Gene Expression Programming: a New Adaptive Algorithm for Solving Problems

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Gene expression programming, a genome/phenome genetic algorithm (linear and non-linear), is presented here for the first time as a new technique for creation of computer programs. Gene expression programming uses character linear chromosomes composed of genes structurally organised in a head and a tail. The chromosomes function as a genome and are subjected to modification by means of mutation, transposition, root transposition, gene transposition, gene recombination, 1-point and 2-point recombination. The chromosomes encode expression trees which are the object of selection. The creation of these separate entities (genome and expression tree) with distinct functions allows the algorithm to perform with high efficiency: in the symbolic regression, sequence induction and block stacking problems it surpasses genetic programming in more than two orders of magnitude, whereas in the density-classification problem it surpasses genetic programming in more than four orders of magnitude. The suite of problems chosen to illustrate the power and versatility of gene expression programming includes, besides the above mentioned problems, two problems of Boolean concept learning: the 11-multiplexer and the GP rule problem.

1. Introduction

Gene expression programming (GEP) is, like genetic algorithms (GAs) and genetic programming (GP), a genetic algorithm as it uses populations of individuals, selects them according to fitness, and introduces genetic variation using one or more genetic operators [1]. The fundamental difference between the three algorithms reside in the nature of the individuals: in GAs the individuals are linear strings of fixed length (chromosomes); in GP the individuals are non-linear entities of different sizes and shapes (parse trees); and in GEP the individuals are encoded as linear strings of fixed length (the genome or chromosomes) which are afterwards expressed as non-linear entities of different sizes and shapes (simple diagram representations or expression trees).

If we have in mind the history of life on Earth [2], we can see that the difference between GAs and GP is only superficial: both systems use only one kind of entity which functions both as genome and body (phenome). These kind of systems are condemned to have one of two limitations: if they are easy to genetically manipulate, they lose in functional complexity (the case of GAs); if they exhibit a certain amount of functional complexity, they are extremely difficult to reproduce with modification (the case of GP).

GAs, with their simple genome and limited structural and functional diversity, resemble a primitive RNA World [2], whereas GP, with its structural and functional diversity, resembles an hypothetical Protein World. Only when molecules capable of replication joined molecules with catalytic activity, forming an indivisible whole, was it possible to create more complex systems and, ultimately, the first cell. Since then, the genome and phenome mutually presume one another and neither can function without the other. Similarly, the chromosomes and expression trees of GEP mutually presume one another and neither exists without the other.

The advantages of a system like GEP are clear from nature, but the most important should be emphasised: First, the chromosomes are simple entities: linear, compact, relatively small, easy to genetically manipulate (replicate, mutate, recombine, transpose, etc.). Second, the expression tress (ETs) are exclusively the expression of the respective chromosomes; they are the entities upon which selection acts and, according to fitness, they are selected to reproduce with modification. During reproduction it is their chromosomes, not the ETs, which are reproduced with modification and transmitted to the next generation.

The interplay of chromosomes and ETs implies a universal translation system to translate the language of chromosomes into the language of ETs. The structural organisation of GEP chromosomes presented in this work allows such an interplay, as any modification made in the genome results always in syntactically correct ETs or programs. The varied set of genetic operators developed to introduce genetic diversity in GEP populations always pro-

duce valid ETs. Thus, GEP is a very simple, life-like complex system capable of adaptation and evolution.

On account of these characteristics, GEP is extremely versatile and greatly surpasses the existing evolutionary techniques. Indeed, in the most complex problem presented in this work, the evolution of cellular automata rules for the density-classification task, GEP surpasses GP in more than four orders of magnitude.

In the present work I show the structural and functional organisation of GEP chromosomes; how the language of the chromosomes is translated to the language of the ETs; how the chromosomes function as genotype and the ETs as phenotype; and how an individual program is created, matured, and reproduced, leaving offspring with new properties, thus, capable of adaptation. The paper proceeds with a detailed description of GEP and the illustration of this technique with six examples chosen from different fields, comparing the performance of GEP with GP.

2. Gene expression algorithms: an overview

The flowchart of a gene expression algorithm (GEA) is shown in Figure 1. The process begins with the random generation of the chromosomes of each individual of the initial population. Then the chromosomes are expressed and the fitness of each individual is evaluated. The individuals are then selected according to fitness to reproduce with modification, leaving progeny with new traits. The individuals of this new generation are, in their turn, subjected to the same developmental process: expression of the genomes, confrontation of the selection environment, and reproduction with modification. The process is repeated for a certain number of generations or until a solution has been found.

Note that reproduction includes not only replication but also the action of genetic operators capable of creating genetic diversity. During replication, the genome is rigorously copied and transmitted to the next generation. Obviously, replication alone can not introduce variation: only with the action of the remaining operators is the genetic variation introduced in the population. These operators randomly select the chromosomes to be modified. Thus, in GEP, a chromosome might be modified by one or several operators at a time or not be modified at all. The details of the implementation of GEP operators are shown in section 5.

3. The genome of GEP individuals

In GEP, the genome or chromosome consists of a linear, symbolic string of fixed length composed of one or more genes. We will see that despite their fixed length, GEP chromosomes code for ETs with different sizes and shapes.

