Equidistant Reorder Operator for Cartesian Genetic Programming

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Abstract: The *Reorder* operator, an extension to *Cartesian Genetic Programming* (CGP), eliminates limitations of the classic CGP algorithm by shuffling the genome. One of those limitations is the *positional bias*, a phenomenon in which mostly genes at the start of the genome contribute to an output, while genes at the end rarely do. This can lead to worse fitness or more training iterations needed to find a solution. To combat this problem, the existing *Reorder* operator shuffles the genome without changing its phenotypical encoding. However, we argue that *Reorder* may not fully eliminate the positional bias but only weaken its effects. By introducing a novel operator we name *Equidistant-Reorder*, we try to fully avoid the positional bias. Instead of shuffling the genome, active nodes are reordered equidistantly in the genome. Via this operator, we can show empirically on four Boolean benchmarks that the number of iterations needed until a solution is found decreases; and fewer nodes are needed to efficiently find a solution, which potentially saves CPU time with each iteration. At last, we visually analyse the distribution of active nodes in the genomes. A potential decrease of the negative effects of the positional bias can be derived with our extension.

1 INTRODUCTION

Cartesian Genetic Programming (CGP) is a form of *Genetic Programming* (GP), based on *directed acyclic graphs* whose nodes are arranged in a two-dimensional grid.

Since its inception in 1999 by Miller, CGP has been used for various applications (Miller, 1999). Originally, Miller used it to evolve digital circuits (Miller, 1999), which is still a use case to this day (Froehlich and Drechsler, 2022; Manazir and Raza, 2022). Furthermore, the CGP concept is used in a diverse field of problem domains like classification or regression (Miller, 2011). Other works utilized CGP for image segmentation (Leitner et al., 2012; Margraf et al., 2017) or the evaluation of sensor data (Huang et al., 2022; Bentley and Lim, 2017).

CGP has some advantages over GP, such as the absence of bloat (Miller, 1999): Solutions becoming larger without an increase in fitness. However, there are also some downsides and limitations in CGP. One of those limitations is its *positional bias*, an effect which potentially limits CGP to fully explore its search space (Goldman and Punch, 2013a). To counteract this problem, Goldman and Punch introduced *Reorder*, an operator to shuffle CGPs genome ordering without changing its phenotype (Goldman and Punch, 2013a). However, we believe that Reorder suffers from some limitations, too, which could lead to the search space being explored inefficiently. This, in turn, could increase the iterations needed for training as CGP gets stuck in local optima. To mitigate this problem, we introduce a modification to Reorder: *Equidistant-Reorder*. With our modification, the genome is not shuffled randomly anymore. By additionally influencing the genomes reordering, the effects of the positional bias may be further lessened. In turn, CGP with *Equidistant-Reorder* needs less iterations to find a solution, which can save computational time.

In the following Section 2, we provide a quick overview of the core principles of CGP and reintroduce the *Reorder* operator. Afterwards, Section 3 gives an overview of related work. In Section 4, we discuss the aforementioned limitation of Reorder more in-depth. Furthermore, we formally introduce and explain our operator: Equidistant-Reorder. Af-

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terwards, its performance is analysed using several Boolean benchmark problems in Section 5. At last, Section 6 summarizes our findings and discusses future research directions.

2 CARTESIAN GENETIC PROGRAMMING

In the following section, the core principles of the supervised learning algorithm called *Cartesian Genetic Programming* (CGP) is reintroduced. In addition, the CGP's extension *Reorder* by Goldman and Punch is presented (Goldman and Punch, 2013a).

The standard CGP variant described in Section 2.1 will be called STANDARD in the next sections to improve readability. Apart from that, a CGP variant with the *Reorder* operator employed will be called REORDER.

2.1 Representation

Traditionally, CGP is represented as a directed, acyclic and feed-forward graph. This graph contains *nodes* which are arranged in a $c \times r$ grid, with $c \in \mathbb{N}_+$ and $r \in \mathbb{N}_+$ defining the number of columns and rows in the grid respectively. Given an arbitrary amount of program inputs, the CGP model feeds those inputs forward through its partially connected nodes to get any desired amount of outputs. Please note that, with today's standards, a CGP model typically consists of only one row (Miller, 2011). That means, $r = 1$.

The set of nodes can be divided into three groups: *input-*, *computational-* and *output-nodes*. Input nodes directly receive a program input. Their only purpose is to relay the program input. Differently, computational nodes are represented by a function gene and a connection genes. Here, $a \in \mathbb{N}_+$ is the maximum arity of all functions in the predefined function set, while the function gene addresses the encoded computational function of the node. Please note that if a function needs less than a inputs, all excessive input genes are ignored. At last, output nodes redirect the calculated output of a computational node and define the model's output. They are represented by a single connection gene, which defines a path between a previous node and the current node.

