Techniques for Inferring Context-Free Lindenmayer Systems With Genetic Algorithm

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Abstract—Lindenmayer systems (L-systems) are a formal grammar system, where the most notable feature is a set of rewriting rules that are used to replace every symbol in a string in parallel; by repeating this process, a sequence of strings is produced. Some symbols in the strings may be interpreted as instructions for simulation software. Thus, the sequence can be used to model the steps of a process. Currently, creating an L-system for a specific process is done by hand by experts through much effort. The inductive inference problem attempts to infer an L-system from such a sequence of strings generated by an unknown system; this can be thought of as an intermediate step to inferring from a sequence of images. This paper evaluates a new tool, the Plant Model Inference Tool for Context-Free L-systems (PMIT-D0L) is implemented based on these techniques. PMIT-D0L has been successfully evaluated on 28 known L-systems, with alphabets up to 31 symbols and a total sum of 281 symbols across the rewriting rules. PMIT-D0L can infer even the largest of these L-systems in less than a few seconds.

Index Terms—Lindenmayer Systems, plant modeling, genetic algorithm, inductive inference

I. INTRODUCTION

Lindenmayer systems (L-systems), introduced in [3], are a bio-inspired grammar system that produces self-similar patterns that appear frequently in nature and especially in plants [4]. L-systems produce a sequence of strings, where a string can be obtained by the parallel application of rewriting rules to the previous word. Certain symbols can be interpreted as instructions to create images, and therefore a sequence of strings can describe a temporal process, which can be visually simulated by software such as the “virtual laboratory” (vlab) [5]. Such simulations can incorporate different geometries [3], [6], [7], environmental factors [8], [9], and mechanistic controls [6], [10], and as such are useful for simulating plants. L-systems often consist of small textual descriptions that require little storage compared to real imagery. Certainly also, they have a low cost in currency, time, and labor to simulate in silico compared to actually growing a plant, and realistic imagery can be produced with a well-constructed L-system.

Formally, L-systems are described by an ordered tuple $G = (V, \omega, P)$ consisting of an alphabet $V$ (a finite set of allowed symbols), an axiom $\omega$ that is a word over $V$, and a finite set of productions, or rewriting rules, $P$. A deterministic context-free L-system (D0L-system) has rules of the form $A \rightarrow x$, where $A \in V$ is called the predecessor, $x$ is a word over $V$ that is called the successor of $A$, with exactly one rule for each $A \in V$ as predecessor. Given a word $\omega_1 = A_1 \cdots A_m$ where each $A_i \in V$, $1 \leq i \leq m$, a derivation step $\Rightarrow$ is defined by $A_1 \cdots A_m \Rightarrow x_1 \cdots x_n$ where $A_i \Rightarrow x_i$ is in $P$, for each $i, 1 \leq i \leq m$. When this process is repeated $n - 1$ times starting with the axiom $(\omega = \omega_1 \Rightarrow \omega_2 \Rightarrow \cdots \Rightarrow \omega_n)$, the sequence $(\omega_1, \ldots, \omega_n)$ is called the length-$n$ developmental sequence. Even though there are more general extensions of D0L-systems, such systems are enough to simulate realistic structures as shown in Figures 1a and 1b.

A difficult challenge is to determine an L-system that can accurately simulate a specific process, for example, modeling plant growth. In practice, this often involves manual measurements over time, scientific knowledge, and is done by hand by experts [4], [6], [7], [11]. Although this approach has been successful, it does have notable drawbacks. Producing a system manually requires an expert that are in limited supply, and it does not scale to producing arbitrarily many (perhaps closely related) models. Indeed, the manual process currently

(a) Fibonacci Bush after 7 generations as produced using vlab

(b) Apple twig with blossoms as produced using vlab
has been described as requiring “tedious and intricate hand-work” [12] that could be improved if an automatic approach could “infer rules and parameters automatically from real ... images” [12]. Furthermore, when constructed manually, the more complex plant models require a priori knowledge of the underlying mechanics of the plant. In contrast, inferring L-systems automatically may be used to reveal scientific principles of the underlying process, or as stated by Godin and Ferraro, automatic inference “could be further exploited in combination with investigations at a biomolecular level to better understand plant development.” [7]

The ultimate goal of this line of research is to automatically determine an L-system from a sequence of plant images over time. There have been simplified variants of this problem that have been attempted thus far in the literature. One approach is to develop a tool as an aide for the expert to reduce the work load [13], [14]. With such approaches, the expert operator guides the tool towards a desirable model. Another approach is to build a fully automated method to find an L-system that produces the length-n developmental sequence given as an input [15], [16]. This is known as the inductive inference problem and it dates back to early work on L-systems studied from the perspective of decidability [17]. This can be thought of as an intermediate step of inferring an L-system from images, with an accurate segmentation of the images into descriptive strings being the second step. A similar type of plant image segmentation used on a temporal image sequence has been studied separately, e.g. [18]. However, for inductive inference to be truly crucial in combination with image segmentation, it would need to be both fast and robust so that it could be expanded to work with realistic complications such as noisy images, imperfect data, and other mechanisms built into L-systems. Existing work on inductive and inductive inference of L-systems is described in Section II-C.

This paper creates the Plant Model Inference Tool for Deterministic Context-Free L-systems (PMIT-D0L) [1], [2] that aims to be an automated approach to solve the inductive inference problem for D0L-systems. Towards that goal, PMIT-D0L uses a genetic algorithm (GA) to search for an L-system that produces a sequence of strings provided as input. In general, GAs search solution spaces in accordance with the encoding scheme used for the problem, and to-date most existing approaches to L-system inference use similar encoding schemes. This paper presents and analyzes different encoding schemes, both new and old, to show which are most effective for inferring L-systems. Additionally, some mathematical properties are used to shrink the solution space.

Between the encoding schemes and the use of mathematical properties based on necessary conditions, PMIT-D0L is able to infer all L-systems in a test suite where the sum of production successor lengths is up to 281 symbols; whereas, other approaches implemented in the literature are limited to about 20 symbols as described in Section II-C. Moreover, the test suite used to test PMIT-D0L is significantly larger than previous approaches, consisting of 28 previously developed D0L-systems. The best encoding scheme, based on the length of successors, took no longer than 3.192 seconds for each L-system, with an average of 0.391 seconds for them all. All L-systems were inferred with 100% accuracy with all encoding schemes. This is notable as the GA is being used to essentially learn the simulations from data. Some encoding schemes used were slower than others; however, the mathematical properties played a larger role in the speed. When multiple properties were combined together, they operated in a synergistic fashion to reduce the search space.

Although there are many future directions required in order to fully realize automatic inference of L-systems, PMIT-D0L provides both a fast and robust implementation of inductive inference that is necessary for L-system inference from images, and is the first inductive inference implementation to do so.

The remainder of this paper is structured as follows. Section II will describe some existing automated approaches for inferring L-systems. Section III will discuss the different encoding schemes that can be used with PMIT-D0L, along with techniques for reducing the search space size, etc. Section IV discusses the data set, performance metrics, and the results of the evaluation of PMIT-D0L. Finally, Section V concludes the work and discusses future directions.

II. BACKGROUND

This section describes useful contextual and background information relevant to understanding this paper. It starts with describing some notation used. Since GA is used as the search mechanism for this work, it contains a brief description of them. The section concludes with a discussion of some existing approaches to L-system inference.

A. Notation

An alphabet is a finite set of symbols. Given an alphabet $V$, a word over $V$ is any finite sequence of letters $A_1 A_2 \cdots A_n$, $A_i \in V, 1 \leq i \leq n$. The set of all words over $V$ is denoted by $V^*$, which contains the empty string denoted by $\lambda$. Given a word $x \in V^*$, $|x|$ is the length of $x$, and $|x|_{B}$ is the number of $B$'s in $x$, where $B \in V$. Given $V = \{B_1, \ldots, B_k\}$, the Parikh vector of a string $x \in V^*$ is $(|x|_{B_1}, \ldots, |x|_{B_k})$.

Given two words $x, y \in V^*$, then $x$ is a substring of $y$ if $y = uxv$, for some $u, v \in V^*$ and in this case $y$ is said to be a superstring of $x$. Also, $x$ is a prefix of $y$ if $y = xv$ for some $v$, and $x$ is a suffix of $y$ if $y = ux$ for some $u$.