3.1. Open reading frames and genes

The structural organisation of GEP genes is better understood in terms of open reading frames (ORFs). In biology, an ORF, or coding sequence of a gene, begins with the

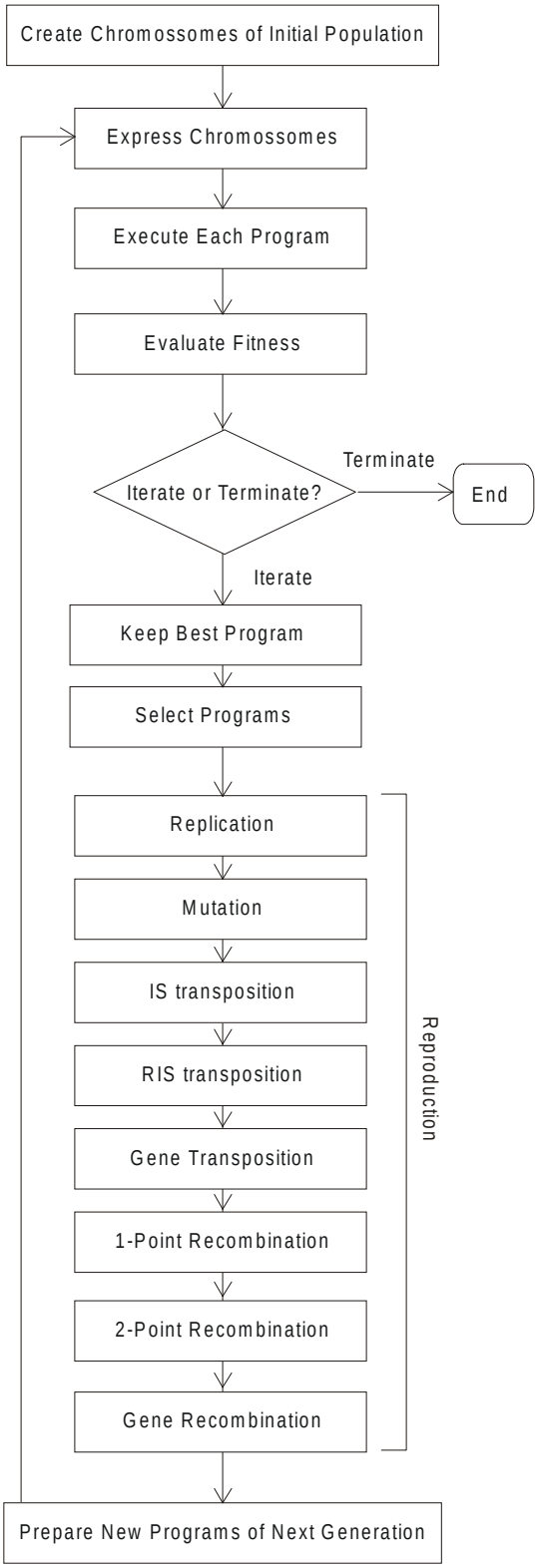


Figure 1. The flowchart of a gene expression algorithm.

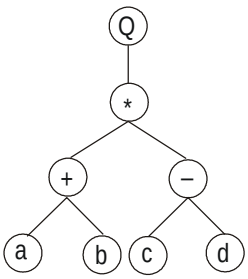
'start' codon, continues with the amino acid codons, and ends at a termination codon. However, a gene is more than the respective ORF, with sequences upstream the start codon and sequences downstream the stop codon. Although in GEP the start site is always the first position of a gene, the termination point not always coincides with the last position of a gene. It is common for GEP genes to

have non-coding regions downstream the termination point. (For now we will not consider these non-coding regions, because they do not interfere with the product of expression.)

Consider, for example, the algebraic expression:

$$\sqrt{(a+b)\times(c-d)} \qquad (3.1)$$

It can also be represented as a diagram or ET:



where 'Q' represents the square root function. This kind of diagram representations are in fact the phenotype of GEP individuals, being the genotype easily inferred from the phenotype as follows:

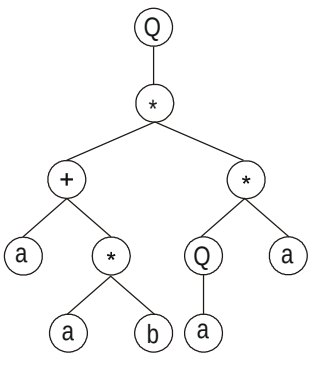
```
01234567
Q*+-abcd
```
(3.2)

which is the straightforward reading of the ET from left to right and from top to bottom. The expression 3.2 is an ORF, starting at 'Q' (position 0) and terminating at 'd' (position 7). These ORFs were named K-expressions (from KARVA language). Note that this ordering differs from both the postfix and prefix expressions used in different GP implementations with arrays or stacks [3].

The inverse process, i.e. the translation of a K-expression into an ET, is also very simple. Consider another ORF, the following K-expression:

```
01234567890
Q*+*a*Qaaba
```
(3.3)

The start position (position 0) in the ORF corresponds to the root of the ET. Then, bellow each function are attached as many branches as there are arguments to that function. The assemblage is complete when a base line composed only of terminals (the variables or constants used in a problem) is formed. In this case, the following ET is formed:



Looking at the structure of GEP ORFs only, it is difficult or even impossible to see the advantages of such a representation, except perhaps for its simplicity and elegance. However, when ORFs are analyzed in the context of a gene, the advantages of such representation become obvious. As I said, GEP chromosomes have fixed length, and they are composed of one or more genes of equal length. Therefore the length of a gene is also fixed. Thus, in GEP, what varies is not the length of genes which is constant, but the length of the ORFs. Indeed, the length of an ORF may be equal or less than the length of the gene. In the first case, the termination point coincides with the end of the gene, and in the last case, the termination point is somewhere upstream the end of the gene.