In this sense, when we mention a graph with $N \in \mathbb{N}_+$ nodes, this graph will have only one row, N computational nodes and additional input and output nodes corresponding to the given learning task.

Another important distinction of computational nodes are *active* and *inactive* nodes. Active nodes are part of a path to an output node. Hence, they actively contribute to a program output. On the contrary, inactive nodes do not contain a path to an output node and do not contribute to the model's output. However, inactive nodes are essential to CGP as they probably aid the evolutionary process through genetic drift (Turner and Miller, 2015).

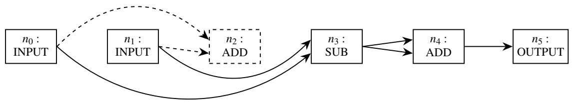


Figure 1: Example graph defined by a CGP genotype. The dashed node and connections are *inactive* due to not contributing to the output.

An illustrative example of a graph defined by a CGP genotype can be seen in Figure 1. It shows a graph with $c = 6$ and $r = 1$, which is supposed to solve a task consisting of two inputs and one output. Here, the first two nodes (n_0 and n_1) are input nodes and provide two different program inputs. The following nodes (n_2–n_4) are computational nodes. At last, the output is provided by one output node n_5. In this example, both inputs are subtracted, with this intermediate result being added to itself and taken as the program output. Thus, every node drawn with a solid line is an active node. The node n_2 is an inactive node (marked by dashed lines) since it does not contribute to the program output nor contains a path to an output node.

2.2 Evolutionary Algorithm Used by CGP

As is standard in most CGP variants, an *elitist* $(\mu + \lambda)$ evolution strategy with $\mu = 1$ and $\lambda = 4$ is used to select the best graph. This is combined with neutral search to improve performance and convergence time (Turner and Miller, 2015; Yu and Miller, 2001; Vassilev and Miller, 2000). Here, neutral search means that, when an offspring and the current parent have the same fitness value, the offspring is always chosen as the next parent. Hence, by always preferring the child, *neutral drift* is allowed to occur. For that reason, the search algorithm is exploring various possible solutions given by different genotypes (Miller, 2020).

Regarding its mutation operator, a *point mutation* is oftentimes found in literature (Miller, 2011; Miller, 2020). Here, the operator simply iterates over all genes, mutating each with a probability defined by the user (Miller, 2011). However, for this mutation operator, it is possible that only inactive genes are mutated. As no active node is changed, it is not possible to evaluate the quality of the newly mutated program. This could potentially lead to more training iterations needed and introduce fitness plateaus.

In order to prevent such plateaus, Goldman and Punch propose an alternative mutation operator which they call *Single* (Goldman and Punch, 2013b). For this method, randomly selected genes are mutated until a gene corresponding to an active node is mutated. This approach has the advantage that no wasted evaluations are performed and a change in the phenotype is guaranteed. Furthermore, as inactive nodes are mutated too, genetic drift is also able to occur. Thus, when the optimal mutation rate is not known, the authors Goldman and Punch claim that *Single* should be preferred (Goldman and Punch, 2013b).

2.3 Extension: Reorder

By enforcing a feed forward grid, Goldman and Punch found a negative impact in CGPs search space (Goldman and Punch, 2013a). One insight is a *positional bias*: a non-uniformity of the probability that a node is active. When nodes are closer to the input nodes, their probability of becoming active is higher. The other way round, nodes closer to the output nodes have the lowest probability of becoming active.

During the mutation of a connection gene, each previous node has the same probability of being chosen as the new starting node for the connection. However, nodes near input nodes have more options for successor nodes, as directed edges are only allowed from left to right. This is why they have a higher chance of becoming active, as a node is only active when it is part of a path to an output node. Nodes closer to output nodes have less options of being chosen by other nodes, as they have less nodes in front.

With the help of Figure 1, the positional bias can be exemplified. In this example, n_1's possible successors are n_2–n_5 whereas n_4's possible successor is just n_5. Hence, four nodes can potentially mutate their connection to n_1 and if one of those nodes is active, n_1 becomes active, too. Contrary, n_4 has only one node in front which could mutate its connection to n_4.

This leads to some drawbacks, as this positional bias makes it difficult or impossible to solve certain problems (Goldman and Punch, 2013a; Payne and Stepney, 2009). To combat such limitations, Goldman and Punch proposed two new operators which are executed before mutation: *DAG* and *Reorder* (Goldman and Punch, 2013a). The first extension, *DAG*, allows each node to mutate connections to every other node in the genome as long as the new connection does not create a cycle. However, as we do not build upon it, we will not discuss *DAG* in further detail. As for *Reorder*, this extension shuffles the genome's node ordering, with the result of a shuffled genotype. Nevertheless, by respecting the sequence of operations of the active nodes, the phenotype does not change.

