1 and H_2
output : The number of common hash values

```
1  i ← 0, j ← 0, count ← 0;
2  while i < |H1| and j < |H2| do
3      if H1[i] = H2[j] then
4          count ← count + 1;
5          i ← i + 1;
6          j ← j + 1;
7      else if H1[i] < H2[j] then
8          i ← i + 1;
9      else
10         j ← j + 1;
11 return 1 − 2 · count / (|H1| + |H2|)
```

TABLE I
RUNTIME PERFORMANCE OF HASH-BASED TREE DISTANCE VS THE BOTTOM-UP TREE DISTANCE

Tree distance method	Elapsed time (s)	Speed-up
Bottom-up	1225.751	1.0x
Hash-based (single-mode)	297.521	4.1x
Hash-based (batch-mode)	3.677	333.3x

Generational Overhead



Distance-based Diversity Control

Idea

- Compute distance matrix every generation
- For each individual, compute average distance to the rest of the population
- Promote diversity: focus on exploration, favour individuals that are farther from the rest

Structural and semantic diversity

- Tree distance inherently structural
- Tree semantics: include node coefficients in hash value calculation
- “strict” hashing → distinguish same structures with different semantics (coefficients)

Implementation

- Standard GA: weighted sum between fitness and average tree distance
- NSGA-II: average tree distance as secondary objective

Empirical Analysis

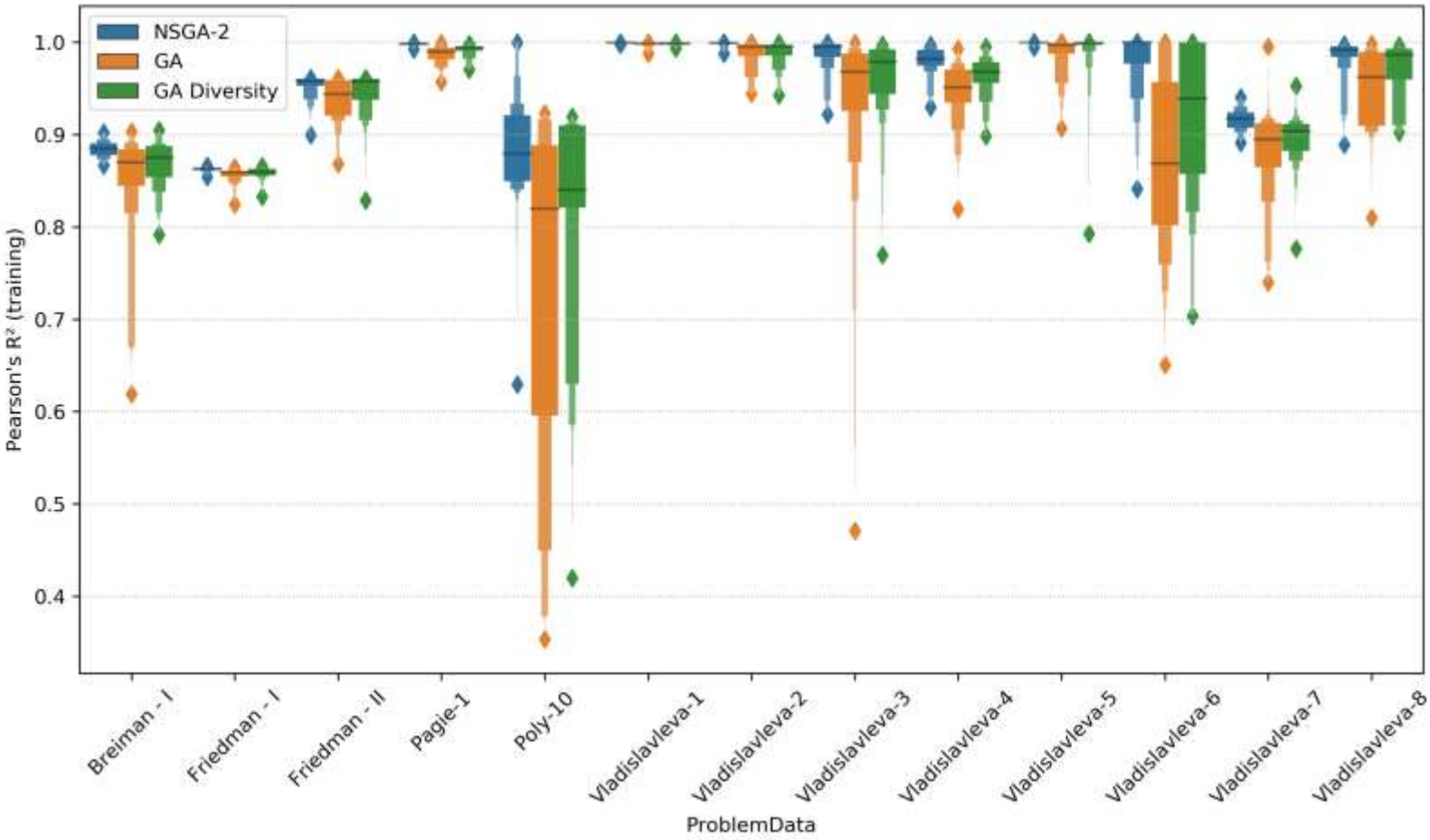
Algorithms: NSGA-2, GA, GA with diversity penalty term