So, what is the function of these non-coding regions in GEP genes? In fact, they are the essence of GEP and evolvability, for they allow the modification of the genome using any genetic operator without restrictions, producing always syntactically correct programs without the need for a complicated editing process or highly constrained ways of implementing genetic operators. Indeed, this is the paramount difference between GEP and previous GP implementations, with or without linear genomes (for a review on GP with linear genomes see [4]).

3.2. GEP genes

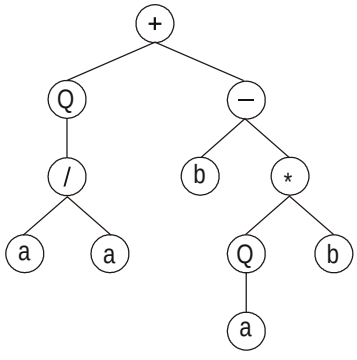
GEP genes are composed of a head and a tail. The head contains symbols that represent both functions and terminals, whereas the tail contains only terminals. For each problem, the length of the head, *h*, is chosen, whereas the length of the tail, *t*, is a function of *h* and the number of arguments of the function with more arguments, *n*, and is evaluated by the equation:

$$t = h \cdot (n-1) + 1 \qquad (3.4)$$

Consider a gene composed of {Q, *, /, -, +, a, b}. In this case $n = 2$. For instance, for an $h = 10$, $t = 11$, and the length of the gene is 10+11=21. One such gene is shown bellow (the tail is shown in bold):

```
012345678901234567890
+Q-/b*aaQbaabaabbaaab
```
(3.5)

It codes for the following ET:

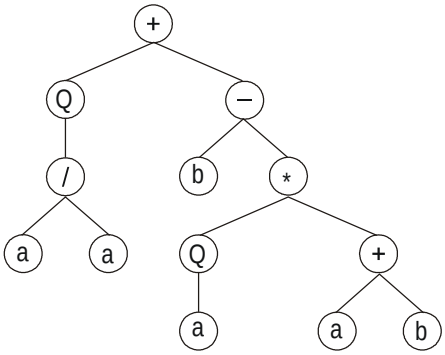


In this case, the ORF ends at position 10, whereas the gene ends at position 20.

Suppose now a mutation occurred at position 9, changing the ‘b’ into ‘+’. Then the following gene is obtained:

```
012345678901234567890
+Q-/b*aaQ+aabaabbaaab          (3.6)
```

And its expression gives:

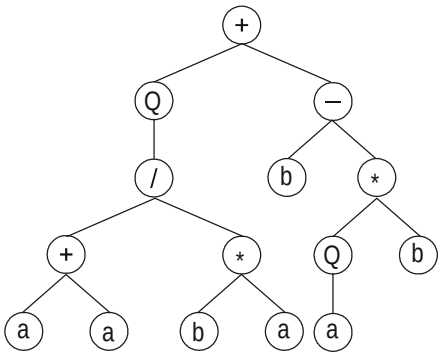


In this case, the termination point shifts two positions to the right (position 12).

Suppose now that a more radical modification occurred, and the symbols at positions 6 and 7 in the gene 3.5 above, change respectively into ‘+’ and ‘*’, creating the following gene:

```
012345678901234567890
+Q-/b*+*Qbaabaabbaaab          (3.7)
```

Its expression gives:

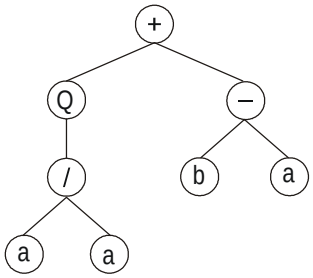


In this case the termination point shifts several positions to the right (position 14).

Obviously the opposite also happens, and the ORF is shortened. For example, consider gene 3.5 above, and suppose a mutation occurred at position 5, changing the ‘*’ into ‘a’:

```
012345678901234567890
+Q-/baaaQbaabaabbaaab          (3.8)
```

Its expression results in the following ET:



In this case, the ORF ends at position 7, shortening the original ET in 3 nodes.

Despite its fixed length, each gene has the potential to code for ETs of different sizes and shapes, being the simplest composed of only one node (when the first element of a gene is a terminal) and the biggest composed of as many nodes as the length of the gene (when all the elements of the head are functions with the maximum number of arguments, *n*).

It is evident from the examples above, that any modification made in the genome, no matter how profound, always results in a valid ET. Obviously the structural organisation of genes must be preserved, always maintaining the boundaries between head and tail and not allowing symbols representing functions on the tail. In section 5 is shown how GEP operators work and how they modify the genome of GEP individuals during reproduction.

3.3. Multigenic chromosomes

GEP chromosomes are usually composed of more than one gene of equal length. For each problem or run, the number of genes, as well as the length of the head, is chosen. Each gene codes for a sub-ET and the sub-ETs interact with one another forming a more complex multi-subunit ET. The details of such interactions will be fully explained in section 3.4.