Given a D0L-system $G = (V, \omega, P)$ as defined in Section 1, the successor of $A$ is indicated by $\text{succ}(A)$. A rewriting rule $A \rightarrow \text{succ}(A)$, and $B \in V$, then the number of symbols $B$ in $\text{succ}(A)$ is called the growth of $B$ by $A$, denoted by $M(A, B)$. These values are stored in a $|V| \times |V|$ matrix called the growth matrix $M(G)$. Commonly, $V$ includes symbols to provide simple graphical instructions to simulation software (such as vlav [5]). One commonly used such instruction set is the “Turtle Graphics” [4]. It is imagined as manipulating a turtle through a 2D or 3D space with a pen on its back. The turtle has a state consisting of its position and orientation. The symbols “F” and “f” move the turtle forward along its current orientation with the pen on or off respectively. In 2D, the symbols “*” and “-” turn the turtle a predefined number.
of degrees left or right. Additional commands are used for re-orienting the turtle in 3D space. For branching processes, the symbols "[" and "]" are used to start and stop a branch, which is implemented as pushing and popping the turtle's state on a stack. It is usually the case that the symbols "[", "]", "+", "−" have identity productions. There are some instances where "F" may not have an identity production (e.g. some of the variants of “Fractal Plant” [4]). Given a sequence of \( n \) words \( \rho, G \) is said to be compatible with \( \rho \) if \( \rho \) is \( G \)’s length-\( n \) developmental sequence. To differentiate the turtle graphic symbols “+”, “−” from the corresponding mathematical operators + and −, the turtle graphics symbols will appear in bold as + and −.

B. Background on Genetic Algorithm

The GA is described as follows by Bück [19]. The GA is an optimization algorithm based on evolutionary principles used to efficiently search \( N \)-dimensional (usually) bounded spaces. An encoding scheme is applied to convert a problem’s solution space into one describable by a virtual genome consisting of \( N \) genes. Each gene can be either a binary, integer, or real value and represents, in a problem specific way, an element of the solution to the problem. While there exists several types of value encoding schemes, a literal encoding directly represents an element of the solution to a problem. An example of a literal encoding scheme uses gene values to represent the length of a successor, so a value of 3 indicates a successor length of 3. In contrast, a mapped encoding could instead use a real value from 0 to 1 subdivided into sections that represent the different possible solutions.

In evolutionary biology, increasingly fit offspring can be created over successive generations by intermixing the genes of parents. Similarly, a GA functions by iterating over the selection, crossover, mutation, and survival operators until at least one termination condition (e.g. a time limit) is met [19]. There exist different types of these operators; however, this paper will describe only those used here. The function of the GA is controlled by the parameters: population size \( P \), crossover weight \( C \), and mutation weight \( M \). Prior to the first iteration, a GA first produces an initial population of \( P \) random solutions. The selection operator chooses some number of pairs of genomes from the population using a selection technique. One such technique, a roulette wheel, is one where the chance of any option being selected (in this case a genome) is proportional to a fitness value (in this case, the genome’s fitness). For each pair of genomes, the crossover operator swaps a random selection of genes between them, resulting in \( P \) child genomes. The chance for any gene to be swapped is equal to \( C \). The mutation operator changes a random selection of genes to a random valid value in each child genome. The chance of any individual gene being mutated is equal to \( M \). The child genomes are added to the population, and the population is culled to size \( P \), thereby keeping the most fit genomes (elite survival).

With PMIT-DOL, the following changes are made to the standard GA to encourage additional exploration. Although an individual genome may be selected for more than one pair, the same pair may not be selected more than once. If any genome has been modified by neither the crossover operator nor the mutation operator, then one gene is selected and mutated to ensure that at least one change has taken place. Where a mapped encoding is used, it is possible for two different genomes to map to the same solution. To prevent such solutions from dominating the population, genomes that map to the same solution are automatically culled (similarly during initialization, duplicated solutions are not permitted in the population).

C. Existing Automated Approaches to L-system Inference

Various approaches to L-system inference were surveyed in [20]. Here, only certain works most closely related to PMIT-DOL are described. There are several different broad approaches towards the problem: building by hand [4, 6], algebraic approaches [15, 21], using mathematical properties [15], and search approaches [16].

Inductive inference was studied theoretically (without implementation) by Hermann and Rozenberg [17], and Doucet [21]. In [21], Doucet defined a set of equations that relate the number of symbols \( a_i \) observed in each string but the last in a sequence of strings \( \rho \) to all strings but the first. The (unknown) growth matrix must be a solution to these equations. Recently, this theoretical approach was extended to work for context-sensitive L-systems [22]. A somewhat similar approach [21] was implemented with a tool called LGIN [15] that infers L-systems from a single string. LGIN looks exhaustively at the successor combinations, extracted from a single string in a developmental sequence that fulfills these equations. Since only a single string is used, it does not guarantee to find a unique solution. LGIN is limited to two symbol alphabets (not including turtle graphic symbols), with larger alphabets described as “immensely complicated” [15]; however, LGIN was evaluated on six variants of “Fractal Plant” [4] and was very fast having a peak time to find the L-system of less than one second for 5 of the 6 variants, and four seconds for the remaining variant.

Runqiang et al. [16] investigated inferring an L-system directly from an image using a GA. In their approach, they encode each symbol within the successors as a gene. The fitness function attempts to match the candidate system to the observed data. As an input, they use an image of the shape produced by an L-system to be inferred, as seen for example in Figure 2. Their fitness function uses image processing to match the image produced by a candidate solution to the input image since their focus is on finding the proper angles and line lengths for drawing the image, in addition to the L-system itself. Their approach is limited to an alphabet size of 2 symbols and a maximum total length of all successors of 14. Their approach is 100% successful for variants of “Fractal Plant” [4] with \( |V| = 1 \), and a 66% success rate for variants of “Fractal Plant” [4] with \( |V| = 2 \). Although they do not list any timings, their GA converged after a maximum of 97 generations, which suggests a short runtime.

1) Scanning for Successors: A technique for finding productions based on the successor lengths for every \( A \in V \) was previously described in [22], which we call the scanning
Fig. 2: “Fractal Plant” variant #5

process. This technique is used extensively in this research, and is described as follows. With L-systems, although the symbols are replaced in parallel, the sequence of successors in the new word is unchanged from the sequence of the original symbols; i.e., if \( \omega_i = A_1 A_2 \ldots A_m \) with \( A_i \in V, 2 \leq i \leq m \), then \( \omega_{i+1} = \text{succ}(A_1)\text{succ}(A_2)\ldots\text{succ}(A_m) \). Consider the case of \( A_1 \) in \( \omega \). To find \( \text{succ}(A_1) \) it is only necessary to know the length of \( \text{succ}(A_1) \). If \( |\text{succ}(A_1)| \) is known (or different values for it are tested by searching), then the successor is the first \( \text{succ}(A_1) \) characters of \( \omega_{i+1} \). The process of taking the next \( l \) symbols (where \( l \) is a hypothetical successor length) may be repeated for every new instance of a symbol encountered while scanning each word of a developmental sequence until every successor has been found, as described in [22]. With this fast algorithm, the goal is therefore to find a list of successor lengths that results in an L-system compatible with a developmental sequence; however, this may be done in a few ways. Most directly, a list of successor length values may be found by searching. Somewhat indirectly, the growth values for every \( A, B \in V \) may instead be found, and a successor length for each \( A \in V \) computed by summing the growth values for every \( B \in V \).

III. METHODOLOGY

This section describes the design, development, and the process for evaluating PMIT-D0L. First, a high level overview of PMIT-D0L will be described, as this helps to contextualize the remainder of the section. This is followed by a description of the different encoding schemes used to define the space searched by PMIT-D0L to infer an L-system. The different techniques used to reduce the size of the defined search space are then discussed. The final two sub-sections describe the process used to optimize the control parameters of the GA, and finally, the fitness function and termination conditions.

Since many symbols, such as the turtle interpretation symbols, usually have identity productions, a set \( \hat{V} \subset V \) is provided as input where it is assumed that all symbols in \( \hat{V} \) have identity productions. Their known values can speed up searches, but they can also be used to set up associations between the strings as described below (see Section III-B2). In addition, let \( V = V - \hat{V} \) (those symbols with unknown productions).