Population size	1000
Generations	500
Crossover probability	100%
Crossover operator	Subtree crossover
Mutation probability	25%
Mutation operator	Remove branch, replace branch, change node type, one-point mutation
Selector	Tournament (GA) / Crowded tournament selector (NSGA-2), tournament size = 5
Tree initialization	Probabilistic tree creator (PTC2)
Maximum tree length	50
Maximum tree depth	12
Function set	$(+, -, \times, \div, exp, log, sin, cos, square)$

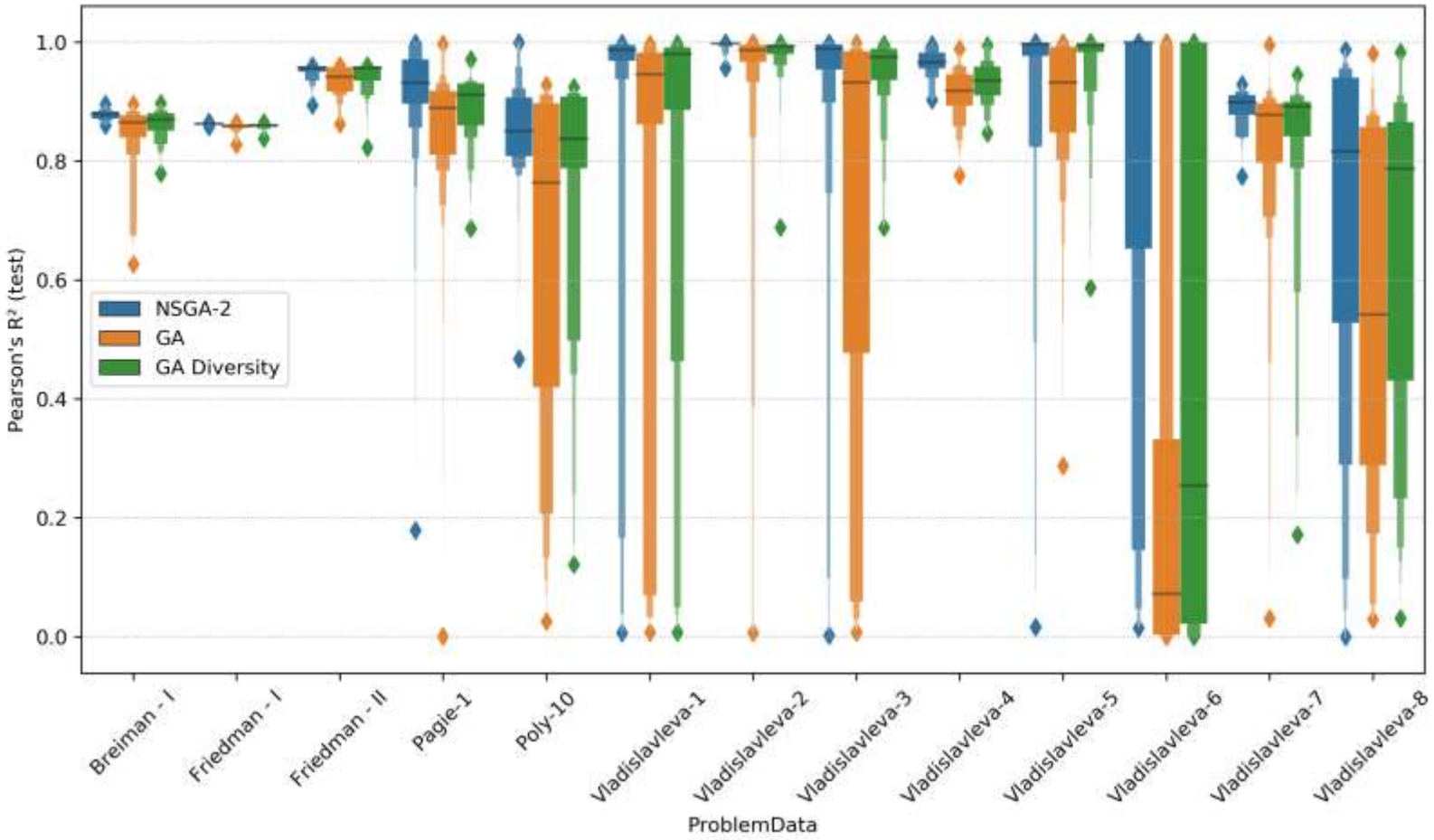
Benchmark problems:

- Vladislavleva $(F_1, \ldots, F_8)$
- Breiman-I, Friedman-I, Friedman-II
- Poly-10, Pagie-1

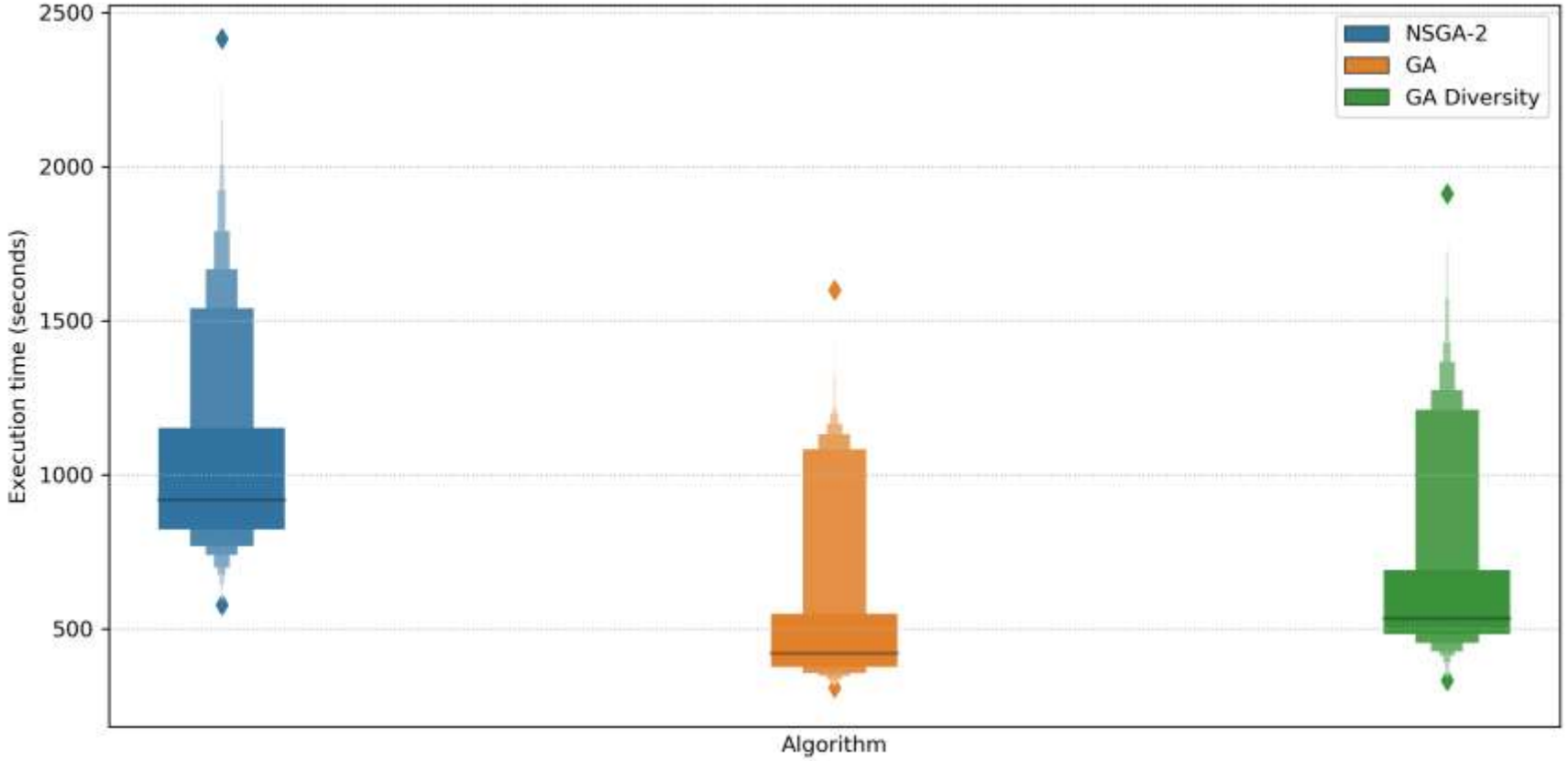