This *Reorder* operator begins by creating a dependency set D, containing each computational node and the nodes from which it gets its input from. In addition, the new genome is initialized. Here, the new genome contains all input and output nodes from the original genome, as they do not get assigned a new position. Afterwards, the set of *addable* nodes Q is created. Initially, this set contains only computational nodes whose dependencies are *satisfied*. Let b be a computational node, and a be a computational or input node from which b gets one input from, with $(b,a) \in D$. This means, there is a directed edge connecting a to b via b's connection gene. Then, in this context, b is satisfied when all nodes from which b gets its input from are mapped into the new genome.

With both sets initialized, the shuffling of the genome is done by repeating the following steps:

1. Select and remove a random node $a \in Q$.
2. Map a sequentially to the next, free location in the new genome.
3. For each node pair $(b,a) \in D$ with b depending on a, do:
   (a) If all dependencies of b are satisfied, add b to Q.

This operator ends when all computational nodes have been assigned a new location in the genotype.

By always satisfying each nodes dependency, the phenotype stays the same. Hence, the fitness value of the genome does not change by re-evaluating. However, by permutating the genome ordering, the authors of (Goldman and Punch, 2013a) show a theoretical improvement of a mutation. This improvement is also shown empirically on four different benchmarks, as utilizing *Reorder* can lead to fewer iterations needed until a solution is found (Goldman and Punch, 2015; Goldman and Punch, 2013a).

3 RELATED WORK

Our work focuses on improving the *Reorder* operator, which has, to the best of our knowledge, not been explored yet. Nevertheless, various other articles layed out the foundation for this work.

Goldman and Punch detected the aforementioned positional bias (Goldman and Punch, 2013a; Goldman and Punch, 2015). To mitigate its effects, they introduced *Reorder* and *DAG*.

Moreover, other works explore new operators for CGP and / or its search space and its limitations, too.

There are various algorithms which extend the basic CGP formula. One such extension was developed by Kalkreuth (Kalkreuth, 2022). By introducing two new operators to duplicate or swap genes in the phenotype, CGP is able to find a solution in less iterations.

Another possibility of changing CGPs geno- and phenotype was introduced by Walker and Miller (Walker and Miller, 2004). With their extension, nodes or subgraphs in the genotype can be dynamically created, evolved, reused and removed. This leads to higher fitness values and less iterations needed to find good solutions.

Harding et al. included a multitude of additional functions in the function pool (Harding et al., 2011). These functions directly change CGPs phenotype and allows it to solve problems with extremely large numbers of inputs. Some of these additional functions were then reused to allow CGP to solve image processing tasks, as was done by Leitner et al. or Harding et al. (Leitner et al., 2012; Harding et al., 2013).

At last, Wilson et al. (Wilson et al., 2018) introduced a different representation of CGP based on a floating point representation. In addition, they included operators to change the genotype, too, which enabled them to add or remove nodes or even whole subgraphs.

CGPs search space is another important factor for its performance. In the context of neural architecture search, Suganuma et al. used a highly specified function set to reduce the size of CGPs search space (Suganuma et al., 2020).

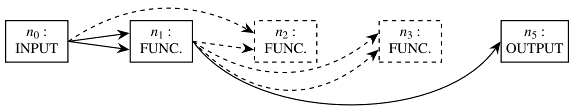
It is also possible to improve the search space by using specific crossover operators, as was done by Torabi et al. (Torabi et al., 2022).

4 EQUIDISTANT-REORDER

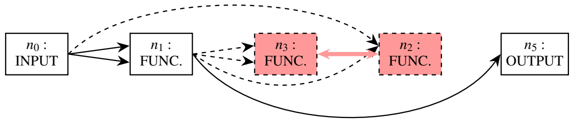
While REORDER has the potential to decrease the number of iterations needed until a solution is found, it is also possible that it does not fully reduce the aforementioned limitation in the search space. This Section argues a potential drawback of REORDER and introduces CGP with *Equidistant-Reorder*, called E-REORDER—a modified variant of REORDER to avoid the flaw.

4.1 Potential Limitation of Reorder

With the *Reorder* operator, a node can only be assigned a new position in the grid when all its dependencies are satisfied. This means that, at first, the only satisfied node dependencies are nodes directly connected to input nodes. Furthermore, computational nodes near input nodes have a higher probability of being connected to input nodes. The reason is that these nodes have little or no computation nodes prior to them. Hence, they are more prone to being connected to input nodes compared to nodes near output nodes.