Algorithm [III] describes PMIT-D0L at a high level. It takes as input a sequence of strings \( \rho = (\omega_1, \ldots, \omega_n), \omega_i \in V^*, 1 \leq i \leq n \), a desired encoding scheme \( En \) (described in Section III-A), and the set of symbols \( \hat{V} \). PMIT-D0L will return either a D0L-system compatible with \( \rho \) or report that no D0L-system was found (as a GA cannot guarantee to find a solution) that is compatible with \( \rho \). Due to the scanning process described in Section II-C1 deducing successor lengths and growth matrix values is particularly important. Thus, the first step is to initialize several programming variables. The current upper and lower bounds for the growth values of every pair of \( A, B \in V \) is denoted by \( (A, B)_{\text{min}} \) and \( (A, B)_{\text{max}} \), and the bounds on successor length for each \( A \in V \) is denoted by \( A_{\text{min}} \) and \( A_{\text{max}} \). An alphabet \( V' \) is initially equal to \( \hat{V} \), and its symbols will be iteratively removed (as described below). Additionally, a prefix, suffix, and superstring of each successor \( A \) is calculated and stored in \( \text{Pre}_A, \text{Suf}_A, \) and \( \text{Sup}_A \) (these are called successor fragments) respectively. They are initially set to \( NULL \) indicating that no successor fragment has yet been found.

Two assumptions are made regarding L-systems in this paper. First, the branching symbols “\( [ \)” and “\( ] \)” are assured to be properly nested within each production. Second, it is assumed that there are no erasing rules (i.e. a successor may not be \( \lambda \)). Most plant models in the literature are of this form. This implies that \( A_{\text{min}} \) is initialized to 1 for each \( A \in V \). For each symbol \( T \in \hat{V}, T_{\text{min}} = T_{\text{max}} = 1. (T, T)_{\text{min}} = (T, T)_{\text{max}} = 0 \) for every \( A \in V, A \neq T \). We assume that all turtle interpretation symbols are in \( \hat{V} \) except possibly \( F \), as this is most common. If \( F \rightarrow F \) is a production, then we assume that \( F \in \hat{V} \).

Following the initialization, an initial analysis is done using the inputs \( \hat{V} \) and \( \rho \) to refine the bounds on growth, the bounds on length, and to find any possible successor relationships by using a set of mathematical properties described in Section III-B. This is done in a loop until no further refinement is found. The main processing then begins consisting of a nested loop. The outermost loop iterates over all symbols in \( V' \); however, if \( V' \) is empty it still executes once (i.e. to account for the case where there are no symbols with already known identity productions). The main purpose of this loop is to search for a solution as if \( \rho \) contained only those symbols currently in \( V - V' \) (as described in Section III-B4) which can simplify the problem. To this end, \( \rho' \) is constructed by filtering out all symbols in \( V' \) from \( \rho \) (i.e. that the symbols in \( V - V' \) remain in \( \rho \)). This is followed by the innermost loop that refines the growth and length bounds and the successor fragments based on the same mathematical properties but using \( \rho' \) (Section III-B). The innermost loop executes until no further refinement occurs during an iteration. The outermost loop then continues by defining a search space (space) in accordance with the desired encoding scheme \( En \) (as described in Section III-A). The bounds on the search space are constructed from the growth and length bounds and the fragments as appropriate. A GA is used to search the defined space until a D0L-system is found that is compatible with \( \rho' \) or a termination condition is reached (as described in Section III-D). Assuming a solution is found, then the solution found
is a D0L-system compatible with ρ'; however, the successor fragments can be refined by adding back the symbols of V' to the solution. The final step is to remove one symbol from V'. Conceptually, this last step can be thought of as iteratively solving simplified problems over smaller alphabets, then gradually reintroducing the symbols until an L-system compatible with ρ is found (described in Section III-B4).

Data: A sequence of strings ρ over V, an encoding scheme En, and a set of symbols with known identity productions V

Result: D0L-system compatible with ρ, or reports that no compatible D0L-system is found

V' ← V (Section III-B4);
// initialize length and growth bound variables;
// initialize fragment variables;

repeat
  refine growth bounds (Section III-B);
  refine length bounds (Section III-B);
  refine fragments (Section III-B);
until there are no changes;

repeat
  ρ' ← filter ρ by removing all symbols in V' (Section III-B4);
  // using V' = V' and ρ';
  repeat
    refine growth bounds (Section III-B);
    refine length bounds (Section III-B);
    refine fragments (Section III-B);
  until there are no changes;

define a search space space based on En (Section III-A);

solution' ← search space using genetic algorithm (Section III-A);

add symbols of V' back to solution' (Section III-B4);

remove some symbol from V' if V' ≠ ∅ (Section III-B4);

until V' ≠ ∅;

Algorithm III.1: D0L-system inference

1) Ordered Sequence of Symbols Encoding: While the technique of building a search space based on the idea of searching for the symbol in each position of each successor has been previously investigated [14], PMIT-D0L creates this search space with additional requirements.

For every A ∈ V, a successor may be encoded as follows. For the remainder of this section, we create a special symbol ∅. A number of genes equal to A_{max} is defined as this is the greatest number of symbols that may exist in the successor. The current values for Pre_A and Suf_A then identify a number of genes at the beginning and end equal to the length of the prefix and suffix respectively. For example, if A_{max} = 7, Pre_A = A, and Suf_A = BB, then the genome would appear as follows A _ _ _ _ _ B B, where _ represents an unknown symbol, which could be set to ∅ if |succ(A)| < 7 (implying no symbol of V exists in that position of this successor considered). Each of the genes are permitted to have a real-value from 0 to 1. The most obvious way to decode a real-value is to map it onto |V| equally sized ranges; however, with the information gathered by PMIT-D0L, a more effective approach can be used by dynamically altering the possible selections for each gene value. For each gene, a list of possible choices can be computed, a so-called symbol pool, based on the state of the successor at the time the choice is being made. To continue the example, if (A, B)_{max} = 2, then since there are already two occurrences of B symbols in the successor, B needs not be a choice for any of the remaining genes. The requirement (A, B)_{min} can be similarly enforced. Continuing the example, if (A, A)_{min} = 3, (A, C)_{min} = 2, and the successor is A A _ _ _ _ B, then the remaining genes must be either A or C regardless of how many symbols are in V. The lower bound on successor length is enforced by making ∅ unable to be selected until |succ(A)|_{min} symbols exist in the successor.

Furthermore, after a list of possible symbols for a gene is determined, instead of giving each symbol an equal chance of selection the ranges can be improved. For example, if the choices for a gene are A, B, ∅, then one approach is to set the ranges from 0 to 0.33, 0.34 to 0.67, and 0.68 to 1.0 for A, B and ∅ respectively. To further improve the searching with OSoS, it is possible to further refine the mapping with a lookahead in ρ. Consider the following string AAAAAAAAAAAABBBBA. If the state of a successor is A _ , then the best choice (barring any additional restrictions or information) for the unknown symbol is A, since the symbol A is quite frequently the next symbol in the string following an A. This logic may be extended out to considering N characters. For example, with the string AABAAACAB, if the successor state is A A _ , then A is impossible, B is 67% likely (occurs two out of three times), and C is 33% likely (occurs one of of three times). Note, these examples consider only a single string; however, in PMIT-D0L all of ρ is used to compute the associated probability. The ∅ symbol is initially assigned a probability equal to 1/(1 + (A_{max} - A_{min})), but since adding this probability with the probabilities for the other symbols in V results in a sum of probabilities greater than 1, the sum is then normalized. This encoding scheme is called OSoS(N), where N is the length of the lookahead. This paper
evaluates both OSoS(1) and OSoS(2).

2) Growth Encoding: The growth-based approach, called PMIT-DOL(G), constructs bounds on each position of a possible growth matrix, of which there are $|V|^2$ values. PMIT-DOL(G) uses a literal encoding scheme and is similar to those seen in [15], [21], where the correct value of a dimension is each value in $M(A, B)$. The GA searches within the computed lower and upper bounds for $M(A, B)$. For each combination of growth matrix tested, the sum of each row is obtained to give a length and then the scanning process is used.

One limitation of this encoding is the possibility that a candidate does not satisfy the property that, for each $B \in V$, $\sum_{A \in V}(|\omega_i|A M(A, B)) = |\omega_{i+1}|_B, 1 \leq i < n$ (total growth constraint). To avoid backtracking with this approach the GA is free to select any values within the lower and upper bounds for each $M(A, B)$. An alternate encoding scheme was also tested by changing the encoding scheme to use a real value from 0 to 1, and then it mapped ranges to the options that would permit the total growth constraint to be satisfied. The results of an evaluation were found to be very similar to those for the encoding scheme described above, and so results for this alternative approach are omitted.