Training Solution Quality



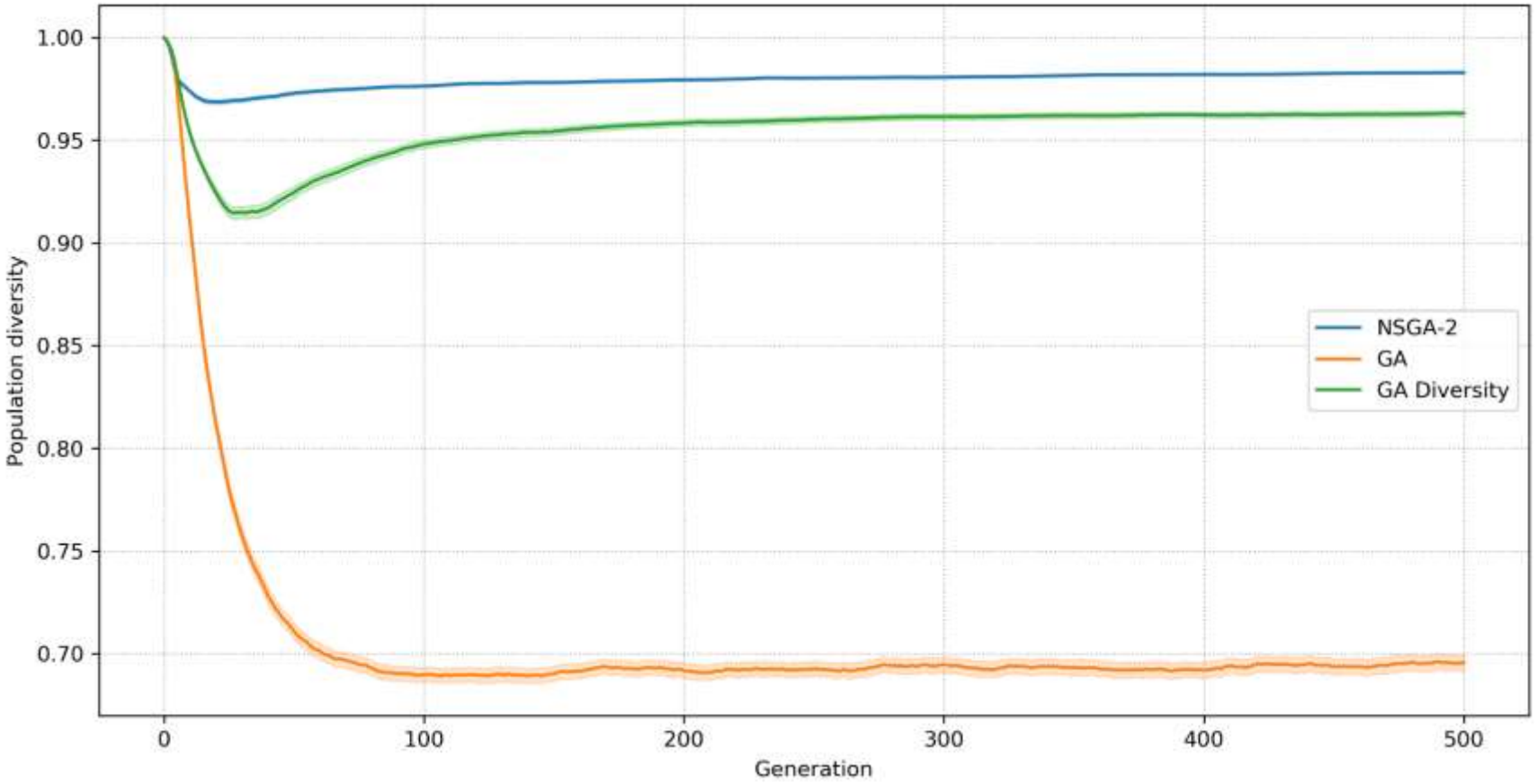
Test Solution Quality