(a) A graph before Reorder. Input and output node are n_0 and n_5, respectively. Nodes n_1–n_3 are computational nodes, with *FUNC.* being an arbitrary function.



(b) The graph after a potential Reorder.

Figure 2: A graph defined by a CGP genome, before and after *Reorder*.

As a consequence, computational nodes near the input nodes have a higher probability of getting added to the set of addable nodes earlier, compared to other computational nodes. This leads to them having a higher probability of being added earlier into to the new, shuffled genome, too. Hence, they get assigned a new position which is, again, closer to the input nodes.

This limitation can be visualized by Figure 2. Here, the aforementioned problem is illustrated. Figure 2a shows a graph before its reordering. As n_1 is only connected to the input node, it is the only node with satisfied dependencies. Hence, it is the only node added to the *addable* set and will be reordered to the first position in the new genome. Therefore, the only active node of the graph will not change its position in the grid. Generally, it is not possible for n_1 to change its position in this graph setup with the *Reorder* operator.

After adding n_1 into the new genome, n_2 and n_3 have satisfied dependencies. They will be placed into the genome afterwards and a potential solution can be seen in Figure 2b.

4.2 Equidistant-Reorder Operator

To circumvent the limitation described in Section 4.1, we propose a different strategy to reorder nodes. For our method, all active nodes are placed equidistantly apart in the grid first; hence we name our method *Equidistant-Reorder*, and a CGP variant with our method will be called E-REORDER in the remainder of this work. Furthermore, as mentioned in Section 2.3, STANDARD suffers from positional bias. By spreading active nodes over the whole genome, this drawback should be lessened, too.

To perform E-REORDER on a genome with N computational nodes, two sets must be obtained. The first set A defined as $A := \{a_1, \cdots, a_n \mid a_i \text{ is active computational node}\}$ contains all active computational nodes. In addition, the set of all inactive computational nodes $\tilde{A} := \{\tilde{a}_1, \cdots, \tilde{a}_m \mid \tilde{a}_i \text{ is inactive computational node}\}$ is needed as well. Afterwards, a new modified genome G is initialized. Initially, G contains all input and output nodes from the original genome, as these two node sets will not be assigned a new position. Please note that the positions of all input and output nodes are not changed in this algorithm. Then, let s be the starting index and e be the last index of computational nodes in the genome.

With these values, a set of equidistantly spaced numbers $L := \left\{ \lfloor s + i \cdot \frac{e-s}{n} \rfloor \mid i = 1, \cdots, n \right\}$ over the interval $[s, e]$ can be generated. Here, L is the set of new positions for active nodes. To further illustrate the generation of L, Algorithm 1 describes it more in-depth. However, if $n = 1$, then $L := \{e\}$. This means, if there is only one active node, it will be placed at the end of the genome just before the output nodes. As a result, the active node is able to mutate its connection to an arbitrary computational node, which should further lessen the positional bias.

On the contrary, $\tilde{L}$ is the set of all genome locations without the positions of active nodes, which is defined as $\tilde{L} := \{s, s+1, \cdots, e\} \cap L := \{\tilde{l}_1, \cdots, \tilde{l}_{N-n}\}$ with $\tilde{l}_1 < \tilde{l}_2 < \cdots < \tilde{l}_n$. Hence, $\tilde{L}$ is the set of new positions for inactive nodes.

Now, active computational nodes can be placed into a new position in G by assigning $a_i \in A$ the position $l_i \in L$, for $i = 1, \cdots, n$. As the order of computational nodes are not modified, the reordering does not change the semantic and no re-evaluation is required.

Next, inactive nodes are placed in order into G by assigning them into the next genome location without an active node in G. As such, the new position of an inactive node $\tilde{a}_j \in \tilde{A}$ is defined by $\tilde{l}_j \in \tilde{L}$ with $j = 1, \cdots, N-n$.

At last, all connection genes must be corrected by changing their connection from the old genome location to the new one. Problems can arise in the case of inactive nodes, as it is possible that a connection gene gets assigned a new position in front of the current node. In this case, a new connection to a previous node must be mutated.