Consider, for example, the following chromosome with length 27, composed of three genes (the tails are shown in bold):

```
012345678012345678012345678
-b*babbab*Qb+abbba-*Qabbaba    (3.9)
```

It has three ORFs, and each ORF codes for a sub-ET (Figure 2). Position zero marks the start of each gene; the end of each ORF, though, is only evident upon construction of the respective sub-ET. As shown in Figure 2, the first ORF ends at position 4 (sub-ET_1); the second ORF ends at position 5 (sub-ET_2); and the last ORF also ends at position 5 (sub-ET_3). Thus, GEP chromosomes code for one or more ORFs, each expressing a particular sub-ET. Depending on the task at hand, these sub-ETs may be selected individually according to their respective fitness (for example, in problems with multiple outputs), or they may form a more complex, multi-subunit ET and be selected according to the fitness of the whole, multi-subunit ET. The patterns of expression and the details of selection will

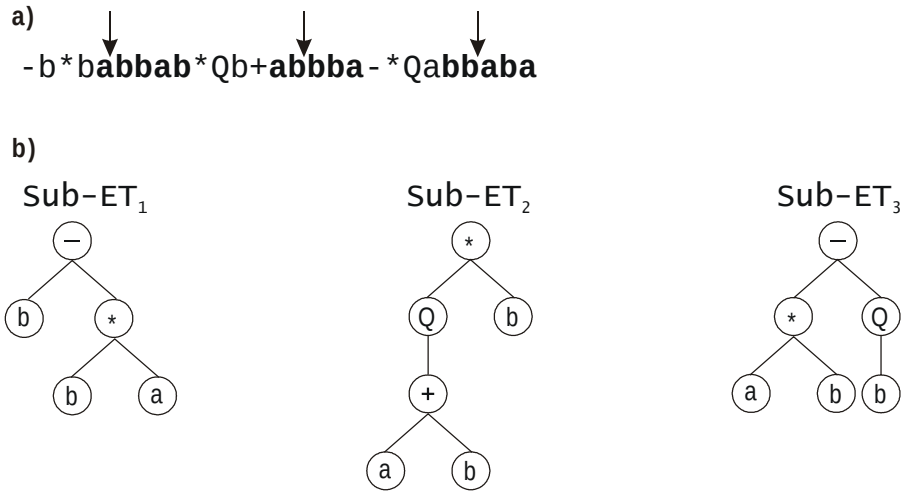


Figure 2. Expression of GEP genes as sub-ETs. **a)** A three-genic chromosome with the tails shown in bold. The arrows show the termination point of each gene. **b)** The sub-ETs codified by each gene.

be discussed throughout this paper. However, keep in mind that each sub-ET is both a separate entity and a part of a more complex, hierarchical structure, and, as in all complex systems, the whole is more than the sum of its parts.

3.4. Expression trees and the phenotype

In nature, the phenotype has multiple levels of complexity, being the most complex the organism itself. But tRNAs, proteins, ribosomes, cells, etc., are also products of expression, and all of them are ultimately encoded in the genome.

In contrast to nature, in GEP the expression of the genetic information is very simple. Nonetheless, GEP chromosomes are composed of one or more ORFs, and obviously the encoded individuals have different degrees of complexity. The simplest individuals are encoded in a single gene, and the 'organism' is, in this case, the product of a single gene - an ET. In other cases, the 'organism' is a multi-subunit ET, in which the different sub-ETs are linked together by a particular function. In other cases, the 'organism' emerges from the spatial organization of different sub-ETs (in planning and problems with multiple outputs, for example). And, in yet other cases, the 'organism' emerges from the interactions of conventional sub-ETs with different domains (neural networks, for example). However, in all cases, the whole 'organism' is encoded in a linear genome.

3.4.1. Posttranslational modifications

We have seen that translation results in the formation of sub-ETs with different complexity but the complete expression of the genetic information requires the interaction of these sub-ETs with one another. One of the most simple interactions is the linking of sub-ETs by a particular function. This process is similar to the assemblage of different protein subunits in a multi-subunit protein.

When the sub-ETs are algebraic expressions or Boolean expressions, any mathematical or Boolean function can be used to link the sub-ETs in a final, multi-subunit ET. The functions most chosen are addition for algebraic sub-ETs, and OR or IF for Boolean sub-ETs.

In the current version of GEP the linking function is a priori chosen for each problem, but it can be easily introduced in the genome, for instance in the last position of chromosomes, and be also subject to adaptation. Indeed, preliminary results suggest that this system works very well.

Figure 3 illustrates the linking of two sub-ETs by addition. Note that the root of the final ET (+) is not encoded by the genome. Note also that the final ET could be linearly encoded as the following K-expression:

```
0123456789012
+Q**-bQ+abbba          (3.10)
```

However, to evolve solutions for complex problems, it is more effective the use of multigenic chromosomes, for they permit the modular construction of complex, hierarchical structures, where each gene codes for a small building block. These small building blocks are separated from each other, and thus can evolve independently. For instance, if we tried to evolve a solution for the symbolic regression problem presented in section 6.1 with single-gene chromosomes, the success rate would fall significantly (see section 6.1). In that case the discovery of small building blocks is more constrained as they are no longer free to evolve independently. These kind of experiments show that GEP is in effect a powerful, hierarchical invention system capable of easily evolving simple blocks and using them to form more complex structures.

Figure 4 shows another example of posttranslational modification, where three Boolean sub-ETs are linked by the function IF. Again, the multi-subunit ET could be linearized as the following K-expression:

```
012345678901234567890123
IINAIAINu1ca3aa2acAOab2          (3.11)
```

a)