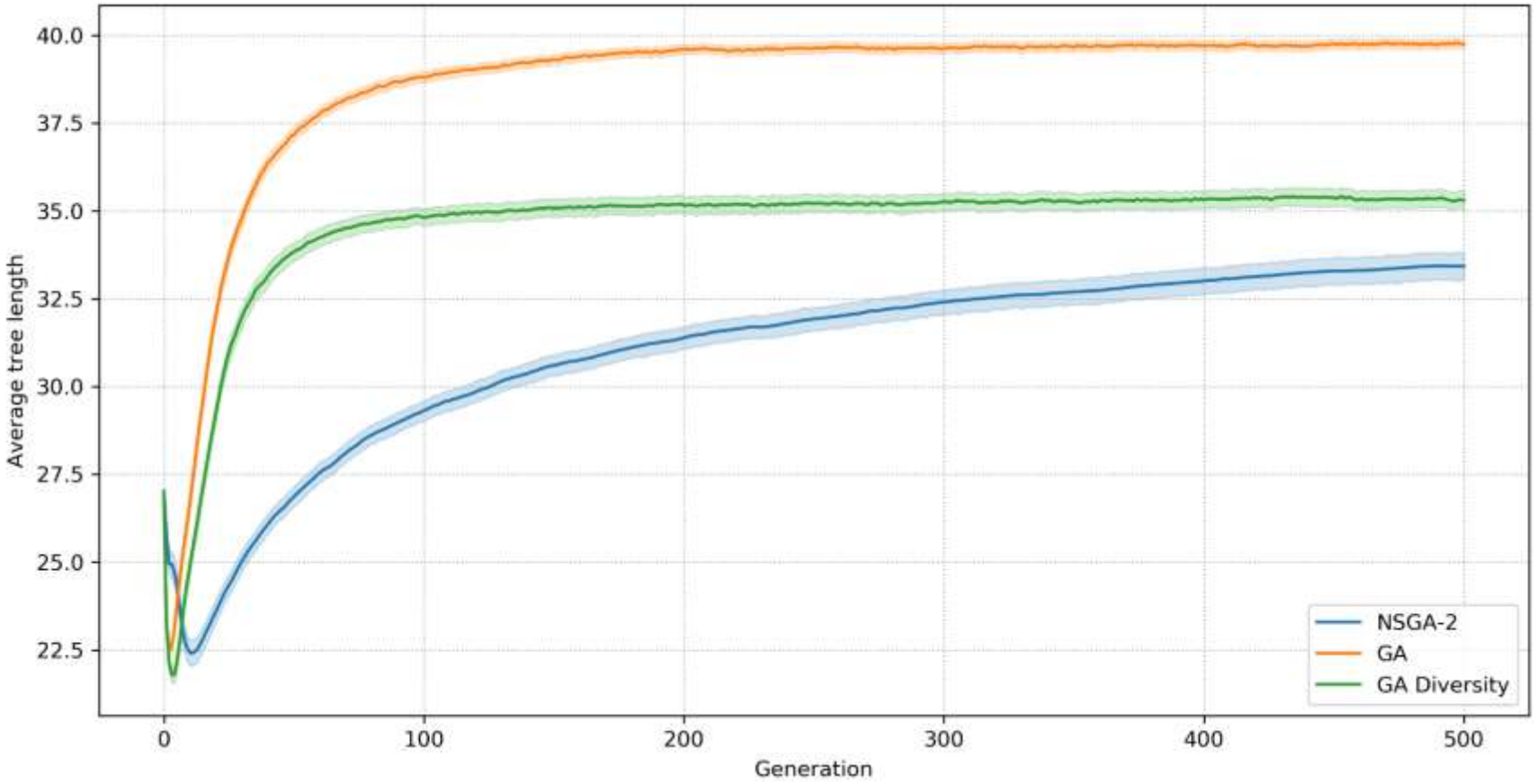
Execution Time



Population Diversity



Average Tree Length