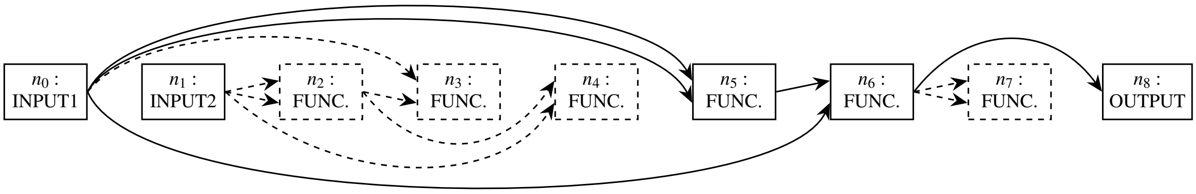
To better illustrate the algorithm of *Equidistant-Reorder*, its workings are depicted in Algorithm 2. Furthermore, Figure 3 shows two example graphs, with Figure 3a depicting an example graph. Figure 3b displays the graph after *E-Reorder*. Both active nodes are placed evenly spaced into the new genome, with the inactive node being assigned to the free position.

```
Function Lin-Space:
    Data:
      • start point s
      • end point e
      • number of evenly spaced values n
    step ← (e − s) / n;
    S ← ∅;
    i ← 1;
    while i ≤ n do
        S ← S ∪ ⌊s + i · step⌋;
        i ← i + 1;
    end
```

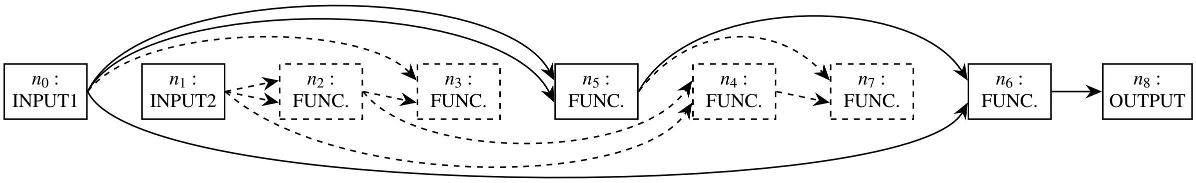
Algorithm 1: Generate a set of equidistantly spaced numbers.

```
Function Equidistant-Reorder:
    A ← all active computational nodes;
    Ã ← all inactive computational nodes;
    initialize new genome G with the same
      input and output nodes from the old
      genome;
    s ← |input_nodes|;
    e ← |input_nodes| + |A| + |Ã|;
    L ← Lin-Space(s, e, |A|);
    L̃ ← {s, s+1, ···, e} ∩ L;
    foreach (a, l) ∈ (A, L) do
        G[l] ← a;
    end
    foreach (ã, l̃) ∈ (Ã, L̃) do
        G[l̃] ← ã;
    end
    foreach node ∈ G do
        foreach connection_i belonging to
          node do
            update(connection_i);
            if connection_i points to the front
              then
                mutate connection_i;
            end
        end
    end
    return G;
```

Algorithm 2: Equidistant-Reorder function.



(a) A graph before E-Reorder. Input and output node are n_0, n_1 and n_8. Nodes n_2–n_7 are computational nodes, with *FUNC.* being an arbitrary function.



(b) The graph after a potential E-Reorder, according to Algorithm 2. Node n_7 must mutate new connections to prevent connections backwards from the new position of n_6 to n_7.

Figure 3: A graph defined by a CGP genome, before and after *E-Reorder*.

4.3 Time Complexity

The modifications of *Equidistant-Reorder* compared to the original *Reorder* operator from Goldman and Punch have the same additional runtime complexity (Goldman and Punch, 2013a). In the following, let $N \in \mathbb{N}_+$ be the number of computational nodes of the considered CGP graph.

To obtain the set of all active and inactive computational nodes, $O(a \cdot N)$ time is needed, where $a \in \mathbb{N}_+$ is the arity of the nodes. Other sets, like L or $\tilde{L}$, need $O(N)$ time. The placing of active and inactive nodes into a new genome takes only $O(N)$ time, as this only requires iterating through the sets of active and inactive nodes and their respective new positions once. At last, the connection genes have to be updated. Nevertheless, this process takes only $O(c \cdot N)$ time by iterating through every computational node and updating its c connection genes. Please note, $a \equiv c$, as the highest arity a is also the number of connection genes c.

Thus, *Equidistant-Reorder* needs $O(a \cdot N)$ time, which is the same as *Reorder* (Goldman and Punch, 2015).

5 EVALUATION OF E-REORDER

In order to find out whether the modification we proposed for *Reorder* truly benefits CGP, we conducted an empirical study[1]. This section describes our experimental design. Afterwards, we attempt to answer the following two questions:

Q1 Which model needs, considering the learning task, less training iterations: REORDER or E-REORDER?

Q2 As mentioned in Section 4.1, REORDER may not reduce the limitation in the search space of CGP. How does E-REORDER perform compared to REORDER?

5.1 Experimental Design

In this section, the evaluated CGP configurations and utilized benchmarks are presented. Afterwards, we briefly describe the Bayesian models used to evaluate and rank different CGP configurations. With these models, the performance of multiple configurations can be compared by calculating a probability of each configuration being the best.