3) Length Encoding: The length-based approach called PMIT-DOL(L) uses the scanning process that requires a successor length for each $A \in V$. Each dimension is ultimately mapped onto an integer value representing the length of a successor of a symbol in $V$. The GA searches within the computed lower and upper bounds for length. Compared to the growth-based approach, although the bounds on the individual dimensions are larger; i.e., typically, the lower bound $A_{min} \geq \sum_{B \in V}(A, B)_{min}$, and the upper bound $A_{max} \leq \sum_{B \in V}(A, B)_{max}$, with the length-based approach. The number of dimensions in the search space is $|V|$ with the length-based approach.

Thus, compared to PMIT-DOL(G), the main advantage is a reduced search space size in almost all but the most trivial of cases (formalized in the remark below). While, the search space size is reduced, a growth-based search space can still be more efficient because the fitness landscape may be more conducive to an effective search (i.e. a partially correct candidate may be a better stepping stone to a solution based on the manner in which a search algorithm exploits existing solutions).

Remark 1. With Algorithm III.1, the search space size in the length-based approach is smaller than the search space size in the growth-based approach when $|V| \geq 2$ and the bounds of the growth-based approach are larger than 3, which can be seen as follows: Let $S_A$ be the size of the dimension for $A$ in the length-based paradigm, and $S_{(A,B)}$ be the size of the dimension for $M(A, B)$ in the growth-based paradigm. Algorithm III.1 refines $S_A$ such that it cannot be larger than $\sum_{B \in V} S_{(A,B)}$, therefore the size of the search space in the length-based paradigm in the worst case is $\prod_{A \in V} \sum_{B \in V} S_{(A,B)}$; however, in the growth-based paradigm the search space is $\prod_{A, B} S_{(A,B)}$. If $|V| \geq 2$, and $S_{(A,B)} \geq 3$ for all $A, B$, then $\prod_{A, B} S_{(A,B)} > \prod_{A \in V} \sum_{B \in V} S_{(A,B)}$.

As with the growth-based approach, an alternative real-value encoding that enforced the constraint that $\sum_{A \in V}(|\omega_i|A succ(A)) = |\omega_{i+1}|_B, 1 \leq i < n$ was implemented. The evaluation showed that the results were also not significantly different overall, and so this approach is not discussed further.

4) Row-Reduced Matrix Encoding: As discussed in Section II Doucet [21] recognized that the productions could be represented as a matrix equation, so as a step towards improving PMIT-DOL, a similar approach was implemented. Let $Y$ be a matrix where each row $i$, from 1 to $n-1$ is the Parikh vector of $\omega_i$ (where $\rho$ has $n$ strings), and let $Z$ be a matrix where each row is a Parikh vector of $\omega_2$ to $\omega_n$. In this case, if $M$ is a growth matrix of an L-system with $\rho$ as its length $n$ developmental sequence, then $YM = Z$ is true. In Doucet’s original work, he proposes to solve for $M$, and where $Y$ is invertible, $Y^{-1}Z$ is a unique solution, and if the solution is not unique, to use linear Diophantine equations.

It is also possible to replace $M$ with the length of each production, called the successor length matrix, and $Z$ is replaced with the length of $\omega_2$ to $\omega_n$. $M$ can then be solved for similarly to the growth matrix. The remainder of this discussion will be presented in the context of a length-based matrix; however, similar logic applies to a growth-based matrix by replacing growth values for successor lengths.

Gauss-Jordan elimination can be applied, and where there is not a unique solution, it results in a set of linear Diophantine equations, where the successor lengths are the variables, e.g. $5X_1 + 3X_2 = 24$. Each successor length only gets substituted for variables that appear in exactly one equation. In these cases, there are an infinite number of possible solutions. However, when inferring L-systems, the successor lengths are constrained to be natural numbers and within the bounds on the lengths provided by the lengths of the words in $\rho$, and it is therefore finite. For each equation, the encoding scheme used to search for a solution has $N$ genes, where $N$ is number of variables in an equation. The range of values for each gene is $A_{min}$ to $A_{max}$ for the symbol $A$ the gene is representing (which can be more restricted than solutions to Diophantine equations due to the additional mathematical properties in Section II-B used that takes the sequences of the words into account). This encoding scheme is designated as PMIT-DOL(M+L) to indicate the addition of the matrix operation. For the matrix based on growth values, it is designated as PMIT-DOL(M+G).

Using the equations means that only possible solutions to the equations need to be checked as opposed to simply iterating over all possible lengths between the lower and upper bounds, thereby reducing the search space size. So, the value of the gene is dynamically changed. For example, say $A + B + C = 10$, and $A, B, C$ have ranges 5 to 7, 1 to 5,1 to 5 respectively. If the GA picks $A = 7$, and $B = 4$ for the second gene, then $B$ can be dynamically reduced to 2 allowing $C = 1$.

This is a deterministic mapping and therefore permissible for a GA.

B. Reducing Search Space Size

In this section, the techniques that are used by PMIT-DOL to reduce the size of the solution space (with any of
the encoding schemes described above) using mathematical properties of D0L-systems will be described. These are applied in Algorithm III.1 everywhere that refine growth bounds, length bounds and refine fragments is performed. Being based on necessary conditions guarantees that all valid solutions are in the remaining search space (if there is a D0L-system that can generate the input strings).

1) Refining Successor Relationships: PMIT-D0L determines successor fragments, of which there are four types.
   - A word $\omega$ is an A-subword fragment if $\omega$ must be a subword of $\text{succ}(A)$.
   - A word $\omega$ is an A-prefix fragment if $\omega$ must be a prefix of $\text{succ}(A)$.
   - A word $\omega$ is an A-suffix fragment if $\omega$ must be a suffix of $\text{succ}(A)$.
   - A word $\omega$ is an A-superstring fragment if $\omega$ must be a superstring of $\text{succ}(A)$.

As PMIT-D0L runs, it can determine additional successor fragments, which can help in turn to reduce growth bounds. Certain prefix and suffix fragments can be found for the first and last symbols in each input word by the following process. Consider two words such that $\omega_1 \Rightarrow \omega_2$. It is possible to scan $\omega_1$ from left-to-right until the first symbol from $\bar{V}$ is scanned (say, $A$, where the word scanned is $\alpha A$). Then, in $\omega_2$, PMIT-DOL skips over the symbols of $\bar{V}$ in $\alpha$ (since each symbol in $\alpha$ has a known identity production), and the next $A_{\min}$ symbols (the current lower bound for $|\text{succ}(A)|$, $\beta$ say, must be an A-prefix fragment. Furthermore, since branching symbols must be well-nested within a successor, if a $\omega$ symbol is met, the prefix fragment must also contain all symbols until a matching $\omega$ symbol is met. Similarly, an A-superstring fragment can be found by skipping $\omega$, then taking the next $A_{\max}$ symbols from $\omega_2$ (the upper bound on $|\text{succ}(A)|$). If a superstring fragment contains a $\omega$ symbol without the matching $\omega$ symbol, then it is reduced to the symbol before the unmatched $\omega$ symbol. The lower and upper bounds $(A,B)_\min$ and $(A,B)_\max$ for each $B \in V$ can be then possibly improved by counting the number of $B$ symbols in any prefix and superstring fragments respectively. For a suffix fragment, the process is identical except the scan goes from right-to-left starting at the end of $\omega_1$.

Example 1: Consider input strings:

$$\omega_1 = + + + A[|FF]|\{F\}B F$$
$$\omega_2 = + + + + + A[|FF]|\{F\}\{F\}B F F .$$

Assume thus far PMIT-DOL has calculated that $A_{\min} = 2$ and $A_{\max} = 8$. It can scan $\omega_1$ until $A$ is found and record that $\alpha = + + +$. An $A$-prefix fragment is $+ A$ as those are the first two $(A_{\min})$ symbols of $\omega_2$ after skipping $\alpha$. An $A$-superstring fragment is $+ A[|FF]$ as those are the first eight $(A_{\max})$ symbols of $\omega_2$ after skipping $\alpha$, which can be reduced to $+ A[|FF]$ due to the unbalanced $|$ symbol. By counting within the prefix fragment, lower bounds on the growth for $A$ are $(A, +)_{\min} := 1$ and $(A, A)_{\min} := 1$, while upper bounds can be found from the superstring fragment to be $(A, +)_{\max} := 1, (A, -)_{\max} := 1, (A, A)_{\max} := 1,(A, |)_{\max} := 1, (A, T)_{\max} := 1$ and $(A, F)_{\max} := 2$.