Mining Common Subtrees

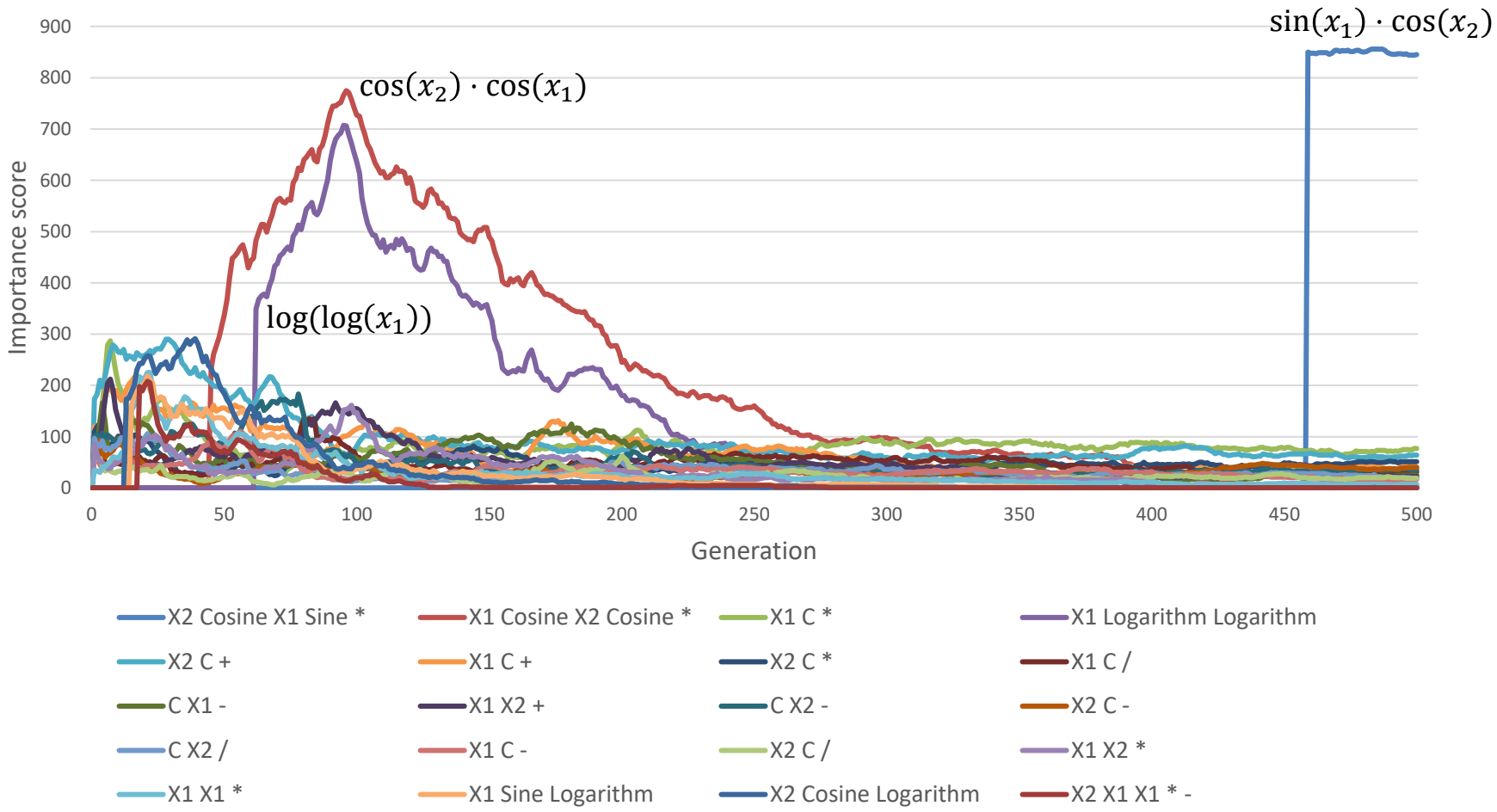
- **Hash entire population and count hash value frequencies**