5.1.1 Settings of CGP

For our experiments, we compared each combination of STANDARD, REORDER and E-REORDER in conjunction with two different mutation strategies: *point mutation* and *Single*. Regarding the hyperparameters, when the mutation operator *Single* is used, the only hyperparameter is the number of nodes N. Thus, we investigated $N \in \{50, 100, 150, \cdots, 2000\}$ and each N was tested 75 times with independent repetitions and different random seeds.

As for the *point mutation*, the number of nodes N and the mutation probability p must be determined.

[1]Implementation and benchmarks can be found at https://github.com/CuiHen/Equidistant_Reorder.

For this task, we performed a hyperparameter search using a Tree-structured Parzen Estimator[2]. The algorithm performed a total of 100 trials to find good hyperparameters. For each trial, the configuration was tested 10 times with independent repetitions and different random seeds. These results were then averaged to obtain a single value. Runs were terminated when a model is able to solve a benchmark completely.

Considering the evolutionary algorithms, we utilized a standard $(1+4)$-ES as described in Section 2.2 for all trainings. Furthermore, to be comparable to the original evaluations by Goldman and Punch, we also compared different mutation strategies as already mentioned above (Goldman and Punch, 2015; Goldman and Punch, 2013a). The original works compared two different strategies for the point mutation: *skip* and *accumulate*. However, they did not change the behaviour of the point mutation but save computational time only. Furthermore, the authors of the work (Goldman and Punch, 2015) found no significant difference between those two operators. Because of that, we employed their point mutation strategy of *skip*. Offsprings, whose phenotype are equal to the parents phenotype, are not evaluated. Instead, they get their parents fitness value assigned.

5.1.2 Problem Set

To evaluate the different settings, we used four Boolean benchmark problems: 3-*bit Parity*, 16-4-*bit Encode*, 4-16-*bit Decode* and 3-*bit Multiply*. In the following, we will call these *Parity*, *Encode*, *Decode* and *Multiply*, respectively. Parity is regarded as too easy by the Genetic Programming community (White et al., 2013). Nevertheless, it is commonly used as a benchmark in the literature (Yu and Miller, 2001; Kaufmann and Kalkreuth, 2020; Kaufmann and Kalkreuth, 2017). Hence, we also included it in our evaluations for ease of comparison. Encode and Decode are problems with different input and output sizes. At last, Multiply is a comparatively hard problem (Walker and Miller, 2008), and recommended by White et al. (White et al., 2013). All four benchmarks are used to evaluate REORDER, too, which is also why we utilized them (Goldman and Punch, 2013a; Goldman and Punch, 2015).

As we employed four Boolean benchmark problems, we also trained them with the standard function set for these problems. They contain the Boolean operators *AND*, *OR*, *NAND* and *NOR*.

These benchmarks also lead to a standard fitness function, which is defined by the ratio of correctly mapped inputs. Let $f:\{0,1\}^n \rightarrow \{0,1\}^m$ be a correct Boolean mapping for $n \in \mathbb{N}_+$ inputs and $m \in \mathbb{N}_+$ outputs. Then, the fitness of an individual $g:\{0,1\}^n \rightarrow \{0,1\}^m$, which relates to the learning task f, is defined as follows:

$$\frac{|\{x \in \{0,1\}^n \mid f(x) = g(x)\}|}{|\{0,1\}^n|} \tag{1}$$

5.1.3 Bayesian Data Analysis

In search of a good number of nodes for *Single*, multiple configurations were investigated. Furthermore, to present our final results, six different, final settings were compared. In all those cases, each configuration has to be ranked to find the respective best solution. However, we only considered the number of training iterations, a unit which can not be negative. Thus, other common distributions such as Student's t distributions can not be expected to model the data well. Hence, we performed a Bayesian data analysis[3] for the posterior distributions of our results. The model to compare the algorithms is based on the Plackett-Luce model described by Calvo et al. (Calvo et al., 2018). It allows the computation of a set of ranked options by estimating the probabilities of each of the options to be the one with the highest rank.

In addition, in our final results, we report for each configuration the 95 % *highest posterior density intervals* (HPDI) of the distribution of μ_{config}, where μ_{config} is a random variable corresponding to the respective *mean numbers of iterations until solution*. At that, the distribution of μ_{config} is estimated by the gamma distribution–based model for comparing non-negative data from *cmpbayes* (Pätzel, 2023). Please note, a 95 % HPDI interval $[l,u]$ can be read as $p(l \leq \mu_{config} \leq u) = 95\,\%$. This means, the probability of the algorithms results lying between the bounds l and u has a probability of 95 %.