012345678012345678
Q*Q+**bbaaa***-ba**baabb**

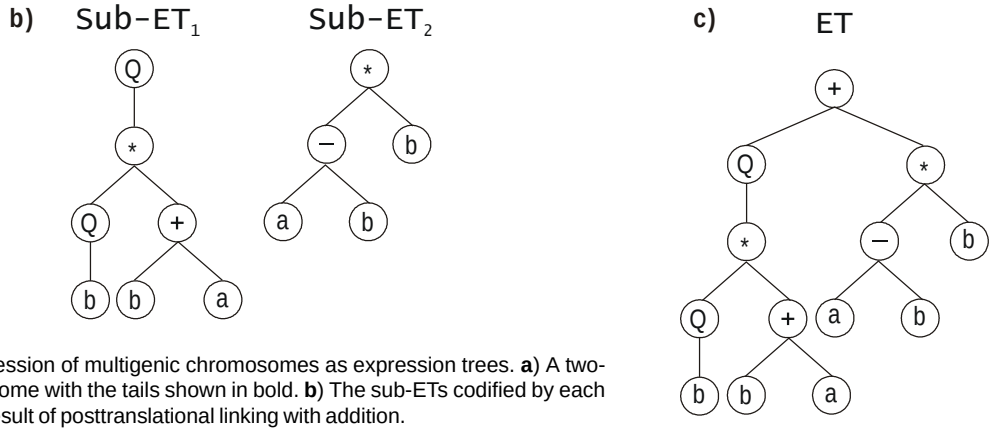


Figure 3. Expression of multigenic chromosomes as expression trees. **a**) A two-genic chromosome with the tails shown in bold. **b**) The sub-ETs codified by each gene. **c**) The result of posttranslational linking with addition.

a)

IIAI**ca3aa2acu**NNAO**ab2u3c31c**Au12**ua3112cac**

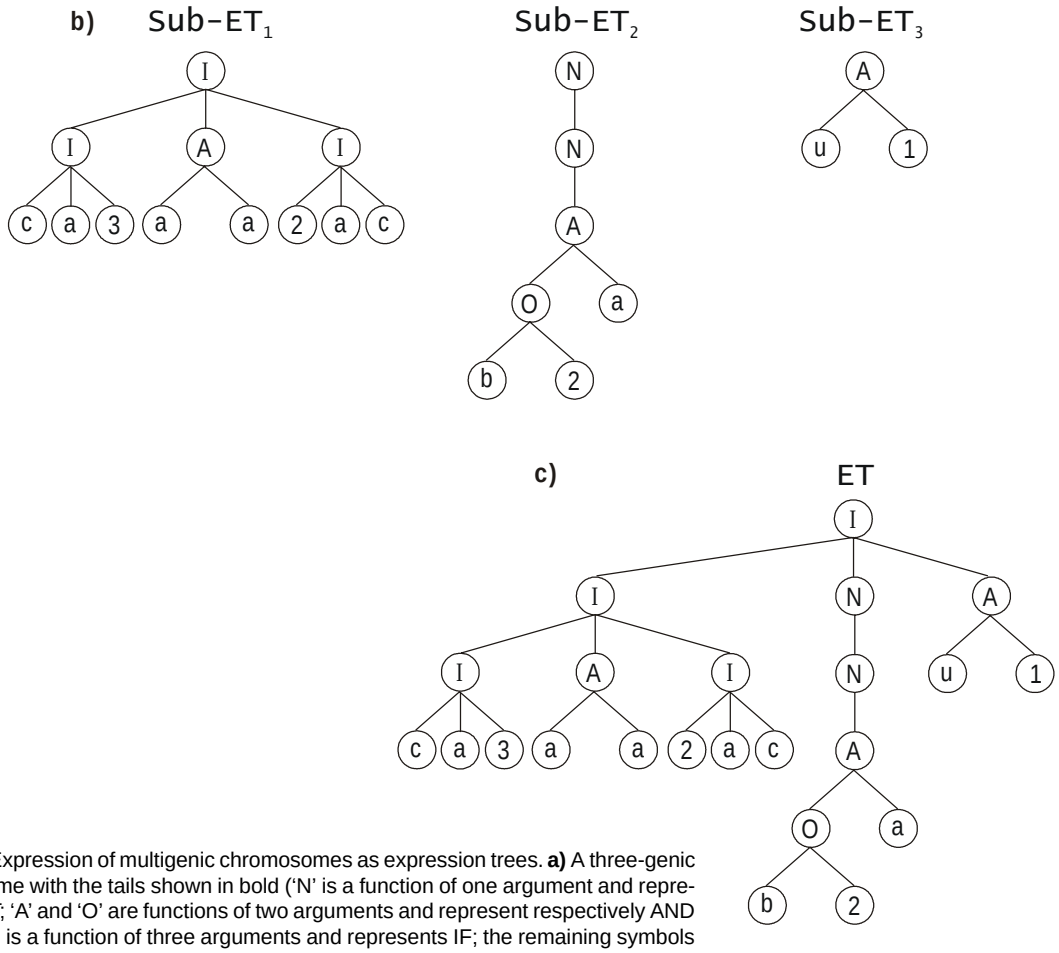


Figure 4. Expression of multigenic chromosomes as expression trees. **a)** A three-genic chromosome with the tails shown in bold ('N' is a function of one argument and represents NOT; 'A' and 'O' are functions of two arguments and represent respectively AND and OR; 'I' is a function of three arguments and represents IF; the remaining symbols are terminals). **b)** The sub-ETs codified by each gene. **c)** The result of posttranslational linking with IF.

a)

131u3ab2ubab23c3ua31a333au3

b)