2) Refining Successor Relationship Using Symbols as Markers: If a symbol has a known successor, then it may be possible under certain circumstances to “line it up” with the symbol(s) it produces. In such circumstances, the derivation is sliced into two parts, and this reduces the possible productions for the symbols in each part. To illustrate the concept, consider the simple example:

$$\omega_1: A + B$$
$$\omega_2: ABA \downarrow BBB$$

$succ(A) \quad succ(B)$

If $\star \in \bar{V}$, then PMIT-DOL assumes that $\star \rightarrow \star$, and the $\star$ symbol in $\omega_1$ may only produce the $\star$ in $\omega_2$. This splits the derivation such that everything to the left of the $\star$ in $\omega_1$ must produce everything to the left of the $\star$ in $\omega_2$, i.e. $A \rightarrow ABA$ is a production. Using similar logic except to the right of the $\star$ implies $B \rightarrow BBB$ is a production.

In practice, it is unusual for a single position of one string to be uniquely associated with a position in the next string, as seen in the example above. More often, any individual position may be associated to multiple positions of the next word. However, a sequence of symbols, each with known successor, may be unique. For example, in the string $A[+B][| - B][A[| - C]][| - | D]$, the individual symbols $[,], +$, and $-$ alone might not uniquely associate to their successors; however, a sequence of symbols such as $| -$ or $| -$ are potentially unique, and as such may be associated to a unique location. To make use of this observation, for each word, a list of possible associations between every position of a symbol in $\bar{V}$ to positions of the next word is constructed. This list of associations is called a marker map. A marker map is constructed based on both individual symbols and sequences of symbols, which are referred to as candidate markers. Associating a candidate marker to potential successors takes into account that a number of symbols must be reserved for symbols that appear before and after the candidate marker. For example, if $\omega_1 = A + BC \rightarrow, \omega_2 = A + BC + C \rightarrow, B_{\min} = C_{\min} = 1$, and $+ \star$ associates with both $\star$s in $\omega_2$, both are candidate markers. But since $B_{\min} + C_{\min} + - m - 3$ the final 3 symbols of $\omega_1$ produce at least the $+ C \rightarrow$ of $\omega_2$. This eliminates the second $\star$ in $\omega_2$ as being produced by the $\star$ in $\omega_1$, and the $\star$ in $\omega_1$ can only be associated to the first $\star$. If, following the construction of the marker map, a candidate marker is not uniquely associated with its successor, then it is removed from the marker map.

Consider a derivation $\omega_i \Rightarrow \omega_{i+1}$ expanded as

$$\omega_{i+1,1}A_{1}\omega_{i+1,2} \cdots A_{m} \Rightarrow$$
$$\omega_{i+1,1} \text{succ}(A_{1})\omega_{i+1,2} \cdots \text{succ}(A_{m})\omega_{i+1,m+1},$$

where each $A_j$ in $\omega_i$ is associated to the annotated successor in $\omega_{i+1}$ forming a marker. It follows that $\omega_{i,j} \Rightarrow \omega_{i+1,j}$ for all
\[ G_{\text{acc}}(i, A) := \sum_{B \in V} (|\omega_{i-1}|B \cdot (B, A)_{\text{min}}). \]

The unaccounted for growth for a symbol \( A \), denoted as \( G_{\text{ua}}(i, A) \), is computed as
\[ G_{\text{ua}}(i, A) := |\omega_i|A - G_{\text{acc}}(i, A). \]

The unaccounted for growth can be used to grow the bounds. In particular, \( (B, A)_{\text{max}} \) is set (if it can be reduced) under the assumption that all unaccounted for symbols are produced by \( B \) symbols. Furthermore, \( (B, A)_{\text{max}} \) is set to be the lowest such value computed for any word from 2 to \( n \), where \( B \) occurs, as any of the \( n - 1 \) words can be used to improve the maximum. And, \( |\text{succ}(B)|A \) must be less than or equal to \( (B, A)_{\text{min}} \) plus the additional unaccounted for growth of \( A \) divided by the number of \( B \) symbols (if there is at least one) in the previous word, as computed by
\[
(B, A)_{\text{max}} := \min_{\substack{2 \leq i \leq n, \\ |\omega_{i-1}|B > 0}} \left( (B, A)_{\text{min}} + \left\lfloor \frac{G_{\text{ua}}(i, A)}{|\omega_{i-1}|B} \right\rfloor \right).
\]

Indeed, the accounted for growth of \( A \) is always updated whenever values of \( (B, A)_{\text{min}} \) change, and the floor function is used since \( |\text{succ}(B)|A \) is a non-negative integer. For example, if \( \omega_{i-1} = ABA \), \( \omega_i = ABABBABABA \), \( (A, A)_{\text{min}} = 1 \), and \( (B, A)_{\text{min}} = 0 \), then the accounted for growth of \( A \) in \( \omega_i \) is computed by \( G_{\text{acc}}(i, A) = (A, A)_{\text{min}} \cdot |\omega_{i-1}|A + (B, A)_{\text{min}} \cdot |\omega_{i-1}|B = 1 \cdot 2 + 0 \cdot 1 = 2 \). This leaves two \( A \)'s in \( \omega_i \), unaccounted for. An upper bound on the value of \( |\text{succ}(A)|A \) is set when the \( A \)'s in \( \omega_i \) produce all of the unaccounted for growth in \( \omega_i \). So, \( A \) produces its minimum \( ((A, A)_{\text{min}} = 1) \) plus the unaccounted for growth of \( A \) in \( \omega_j \) divided by the number of \( A \)'s in \( \omega_{i-1} \) \( |\omega_{i-1}|A = 2 \), hence \( (A, A)_{\text{max}} := 2 \). Similarly, \( (B, A)_{\text{max}} \) is achieved when only \( B \)'s produce all unaccounted for growth of \( A \); this sets \( (B, A)_{\text{max}} \) to \( (B, A)_{\text{min}} = 0 \) plus the unaccounted for growth (2) divided by the number of \( B \)'s in \( \omega_{i-1} \), (1), which is 2.

Once \( (B, A)_{\text{max}} \) has been determined for every \( A, B \in V \), the observed words are re-processed to compute possibly improved values for \( (B, A)_{\text{min}} \). Indeed for each \( (B, A) \), if \( x := \sum_{C \in V} (C, A)_{\text{max}} \), and \( x < |\omega_i|A \), then this means that \( |\text{succ}(B)|A \) must be at least \( \left\lceil \frac{|\omega_i|A - x}{|\omega_{i-1}|B} \right\rceil \), and then \( (B, A)_{\text{min}} \) can be set to this value if its bound is improved. For example, if \( \omega_{i-1} \) has 2 \( A \)'s and 1 \( B \), and \( \omega_i \) has 10 \( A \)'s, and \( (A, A)_{\text{max}} = 4 \), then at most two \( A \)'s produce eight \( A \)'s, thus one \( B \) produces at least two \( A \)'s (10 total minus 8 produced at most by \( A \)), and \( (B, A)_{\text{min}} \) can be set to \( 2 \).

In a similar fashion, the length bounds \( A_{\text{min}} \) and \( A_{\text{max}} \) can be set using unaccounted for length.

4) Refining Successor Relationships from Solution Projection: As previously defined, \( \hat{V} \subset V \) where all symbols in \( \hat{V} \) have a known identity production, and \( \hat{V} = V - \hat{V} \). Since a symbol in \( \hat{V} \) cannot be produced by a symbol in \( \hat{V} \), in the nested loop of Algorithm III.1, it is possible to first infer an L-system over \( V' \) (\( V' \) is a programming variable initially set to \( \hat{V} \)). For example, if \( V = \{ A, B, C, [], +, - \} \) and \( V' = \{ [], +, - \} \), then the first problem is to find each successor of \( A, B, C \) projected to \( \{ A, B, C \} \). After solving this initial problem, then a series of problems are solved for each symbol of \( \hat{V} \) to determine where it belongs in each successor. Note that “[]” and “[]” may be completed together due to the assumption that they are properly nested. Overall, symbol filtering simplifies the inference problem by making the difference between \( A_{\text{min}} \) and \( A_{\text{max}} \) smaller. Although more searches are needed, up to one additional search for each symbol in \( \hat{V} \), they are each in a smaller search space.