On another note, prior sensitivity analyses were conducted prior to ensure the robustness of all models. As they always display similar results, robust and meaningful models are implicated. Finally, please note that *cmpbayes* uses Markov Chain Monte-Carlo sampling to obtain its distributions. Therefore, the usual checks to ensure convergence and well-behavedness (trace plots, posterior predictive checks, $\hat{R}$ values, effective sample size) were performed. For more information regarding the models, we refer to Kruschke and Pätzel (Kruschke, 2013; Pätzel, 2023).

[2]For the hyperparameter search, we utilized the Python library Optuna (Akiba et al., 2019).

[3]We utilized the Python library *cmpbayes* (Pätzel, 2023) for all statistical models.

5.2 Performance on Training Iterations

As already mentioned, we performed a hyperparameter search and determined the best configuration via a Plackett-Luce model described by Calvo et al. (Calvo et al., 2018).

The best results found by the hyperparameter search can be seen in Table 1. For each benchmark, the configurations are sorted from best to worst in descending order. We report the CGP variant and its mutation operator. Furthermore, we list, with their respective averaged number of iterations needed until a solution is found, its HPDI, the number of nodes needed, their mutation rate, the number of active nodes and the probability of a solution being the best.

For all four benchmarks, our novel variant E-REORDER probably performed best. For Encode and Decode, E-REORDER with *Single* lead to the best results while Encode and Parity performs best with the point mutation. This could also mean that we were not able to find the best mutation rate with our hyperparameter search. Albeit when looking at the results for E-REORDER in the context of Encode, the differences of both mutation operators are almost negligible. The average number of iterations needed are almost identical and their HPDI are close, too. Although, according to the Calvo model, the probabilities for E-REORDER with its respective mutation operators are not equal but differ about 5 percentage points—indicating a preference for the point mutation. On another note, *Single* needs less nodes to find a solution compared to the point mutation.

Generally, E-REORDER with *Single* tends to need the least amount of computational nodes. While STANDARD with point mutation needs the least amount of nodes for Multiply, it is also the worst algorithm in this case. This may also be a reason why E-REORDER needs the least amount of iterations until a solution is found. With less nodes, the search space for E-REORDER decreases, too. Hence, it may find a solution faster. Furthermore, with less nodes, CPU time can be saved with each iteration, as less potential computations take place.

Interestingly, E-REORDER and REORDER with the point mutation tend to have similar mutation rates. Except for Encode, both rates only differ marginally and varies vastly from STANDARD's mutation rate. In our experiments, STANDARD favours a lower mutation rate compared to the other two algorithms, which could also indicate that REORDER and E-REORDER favours a higher change in the genotype per mutation.

Another factor for E-REORDER's better performance may be the additional mutations of inactive nodes. With their reordering, some connection genes must be mutated to prevent backward-connections. This could lead to more genetic drift, which may improve its performance.

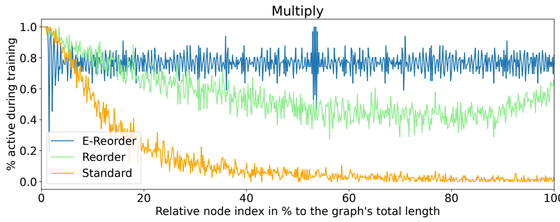


Figure 4: Active node distribution of STANDARD, REORDER and E-REORDER. Each distribution shows the averaged result of 75 aggregated solutions for Multiply.

5.3 Distribution of Active Nodes

In Section 4.1, we hypothesize a potential limitation of REORDER and speculate in Section 4.2 that E-REORDER may further lessen the effects of a positional bias. Hence, one question we would like to answer is the effect of E-REORDER on the distribution of active nodes, compared to REORDER and STANDARD. For this task, a visualization of the active node distribution of the final results for all three CGP variants is given in Figure 4. The x-axis shows the relative node index in percent, while the y-axis shows the probability of that node being active.

Please note that we only visualize our findings for Multiply, as the other three benchmarks show almost identical plots and behaviours. In addition, we always compare the best configurations found, as reported in Table 1. Again, we averaged the active node distribution of 75 independent repetitions with random seeds. Furthermore, the figure only depicts the *Single* mutation strategy, as this was the best mutation operator for all three CGP variants. Besides, the visualization for the point mutation strategy shows only marginal differences compared to *Single*. At last, as the CGP variants have different number of nodes, we do not report the actual node indices in Figure 4. Instead, we report the relative node index in percent to the graphs total length.

In the context of STANDARD, the positional bias can be clearly seen. At the beginning of the genome, nodes have a high probability of being active. However, after the first 30 % of the genome, this probability decreases to 10 % or less.

As for REORDER, this variant is able to moderately overcome the bias. While it also contains a drop in node activity, the decrease is far less pronounced compared to STANDARD. Furthermore, the probability of active nodes increases in the last 10 % of node indices.