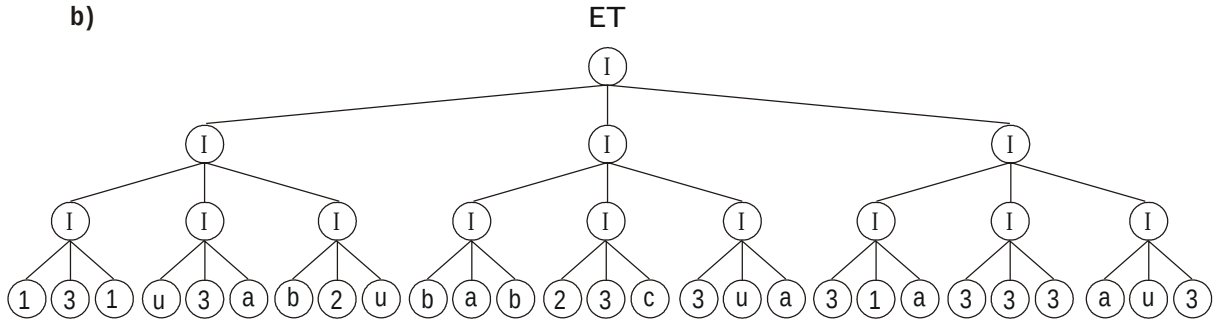


Figure 5. Expression of multigenic chromosomes as expression trees. **a)** A 27-genic chromosome composed of one-element genes. **b)** The result of posttranslational linking with IF.

Figure 5 shows another example of posttranslational modification, where the sub-ETs are of the simplest kind (one-element sub-ETs). In this case, the sub-ETs are linked 3 by 3 with the IF function, then these clusters are, in their turn, linked also 3 by 3 with another IF function, and the three last clusters are also linked by IF, forming a large multi-subunit ET. This kind of chromosomal architecture was used to evolve solutions for the 11-multiplexer problem of section 6.5.2 and also to evolve cellular automata rules for the density-classification problem (results not shown). Again, the individual of Figure 5 could be converted in the following K-expression:

IIIIIIIIIIIII131u3ab2ubab23c3ua31a333au3 (3.12)

And finally, the full expression of certain chromosomes requires the sequential execution of small plans, where the first sub-ET does a little work, the second continues from that, etc. The final plan results from the orderly action of all sub-plans (see the block stacking problem in section 6.3).

The type of linking function, as well as the number of genes and the length of each gene, are a priori chosen for each problem. So, we can always start by using a single-gene chromosome, gradually increasing the length of the head; if it becomes very large, we can increase the number of genes and of course choose a function to link them. We can start with addition or OR, but in other cases another linking function might be more appropriate. The idea, of course, is to find a good solution, and GEP provides the meanings of finding one.

4. Fitness functions and selection

In this section, two examples of fitness functions are described. Other examples of fitness functions are given in the problems studied in section 6. The success of a problem greatly depends on the way the fitness function is designed: the goal must be clearly and correctly defined in order to make the system evolve in that direction.

4.1. Fitness functions

One important application of GEP is symbolic regression, where the goal is to find an expression that performs well for all fitness cases within a certain error of the correct value. For some mathematical applications it is useful to use small relative or absolute errors in order to discover a very good solution. But if the range of selection is excessively narrowed, populations evolve very slowly and are incapable of finding a correct solution. In the other hand, if the opposite is done and the range of selection is broaden, numerous solutions will appear with maximum fitness that are far from good solutions.

To solve this problem, an evolutionary strategy was devised that permits the discovery of very good solutions without halting evolution. So, the system is left to find for itself the best possible solution within a minimum error. For that a very broad limit for selection to operate is given, usually an absolute error of 100, that allows the selection of very unfit individuals in earlier generations. However, in later generations selection operates over these cumbersome individuals and populations adapt wonderfully, finding very good solutions that progressively approach a perfect solution. Mathematically this can be expressed by the equation:

$$f = M - |E| \qquad (4.1)$$

where M is the range of selection, and E is the absolute error between the number generated by the ET and the target value. The precision for the absolute error is usually very small, for instance 0.01, but if a perfect solution could not be found within this value, the system can find the optimal solution for itself. For example, for a set of 10 fitness cases and an M = 100, f_{max} = 1000 if all the values are within 0.01 of the correct value.

In another important GEP application, Boolean concept learning, the fitness of an individual is a function of the number of fitness cases on which it performs correctly. For most Boolean applications, though, it is fundamental to penalize individuals able to correctly solve about 50%

of fitness cases, as most probably this only reflects the 50% likelihood of correctly solving a 2-binary Boolean function. So, it is advisable to only select individuals capable of solving more than 50-75% of fitness cases. Below that mark a symbolic value of fitness can be attributed, for instance $f = 1$. Usually the process of evolution is put in motion with this unfit individuals, for they are very easily created in the initial population. However, in future generations, highly fit individuals start to appear, rapidly spreading in the population. For easy problems, like Boolean functions with 2-5 arguments, this is not really important, but for more complex problems it is convenient to choose a bottom line for selection. For these problems, the following fitness function can be used:

$$\text{If} \quad i \geq \tfrac{3}{4}C \ , \text{then} \quad f = i \ ; \text{else} \quad f = 1 \qquad (4.2)$$

where i is the number of fitness cases correctly evaluated, and C is the total number of fitness cases.

4.2. Selection

In GEP, individuals are selected according to fitness by roulette-wheel sampling [5]. In truth, I never experimented with other selection methods for I'd rather let 'nature' take its course. It is true that with this method, often the best individuals are lost, but this might have some advantages and make populations jump to another, very distant fitness optimum. Of course, this deserves a careful study, but the high performance of GEP indicates that this algorithm can very efficiently walk (I would say fly, even) the fitness landscape, easily finding one of the highest optima. However, the simple form of elitism implemented in GEP guarantees the survival and cloning of the best individual to the next generation. This way the best trait is never lost.

5. Reproduction with modification

According to fitness and the luck of the roulette, individuals are selected to reproduce with modification, creating the necessary genetic diversification that allows adaptation in the long run.