- **Building blocks**
  - Building blocks discovered later in the run should count more
  - Use a weighted sum approach
  - Importance score calculated as

$$Score = \sum_{i=0}^{MAXGEN} i \cdot freq_i$$

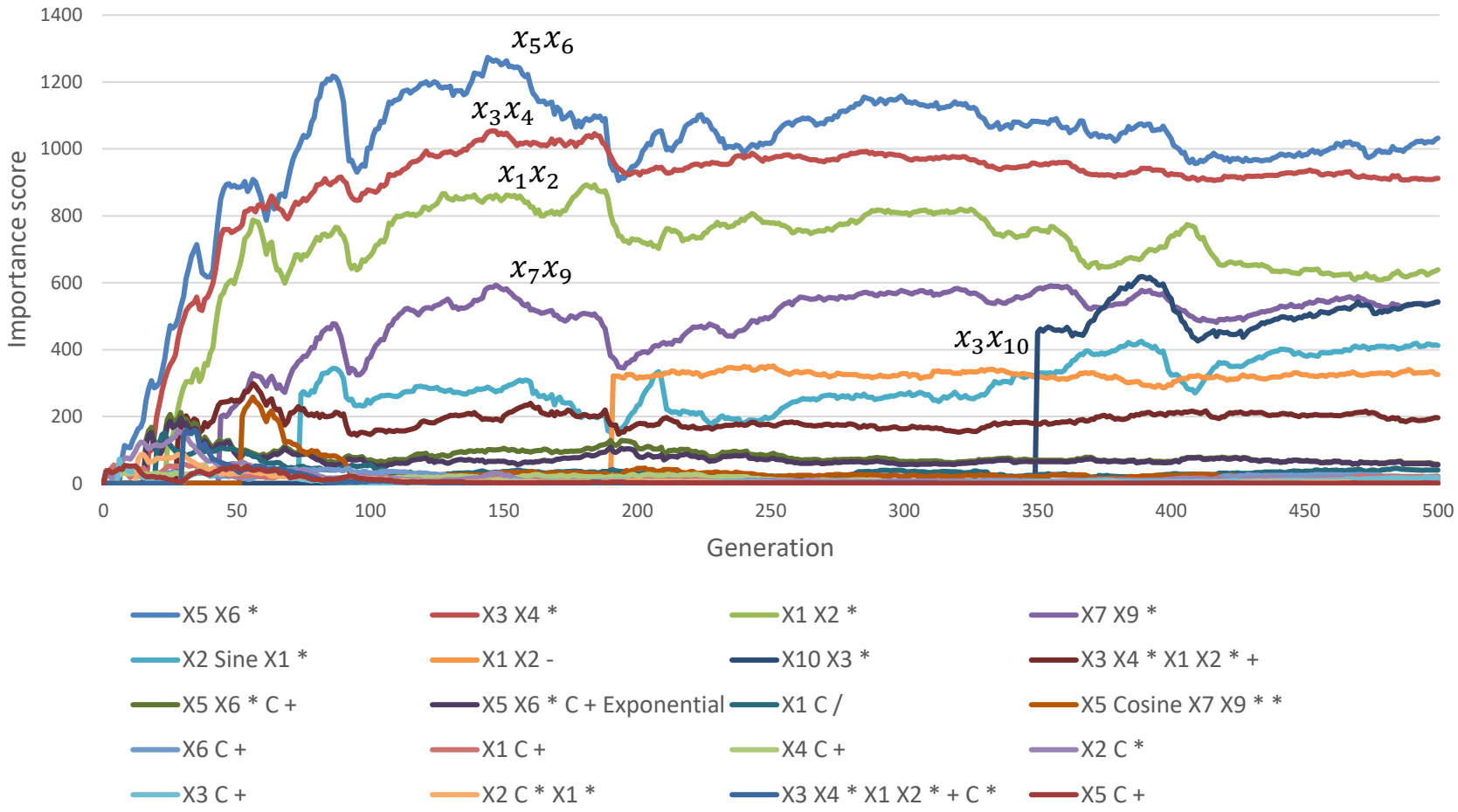
Most Common Subtrees – Example 1

Vladislavleva-6 $F(\mathbf{x}) = 6 \cdot \sin(x_1) \cdot \cos(x_2)$



Most Common Subtrees – Example 2

Poly-10 $F(\mathbf{x}) = x_1x_2 + x_3x_4 + x_5x_6 + x_1x_7x_9 + x_3x_6x_{10}$



Conclusion

Efficient hashing method for expression trees

- Simple, linear data structures
- Sorting of node arguments for handling unordered trees and commutative symbols
- Each tree hashed only once
- Mining of common subtrees in the population

Used to identify equivalent expressions

- Simplification of same terms

Hash-based tree distance feasible to use online

- Incorporates tree semantics by hashing leaf node coefficients
- Diversity measure prevents premature convergence
- Helps create solutions with better generalization capabilities
- Suitable as secondary objective (NSGA-2)

Discussion

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