Table 1: Best results found for each E-Reorder, Reorder and Standard configuration. Algorithms are sorted from best to worst in descending order. Here, *Avg* is the average number of iterations until a solution is found; *# Nodes* is the number of computational nodes used; $p(mut)$ is the mutation rate; *# active* is the number of active nodes for this solution; and $p(best)$ the probability of the solution being the best among the other six.

Variant	Mutation	Avg	HPDI	# Nodes	$p(mut.)$	# Active	$p(best)$
			Parity				
E-Reorder	Prob.	322	$[278, 371]$	350	0.081	129	0.26
Standard	Single	342	$[289, 404]$	600	—	42	0.23
Reorder	Prob.	400	$[341, 471]$	450	0.085	85	0.21
E-Reorder	Single	471	$[395, 561]$	50	—	27	0.16
Reorder	Single	739	$[606, 902]$	200	—	57	0.11
Standard	Prob.	2,524	$[2{,}063, 3{,}084]$	750	0.009	43	0.02
			Encode				
E-Reorder	Prob.	5,294	$[4{,}656, 6{,}049]$	650	0.014	336	0.32
E-Reorder	Single	5,296	$[4{,}759, 5{,}908]$	150	—	87	0.27
Standard	Single	6,213	$[5{,}550, 6{,}947]$	200	—	65	0.22
Reorder	Prob.	8,642	$[7{,}644, 9{,}787]$	550	0.018	249	0.12
Reorder	Single	14,733	$[12{,}786, 16{,}977]$	600	—	258	0.04
Standard	Prob.	20,378	$[17{,}592, 23{,}557]$	700	0.009	103	0.03
			Decode				
E-Reorder	Single	12,119	$[11{,}174, 13{,}142]$	250	—	145	0.39
E-Reorder	Prob.	14,596	$[13{,}154, 16{,}153]$	650	0.008	345	0.26
Reorder	Single	15,017	$[13{,}826, 16{,}295]$	700	—	186	0.21
Standard	Single	23,132	$[20{,}959, 25{,}482]$	400	—	242	0.07
Standard	Prob.	28,510	$[25{,}868, 31{,}349]$	700	0.009	183	0.04
Reorder	Prob.	32,902	$[30{,}227, 35{,}857]$	800	0.003	402	0.03
			Multiply				
E-Reorder	Single	70,304	$[59{,}647, 82{,}144]$	700	—	362	0.41
Reorder	Single	90,370	$[79{,}273, 103{,}286]$	750	—	118	0.23
Standard	Single	129,739	$[110{,}948, 150{,}742]$	700	—	411	0.14
Reorder	Prob.	119,426	$[104{,}665, 135{,}512]$	1000	0.013	540	0.13
E-Reorder	Prob.	194,044	$[163{,}843, 227{,}740]$	700	0.012	363	0.08
Standard	Prob.	414,639	$[360{,}719, 472{,}413]$	500	0.007	102	0.02

The distribution for E-Reorder differs compared to the last two CGP variants. For the first 5 % of nodes of graph, the probability for nodes being active oscillates in the range of $[0.2, 1.0]$. Afterwards, it fluctuates around a probability of 0.75 % with occasional spikes in probability. Nevertheless, such fluctuating behaviour should be anticipated, as E-Reorder places active nodes equidistantly apart. In addition, by forcing a uniform distribution of active nodes in combination with a better fitness value as seen in Section 5.2, we believe that we lessened the effects of a positional bias.

6 CONCLUSION

The existing *Reorder* operator introduced by Goldman and Punch is able to moderately overcome a positional bias, from which Cartesian Genetic Programming (CGP) suffers (Goldman and Punch, 2013a). Nonetheless, we theorized that Reorder might have a small limitation, which may hinder a complete exploration of the search space. A node may only be reordered into the new genome when all of its dependencies are satisfied—which means that all input nodes must be mapped into the genome beforehand. This may slightly favour nodes near input nodes, which could potentially limit Reorders full potential.

With our novel modification to Reorder, called *Equidistant-Reorder*, we are able to evade the limitation of Reorder. The algorithm works by reordering active nodes equidistantly apart throughout the whole genome. As a result, CGP with Equidistant-Reorder is able to find a solution for a given problem in less iterations compared to the CGP baseline or with the Reorder extension. In most cases, the total number of nodes needed to train CGP is reduced, too.

As for future work, different reorder strategies could be examined as we only focused on equidistant spacing. It would also be possible to apply a uniform distribution instead of enforcing an equidistant distance. Another interesting aspect would be to move all or the majority of active nodes to the end of the genome. Then, there are almost no nodes with a higher probability of becoming active. As all active nodes are at the end of the genome, each node is able to mutate a connection to an arbitrary node behind. It may lead to less positional bias, too, but could also lead to other potential problems.

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