Except for replication, where the genomes of all the selected individuals are rigorously copied, all the remaining operators randomly pick chromosomes to be subjected to a certain modification. However, except for mutation, each operator is not allowed to modify a chromosome more than once. For instance, for a transposition rate of 0.7, seven out of 10 different chromosomes are randomly chosen.

Furthermore, in GEP, a chromosome might be chosen by one or several genetic operators that introduce variation in the population. This feature also distinguishes GEP from GP where an entity is never modified by more than one operator at a time [6]. Thus, in GEP, the modifications of several genetic operators accumulate during reproduction, producing offspring very different from the parents.

The section proceeds with the detailed description of GEP operators, starting obviously with replication.

5.1. Replication

Although vital, replication is the most uninteresting operator: alone it contributes nothing to genetic diversification. (Indeed, replication, together with selection, is only capable of causing genetic drift.) According to fitness and the luck of the roulette, chromosomes are faithfully copied into the next generation. The fitter the individual the higher the probability of leaving more offspring. Thus, during replication the genomes of the selected individuals are copied as many times as the outcome of the roulette. The roulette is spun as many times as there are individuals in the population, maintaining always the same population size.

5.2. Mutation

Mutations can occur anywhere in the chromosome. However, the structural organisation of chromosomes must remain intact. In the heads any symbol can change into another (function or terminal); in the tails terminals can only change into terminals. This way, the structural organisation of chromosomes is maintained, and all the new individuals produced by mutation are structurally correct programs. Typically, a mutation rate (p_m) equivalent to 2 point mutations per chromosome is used. Consider the following 3-genic chromosome:

```
012345678012345678012345678
-+-+abaaa/bb/ababb*Q*+aaaba
```

Suppose a mutation changed the element in position 0 in gene 1 to 'Q'; the element in position 3 in gene 2 to 'Q'; and the element in position 1 in gene 3 to 'b', obtaining:

```
012345678012345678012345678
Q+-+abaaa/bbQababb*b*+aaaba
```

Note that if a function is mutated into a terminal or vice versa, or a function of one argument is mutated into a function of two arguments or vice versa, the ET is modified drastically. Note also that the mutation on gene 2 is an example of a neutral mutation, as it occurred in the non-coding region of the gene.

It is worth noticing that in GEP there are no constraints both in the kind of mutation and the number of mutations in a chromosome: in all cases the newly created individuals are syntactically correct programs.

In nature, a point mutation in the coding sequence of a gene can slightly change the structure of the protein or not change it at all, as neutral mutations are fairly frequent (for instance, mutations in introns, mutations that result in the same amino acid due to the redundancy of the genetic code, etc). Here, although neutral mutations exist, a mutation in the coding sequence of a gene has a much more profound effect: it usually drastically reshapes the ET.

In contrast to the current thought in evolutionary computation, this capacity to reshape profoundly the ET is fundamental for evolvability. An exhaustive analysis of GEP operators is beyond the scope of this paper, however, the

results presented in this work clearly show that our very human wish not to disrupt the small functional blocks as they appear in the expression trees and recombine them carefully (as is done in GP) is conservative and works poorly. In a genome/phenome system like GEP, the system can find ways of creating and using these functional blocks much more efficiently. The system's ways are only evident when they emerge in the expression tree.

5.3. Transposition and insertion sequence elements

The transposable elements of GEP are fragments of the genome that can be activated and jump to another place in the chromosome. In GEP there are three kinds of transposable elements: i) short fragments with a function or terminal in the first position that transpose to the head of genes except to the root (insertion sequence elements or IS elements); ii) short fragments with a function in the first position that transpose to the root of genes (root IS elements or RIS elements); iii) and entire genes that transpose to the beginning of chromosomes.

The existence of IS and RIS elements is a remnant of the developmental process of GEP, as the first GEA used only single-gene chromosomes, and in such systems a gene with a terminal at the root was of little use. When multigenic chromosomes were introduced this feature remained as these operators are important to understand the mechanisms of genetic variation . Indeed, the transforming power of these operators show clearly that there is no need to be conservative in evolutionary computation. For instance, root insertion (the most disruptive operator) alone is capable of finding solutions by creating repetitive patterns (this is one of the patterns observed, but certainly others exist).

5.3.1. Transposition of IS elements

Any sequence in the genome might become an IS element, being therefore these elements randomly selected throughout the chromosome. A copy of the transposon is made and inserted at any position in the head of a gene, except at the start position.

Typically, a transposition rate (p_{is}) of 0.1 and a set of three IS elements of different length are used. The transposition operator randomly chooses the chromosomes, the IS element, the target site, and the length of the transposon. Consider the 2-genic chromosome bellow:

```
012345678901234567890012345678901234567890
*-+*a-+a*bbabbaababQ**+abQbb*aabbaaabba
```

Suppose that the sequence 'bba' in gene 2 (positions 12-14) was chosen to be an IS element, and the target site was bond 6 in gene 1 (between positions 5 and 6). Then, a cut is made in bond 6 and the block 'bba' is copied into the site of insertion, obtaining:

```
012345678901234567890012345678901234567890
*-+*a-bba+babbaababQ**+abQbb*aabbaaabba
```

During transposition, the sequence upstream the insertion site stays unchanged, whereas the sequence downstream the copied IS element loses, at the end of the head, as many symbols as the length of the IS element (in this case the sequence 'a*b' was deleted). Note that, despite this insertion, the structural organisation of chromosomes is maintained, and therefore all newly created individuals are syntactically correct programs. Note also that transposition can drastically reshape the expression tree, and the more upstream the insertion site the more profound the change.