As described above, PMIT-D0L removes the symbols of \( \hat{V} \) temporarily by projecting \( \rho \) onto a reduced alphabet, and then iteratively adding each symbol of \( \hat{V} \) back into the problem one at a time. Additional information about the successors of an L-system, i.e. the successor relationships, that produces \( \rho \) as its length-\( n \) developmental sequence may be gleaned by analyzing the solution to each sub-problem. Let a solution to one of these sub-problems be called a projected solution, as it partly describes the final successors. The process for using the projected solutions is conceptually similar to that used for markers as positions in pairs of consecutive words will be “lined up”, and from there successor relationships deduced. To begin some terminology for this process is provided. For every derivation step \( \omega_i \) \( \Rightarrow \omega_i \), every position in \( \omega_i \) is scanned, and associated to the possible locations in \( \omega_i \) that it may produce. If a position may be associated to only one locale it is called certain; otherwise, the position is called uncertain. Uncertain positions are excluded from any subwords that are produced (described in detail by example next); thereby, resulting in the longest possible subword produced only of certain positions. If the positions before and/or after are certain, then an A-prefix (before certain and after uncertain), A-suffix (before uncertain and after certain), or succ(A) (before and after certain) can be found.

For example, assume that the first sub-problem is to solve the successors projected onto the symbols of \( V' \) resulting in the projected successor of \( A \) as \( BAB \) and of \( B \) as \( AB \). Equations 1 to 3 show an example of the process of finding successor relationships from this projected solution. In Equation 1 it can be seen that the + is uncertain; however, it must produce one of the two annotated + symbols (it cannot produce the first + as there are no surrounding [ and ] symbols). Since + is uncertain, it cannot be said definitively whether \( A \) produces the first annotated + in \( \omega_2 \) or not. It could be that \( A \) produced it, or it could be that + produced it. However, an A-subword can be properly calculated, but the + cannot be included in it. Since the projected solution of \( A \) is \( BAB \), then succ(A) must contain everything between the \( BAB \), which is \( B[\text{+}]A|B| (\alpha \text{ in Equation 1}) \) and this is declared an A-prefix due to the uncertainty of the + symbol. In Equation 2 the + production is uncertain so the association used is that which
ensures that the $B$-subword is valid; i.e., that the $+$ produces the second annotated $+$ of the pair. With respect to the $-$, at first glance it may appear uncertain; however, from the projected solution of $B$ as $AB$, the $-$ cannot produce the $-$ between the $A$ and $[+B]$. The subword $A-[+B]$ $(\beta)$ is a $B$-suffix due to the uncertainty of the preceding symbol. Finally, shown in Equation (3) an $A$-subword is formed for $A$ based on the projected solution; however, in this case, both the preceding symbol is certain and there are no following symbols; therefore, this is $\text{succ}(A)$. Note, that since $\text{succ}(A)$ is now known, this makes the production of the first $+$ certain (in Equation [1]), since it is now known that $A$ did not produce it. Therefore $\text{succ}(B)$ can be deduced as $+A-[+B]$ could be produced. Since all of the properties are computed in a loop until no new information is found, this would be found on the next pass.

\[
\begin{align*}
\omega_1 & : A + B - A \\
\omega_2 & : B[A]B[+A] - [+B] - B[+A]B
\end{align*}
\]

As described in Section II-B the function of the GA is controlled by the population size ($P$), crossover weight ($C$), and mutation weight ($M$) parameters. Optimizing these parameters is difficult based on general principles, since they are the optimal settings will depend on the characteristics of the fitness landscape, which is problem specific [23]. As such, typically, the parameters are set by doing a hyperparameter search. Bergstra and Bengio [23] found that using a Random Search provides an effective means to optimize the GA's parameter settings. Using Random Search works as follows. A range of good values is selected for each control parameter. In this case, based on the work by Grefenstette [24], the ranges were set to $10 \leq P \leq 125$ in increments of 5, $0.6 \leq C \leq 0.95$ in increments of 0.05, and $0.01 \leq M \leq 0.20$ in increments of 0.01, with additional values of 0.001 and 0.0001 permitted. An initial mid-range value is selected for each parameter ($P = 60, C = 0.8, M = 0.10$), and this is considered the current parameter value set. Iteratively, sixteen trials of PMIT-D0L are executed with a random variant of the current parameter value set. Each parameter is randomly modified up or down by no more than two increments, i.e. $P$ may be modified by $-10, -5, 0, +5, +10$, while also remaining within the ranges above. The variant parameter set that provides the best fitness value is considered the new current parameter value set. In the case of a tie, which was quite common with PMIT-D0L, the fastest execution time is used. When none of the sixteen trials provide an improvement over the current parameter value set, the hyperparameter search terminates. The resulting parameter value sets for each variant of PMIT-D0L is shown in Table I.

\begin{table}[h]
\centering
\begin{tabular}{|c|c|c|c|c|c|c|}
\hline
\textbf{Parameter} & \textbf{OSoS(1)} & \textbf{OSoS(2)} & \textbf{G} & \textbf{M+G} & \textbf{L} & \textbf{M+L} \\
\hline
$P$ & 110 & 105 & 95 & 105 & 100 & 95 \\
$C$ & 0.20 & 0.80 & 0.85 & 0.90 & 0.85 & 0.85 \\
$M$ & 0.17 & 0.14 & 0.07 & 0.09 & 0.10 & 0.10 \\
\hline
\end{tabular}
\caption{Optimized parameters for each variant of PMIT-D0L}
\end{table}

D. Fitness Function and Termination Conditions

After a candidate L-system $G$ is produced from the solution $S$, the following process is used to evaluate fitness. To begin, any $G$ which produces more than double the expected number of symbols is assigned the maximum fitness value so it (practically) guaranteed to be culled in the survival step. Starting with $\omega_1$, a developmental sequence of length $n$ is produced using $G$ denoted as $\overline{p}$. For each $\overline{\omega}_i \in \overline{p}$, or until it terminates (see below), the symbol in each position of $\omega_i$ is compared to the corresponding position in $\overline{\omega}_i$. An error is counted if the symbol does not match (like Hamming distance), or if there is no corresponding symbol (i.e., one of the strings is longer or shorter than the other). For example, when comparing $\omega_i = XXYXXXY$ to $\overline{\omega}_i = XYYX$, there are four errors. The third and fourth symbols differ, and additionally $\omega_i$ has six symbols, while $\overline{\omega}_i$ has only four. This process terminates when the number of errors for the $i^{th}$ derivation is greater than zero, as any errors will cascade forward. The fitness value is computed as the number of errors divided by the number of expected symbols (e.g., $4/6$), plus the number of unchecked derivations $(n - i)$. This encourages the GA to find solutions that incrementally match $\rho$.

PMIT-D0L uses a three-part termination condition to determine when to stop running. Ideally, PMIT-D0L terminates when a solution is found with a fitness value of 0.0 as this corresponds to an L-system that produces $\rho$ as its length $n$ developmental sequence. PMIT-D0L will also terminate when the population is considered to have converged to prevent the GA from acting as a random search and skewing the results. First, the current generation $\text{Gen}_{\text{best}}$ is recorded whenever a new best solution is found. If an additional $\text{Gen}_{\text{best}}$ generations pass without finding a new best solution, the population is considered converged. To prevent random chance from causing early termination, PMIT-D0L must process at least 1,000 generations. PMIT-D0L also terminates after a time limit is reached. For this paper, the time limit was set to four hours; however, this was mainly used to control the overall

\[
\begin{align*}
\omega_1 & : A + B - A \\
\omega_2 & : B[A]B[+A] - [+B] - B[+A]B
\end{align*}
\]
IV. Evaluation

A. Data Set

To evaluate PMIT-D0L’s ability to infer D0L-systems, ten fractals, plus the six plant-like fractal variants (one shown in Figure 2) inferred by the existing program LGIN [3], [15], and twelve other biological models were selected from the vlab online repository [5]. The biological models consist of ten algae, apple twig with blossoms (shown in Figure 15), and a “Fibonacci Bush” (shown in Figure 13), which was found to be aesthetically realistic [4]. The dataset compares favourably to similar studies where only some variants of one or two models are considered [15], [16]. The data set is also of greater complexity by considering models with alphabets from between 2 to 31 symbols compared to two symbol alphabets [15], [16].

B. Performance Metrics

Two performance metrics are used to measure how well PMIT-D0L can infer D0L-systems. The first metric is success rate (SR) which is defined as the percentage of times PMIT-D0L can find any L-system compatible with the input sequence. The second metric is mean time to solve (MTTS) measured to the millisecond level since some models solve in sub-second time. Time was measured using a single core of an Intel 4770 @ 3.4 GHz with 12 GB of RAM on Windows 10. PMIT-D0L is only allowed to execute for at most 4 hours (14400 seconds) and reaching this limit is considered a failure. These metrics are consistent with those found in literature [15], [16].

C. Results

There are three results discussed in this section. The first set of results is the performance metrics shown in Table II. For PMIT-D0L(M+G) and PMIT-D0L(M+L), the systems where the matrix was invertible are marked with “*” as no searching was required. A raw average for each encoding technique is also provided. Brute force was also implemented to highlight the effect of the GA over brute force, Table III shows a comparison of MTTS between these two search algorithms using the PMIT-D0L(M+L) (selected as it was overall the best algorithm for the brute force implementation). For brute force, the mathematical properties were still used, but to emphasize the effect of the search algorithm, the mathematical properties were only computed once instead of in a loop. The MTTS results are shown explicitly in seconds with the best result for a system bolded. SR is always 100% with the GA, and was either 0% or 100% for brute force. In cases where it is 0%, the MTTS result is bold, and the MTTS is 14000 (the max value). The second set of results, shown in Table IV are based on examining the effect of different search space reduction techniques on search space size. A discussion is provided on a fitness landscape analysis of the different encoding schemes. The fitness landscape analysis examined the manner in which the GA traversed the search space, and examined the local neighborhood of candidate solutions.

D. Discussion

It is evident from Table II and the average row that OSoS(1) and OSoS(2) are worse than the other encoding schemes, and therefore using some form of length with the scanning process seems to be best. However, OSoS(2) is faster overall than OSoS(1) (especially for Metamorpha), and therefore additional lookahead is helping with OSoS. With respect to using Doucet’s [21] approach to find a unique solution, the matrix is found to be invertible for a little less than half of the L-systems in the test set, but never for any of the biological models. However, for both PMIT-D0L(M+G) and PMIT-D0L(M+L) the addition of the matrix operation to reduce the search space provides a benefit over PMIT-D0L(G) and PMIT-D0L(L) respectively. It is not so clear cut as to which encoding scheme is best, although PMIT-D0L(M+L) is the fastest overall, finishing in an average of 0.391 seconds. Certainly, it can be seen that PMIT-D0L(M+G) and PMIT-D0L(M+L) tend to be better than those without the matrix operations, but the timings tend to be close. However, for Fibonacci Bush, PMIT-D0L(M+L) performed much better than PMIT-D0L(M+G). Overall, both are quite fast, and the same can be said for all of the growth-based and length-based encoding schemes. This leads perhaps to the conclusion that choosing between a growth-based or length-based encoding scheme is not so important, but rather the success of PMIT-D0L (of any type) is largely attributed to the space reduction techniques. This observation is further reinforced by the results in Table III. Except where there are ties at 0.001 seconds, the data indicates not only that a GA provides substantial improvement over brute force, but also a single pass of computing growth and length bounds does not provide as much improvement when compared to PMIT-D0L(M+L) (Dipterosiphonia v1, Pterocladellium, and Tenuissimum). The conclusion that the success is tied mainly to search space reduction led to evaluating the effect more explicitly (described in the next paragraph). Additionally, this conclusion suggests as a future work to incrementally increase |V| (or make other systematic changes to the test data) to see if a difference emerges between growth-based and length-based approaches.

Table IV shows the length-based search space size for each L-system in the test set projected onto V with a different set of space reduction techniques applied (in the columns). In Table IV the “Trivial” column shows the search space for a single execution of the length bounds reduction technique (Section III-B3) as this is the least amount of analysis possible with PMIT-D0L while still allowing it to function (this is a necessary first step to initialize the $A_{\max}$ bounds). The “All” columns shows the search space size when all techniques are applied. The “Only Growth and Length Reduction” columns shows the search space size when only the Parikh vectors and word lengths are examined (Section III-B3). The “Only Successor Relationships” column shows the search space size when the techniques related to successor relationships are used alone (Sections III-B1 and III-B2), after a single execution of the length reduction techniques.

For this table, only the V alphabet was used as the search spaces for each additional problem where a symbol from V
is added to determine to which successor they belong are often small (≤16) in comparison after applying the solution projection technique (Section III-B4), with some exceptions. In particular, *Dipterosiphonia* v1, *Pterocladelium* and *Tenuissimum* had exceptional cases where the search spaces were larger for symbols from $V$ than the problem for $V$, although even in the worst case the search spaces were still on the order of $10^4$ or less when all of the techniques were applied. This was due to the solution projection technique being unable to mark the “f” and “F” symbols as certain. An examination of the three L-systems shows that more so than other L-systems since it mainly excels at finding symbols that lay between the scenario is the worst case for the solution projection technique (Section III-B4), with some exceptions.TABLE II: Comparison of MTTS in seconds for different encoding schemes for PMIT-D0L with the best MTTS bolded. SR is 100% for all executions. Results with “*” indicate an invertible matrix.

| Model                              | MTTS (s) |
|------------------------------------|----------|
| OSoS(1)                            | 0.001    |
| OSoS(2)                            | 0.001    |
| G                                  | 0.001    |
| M+G                                | 0.001    |
| L                                  | 0.001    |
| M+L                                | 0.001    |
| Algae                              | 0.001    |
| Cantor Dust                        | 0.001    |
| Dragon Curve                       | 0.001    |
| E-Curve                            | 0.001    |
| Fractal Plant v1                   | 0.001    |
| Fractal Plant v2                   | 0.001    |
| Fractal Plant v3                   | 0.001    |
| Fractal Plant v4                   | 0.001    |
| Fractal Plant v5                   | 0.001    |
| Fractal Plant v6                   | 0.001    |
| Gosper Curve                       | 0.001    |
| Koch Curve                         | 0.001    |
| Peano                              | 0.001    |
| Pythagoras Tree                    | 0.001    |
| Sierpinski Triangle v1             | 0.001    |
| Sierpinski Triangle v2             | 0.001    |
| Dipterosiphonia v1                 | 0.001    |
| Dipterosiphonia v2                 | 0.001    |
| Ditira Reptans                     | 0.001    |
| Ditira Zonaricola                  | 0.001    |
| Herposiphonia                      | 0.001    |
| Herposiphonia                      | 0.001    |
| Metamorphe                         | 0.001    |
| Pterocladelium                     | 0.001    |
| Tenuissimum                        | 0.001    |
| Apple Twig                         | 0.001    |
| Pterocladellium                    | 0.001    |
| Tenuissimum                        | 0.001    |
| Average                            | 0.001    |
| **Total**                          | **0.001**|

| Model                              | MTTS (s) |
|------------------------------------|----------|
| L-system                           |          |
| Algae                              | 0.001    |
| Cantor Dust                        | 0.001    |
| Dragon Curve                       | 0.001    |
| E-Curve                            | 0.001    |
| Fractal Plant v1                   | 0.001    |
| Fractal Plant v2                   | 0.001    |
| Fractal Plant v3                   | 0.001    |
| Fractal Plant v4                   | 0.001    |
| Fractal Plant v5                   | 0.001    |
| Fractal Plant v6                   | 0.001    |
| Gosper Curve                       | 0.001    |
| Koch Curve                         | 0.001    |
| Peano                              | 0.001    |
| Pythagoras Tree                    | 0.001    |
| Sierpinski Triangle v1             | 0.001    |
| Sierpinski Triangle v2             | 0.001    |
| Dipterosiphonia v1                 | 0.001    |
| Dipterosiphonia v2                 | 0.001    |
| Ditira Reptans                     | 0.001    |
| Ditira Zonaricola                  | 0.001    |
| Herposiphonia                      | 0.001    |
| Herposiphonia                      | 0.001    |
| Metamorphe                         | 0.001    |
| Pterocladelium                     | 0.001    |
| Tenuissimum                        | 0.001    |
| Apple Twig                         | 0.001    |
| Pterocladellium                    | 0.001    |
| Tenuissimum                        | 0.001    |
| Average                            | 0.001    |
| **Total**                          | **0.001**|

From this table, it is evident that there exists a synergistic effect between the growth and length reduction, and the techniques for refining successor fragments. The resulting search space is much lower when all of the techniques are applied than when only one category of techniques is applied. While all of the techniques are essential overall, the use of successor relationships extracts information from $\rho$ by utilizing the sequence of symbol and this is one of the main differences between PMIT-D0L and other existing approaches. Capturing information from the symbol sequence of strings in $\rho$ should provide guidance towards future investigations on inferring L-
### TABLE IV: Comparison of search space size for different encoding schemes for PMIT-D0L. All values larger than 100,000 shown in scientific notation.

| L-system                     | Trivial | All | Only Growth and Length Reduction | Only Successor Relationships |
|------------------------------|---------|-----|----------------------------------|-----------------------------|
| Algae                        | 1       | 1   | 1                                |                             |
| Cantor Dust                  | 9       | 1   | 4                                | 9                           |
| Dragon Curve                 | 4       | 1   | 4                                | 9                           |
| E-Curve                      | 6557    | 4   | 2070                            | 4                           |
| Fractal Plant v1             | 4       | 1   | 1                                | 1                           |
| Fractal Plant v2             | 4       | 1   | 1                                | 1                           |
| Fractal Plant v3             | 4       | 1   | 1                                | 1                           |
| Fractal Plant v4             | 4       | 1   | 1                                | 1                           |
| Fractal Plant v5             | 4       | 1   | 1                                | 1                           |
| Fractal Plant v6             | 4       | 1   | 1                                | 1                           |
| Gazper Curve                 | 525     | 4   | 90                              | 1368                        |
| Koch Curve                   | 1       | 1   | 1                                | 1                           |
| Peano                        | 35144   | 1   | 2352                            | $3 \times 10^3$            |
| Pythagoras Tree              | 1       | 1   | 1                                | 1                           |
| Sierpinski Triangle v1       | 4       | 1   | 1                                | 12                          |
| Sierpinski Triangle v2       | 2       | 1   | 1                                | 20                          |
| Aphanocladia                 | $2 \times 10^5$ | 36 | 392 | 45 |
| Dipterosiphonia v1           | $1 \times 10^{18}$ | 16 | $1 \times 10^{18}$ | $4 \times 10^{14}$ |
| Dipterosiphonia v2           | $2 \times 10^5$ | 81 | 12615 | $1 \times 10^5$ |
| Ditira Keptans               | 6084   | 49  | 196                             | 49                          |
| Ditira Zonaricola            | $1 \times 10^4$ | 49 | 196 | 49 |
| Herpopteris                  | $6 \times 10^5$ | 25 | 1350 | 74 |
| Herposiphonia                | $6 \times 10^4$ | 1  | 39520 | $3 \times 10^6$ |
| Metamorpha                   | $2 \times 10^5$ | 576 | 85698 | $4 \times 10^6$ |
| Pierocladellium              | $6 \times 10^{18}$ | 81 | $1 \times 10^{18}$ | $5 \times 10^{14}$ |
| Tenaisadium                  | $1 \times 10^4$ | 96 | $2 \times 10^4$ | $1 \times 10^4$ |
| Apple Twig                   | $1 \times 10^4$ | 1  | $3 \times 10^4$ | $2 \times 10^4$ |
| Fibonacci Bush               | $1 \times 10^5$ | 576 | 7200 | 7200 |

### TABLE V: L-system for Dipterosiphonia v1 [25].

| Productions                  |
|------------------------------|
| $c \rightarrow FFFz[+k]$$−r[FF]f d$ |
| $z \rightarrow Fz$           |
| $k \rightarrow tmFF$         |
| $r \rightarrow stFF$         |
| $d \rightarrow FFFz[+k]$$−r[FF]f c$ |
| $t \rightarrow jF$           |
| $m \rightarrow n$           |
| $s \rightarrow jF$           |
| $t \rightarrow u$           |
| $e \rightarrow FFFz[+fj]FFf g$ |
| $n \rightarrow jFF[−A]F o$   |
| $u \rightarrow jFF[+A]F v$   |
| $j \rightarrow abF$         |
| $g \rightarrow FFFz[+k]$$−r[FF]f n$ |
| $A \rightarrow jFB$         |
| $o \rightarrow jFF[−B]F p$   |
| $v \rightarrow jFF[+B]F w$   |
| $a \rightarrow F f$         |
| $b \rightarrow c$           |
| $h \rightarrow FFFz[+k]$$−r[FF]f i$ |
| $B \rightarrow jFC$         |
| $p \rightarrow jFF[−C]F q$   |
| $w \rightarrow jFF[+C]F x$   |
| $i \rightarrow jFFz[−fj]FFf c$ |
| $C \rightarrow jFD$         |
| $q \rightarrow jFF[−D]F$     |
| $s \rightarrow jFF[+D]F$     |
| $D \rightarrow jF$          |

The fitness landscape analysis was conducted in two parts. First, a number ($r$) of random points were selected in the search space. The fitness function was applied to the selected point and to each point in a local neighborhood around it within $±3$ in each dimension. The count of each unique fitness value was collected for the neighborhood. Second, the best and worst fitness values collected from the executions were examined from the perspective of how they change as the GA converges towards the solution. Although the analysis was done for each encoding scheme, and across all of the systems, ultimately the observations can be made mainly collectively. Any observations that were made for a specific encoding scheme will be specified.

The fitness values are extremely stratified, i.e. there are relatively few unique fitness values for any system. There are almost always less strata for the length-based encoding schemes versus the growth-based encoding schemes, and the growth-based schemes in turn have less than OSoS(2). This means that it can be difficult to find a better solution since so many solutions have the same fitness value and the GA will get stuck in a local optima (this can be seen in the figures as a plateau). The main difference is that the length-based schemes tend to have a local optima with relatively high fitness. OSoS and growth-based encoding schemes, by contrast, have a local optima with a low fitness. This suggests that there is a tighter relationship, or more information revealed, in the growth-based and OSoS encoding schemes with respect to the actual solution, and that minor variations from the solution in length-based approaches generates much more error. Especially with respect to OSoS encoding, even though it was not as good with respect to MTTS, maybe there is a way to use the systems.
information revealed to help guide the other encoding schemes more quickly towards a solution using hybridization. Finally, the stratified nature of the search space suggests a probable reason why the mutation weight for the GA tends to be high; exploration is more important than exploitation for these encoding schemes and the L-system inductive inference problem.

In examining the local neighborhood, it was observed that it is rarely very uniform. Even small variations to gene values can have an impact on fitness values. This lack of uniformity suggests that global/local hybrid search, or a swarm-based search that focuses on searching the neighborhood of local optima (e.g. particle swarm optimization), should be effective choices. Alternatively, differential evolution may be a good choice since it has been shown to be effective on search spaces that are similar to the one found in this research [26].

V. Conclusions

This paper presented an evaluation and analysis of different encoding schemes for the Plant Model Inference Tool for deterministic context-free L-systems (PMIT-D0L) to infer L-systems from a sequence of strings. Some of the encoding schemes are based on or modifications of earlier works, while some are novel. The classical encoding schemes look at the problem of inferring successors as finding an ordered sequence of symbols for the successors [16]. Alternatively, considering the input strings and successors as Parikh vectors, a so-called growth-based or length-based approach can be used.

The evaluation of the different encoding schemes does not indicate a clear best encoding, however length-based approaches are the fastest for this test set. Much of this paper focused on techniques for reducing the search space size, mainly using necessary conditions. While all of the different techniques were found to reduce the search space, there was an observed synergistic effect when used in combination. The techniques are effective to the degree that the choice between growth-based and length-based is not particularly critical for this particular test set. Additional investigation should be done on larger or more complex L-systems to determine if this still holds true.

A fitness landscape analysis was also conducted and it was observed that the landscape is very stratified and very non-uniform in the local neighborhood of an arbitrary point. This suggests that exploration, especially of a local neighborhood, might be an opportunity for future improvement over genetic algorithm. A global/local hybrid or a swarm algorithm may be good choices, alternatively differential evolution has been previously shown to be a good choice for the types of fitness landscapes observed [26].

The inductive inference of L-systems from input strings allows for much more rapid development of models than the current approach of building models by hand [11], which can take weeks or months. Additionally, by going directly from observation (strings) to a model, allows for mechanistic principles to be possibly revealed, as opposed to requiring expert knowledge to build the model.

Since PMIT-D0L seems capable of inferring L-systems with fairly large alphabets (at least 31 symbols in the test set in a fast manner), this work will be used as a base for investigating the inference of other, more complex, L-system extensions such as stochastic L-systems, parametric L-systems, and for using images as input.

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