5.3.2. Root transposition

All RIS elements start with a function, and thus are chosen among the sequences of the heads. For that, a point is randomly chosen in the head and the gene is scanned downstream until a function is found. This function becomes the start position of the RIS element. If no functions are found, it does nothing.

Typically a root transposition rate (p_{ris}) of 0.1 and a set of three RIS elements of different sizes are used. This operator randomly chooses the chromosomes, the gene to be modified, the RIS element, and its length. Consider the following 2-genic chromosome:

```
012345678901234567890012345678901234567890
-ba*+-+-Q/abababbbaaaQ*b/+bbabbaaaaaaaabbb
```

Suppose that the sequence '+bb' in gene 2 was chosen to be an RIS element. Then, a copy of the transposon is made into the root of the gene, obtaining:

```
012345678901234567890012345678901234567890
-ba*+-+-Q/abababbbaaa+bbQ*b/+bbaaaaaaaabbb
```

During root transposition, the whole head shifts to accommodate the RIS element, losing, at the same time, the last symbols of the head (as many as the transposon length). As with IS elements, the tail of the gene subjected to transposition and all nearby genes stay unchanged. Note, again, that the newly created programs are syntactically correct because the structural organisation of the chromosome is maintained.

The modifications caused by root transposition are extremely radical, because the root itself is modified. In nature, if a transposable element is inserted at the beginning of the coding sequence of a gene, it will certainly drastically change the corresponding protein, specially if the insertion caused a frameshift mutation. Like mutation and IS transposition, root insertion has a tremendous transforming power and is excellent to create genetic variation. This kind of operators prevent populations from becoming stuck in local optima, finding easily and rapidly good solutions.

5.3.3. Gene transposition

In gene transposition an entire gene functions as a transposon and transposes itself to the beginning of the

chromosome. In contrast to the other forms of transposition, in gene transposition the transposon (the gene) is deleted in the place of origin. This way, the length of the chromosome is maintained.

The chromosome to undergo gene transposition is randomly chosen, and one of its genes (except the first, obviously) is randomly chosen to transpose. Consider the following chromosome composed of 3 genes:

```
012345678012345678012345678
*a-*abbab-QQ/aaabbQ+abababb
```

Suppose gene 2 was chosen to undergo gene transposition. Then the following chromosome is obtained:

```
012345678012345678012345678
-QQ/aaabb*a-*abbabQ+abababb
```

Note that for numerical applications where the function chosen to link the genes is addition, the expression evaluated by the chromosome is not modified. But the situation differs in other applications where the linking function is not commutative, for instance, the IF function chosen to link the sub-ETs in the 11-multiplexer problem (section 6.5.2). However, the transforming power of gene transposition reveals itself when this operator is conjugated with crossover. For example, if two functionally identical chromosomes or two chromosomes with an identical gene in different positions recombine, a new individual with a duplicated gene may appear. It is know that the duplication of genes plays an important role in biology and evolution (for a general reference see [7]). Interestingly, in GEP, individuals with duplicated genes are commonly found in the process of problem solving.

5.4. Recombination

In GEP there are three kinds of recombination: 1-point, 2-point, and gene recombination. In all cases, two parent chromosomes are randomly chosen and paired to exchange some material between them.

5.4.1. One-point recombination

During 1-point recombination, the chromosomes cross over a randomly chosen point to form two daughter chromosomes. Consider the following parent chromosomes:

```
012345678012345678
-b+Qbbabb/aQbbbaab
/-a/ababb-ba-abaaa
```

Suppose bond 3 in gene 1 (between positions 2 and 3) was randomly chosen as the crossover point. Then, the paired chromosomes are cut at this bond, and exchange between them the material downstream the crossover point, forming the offspring below:

```
012345678012345678
-b+/ababb-ba-abaaa
/-aQbbabb/aQbbbaab
```

With this kind of recombination, most of the times, the offspring created exhibits different properties from those of the parents. One-point recombination, like the above mentioned operators, is a very important source of genetic variation, being, after mutation, one of the operators most chosen in GEP. The 1-point recombination rate (p_{1r}) used depends on the rates of other operators. Typically a global crossover rate of 0.7 (the sum of the rates of the three kinds of recombination) is used.

5.4.2. Two-point recombination

In 2-point recombination the chromosomes are paired and the two points of recombination are randomly chosen. The material between the recombination points is afterwards exchanged between the two chromosomes, forming two new daughter chromosomes. Consider the following parent chromosomes:

```
012345678900123456789 0
+*a*bbcccac*baQ*acabab-[1]
*cbb+cccbcc++**bacbaab-[2]
```

Suppose bond 7 in gene 1 (between positions 6 and 7) and bond 3 in gene 2 (between positions 2 and 3) were chosen as the crossover points. Then, the paired chromosomes are cut at these bonds, and exchange the material between the crossover points, forming the offspring below:

```
012345678900123456789 0
+*a*bbccbcc++*Q*acabab-[3]
*cbb+ccccac*ba*bacbaab-[4]
```

Note that the first gene is, in both parents, split downstream the termination point. Indeed, the non-coding regions of GEP chromosomes are ideal regions where chromosomes can be split to cross over without interfering with the ORFs. Note also that the second gene of chromosome 1 was also cut downstream the termination point. However, gene 2 of chromosome 2 was split upstream the termination point, changing profoundly the sub-ET. Note also that when these chromosomes recombined, the non-coding region of chromosome 1 was activated and integrated in chromosome 3.

The transforming power of 2-point recombination is greater than 1-point recombination, and is most useful to evolve solutions for more complex problems, specially when multigenic chromosomes composed of several genes are used.

5.4.3. Gene recombination

In gene recombination an entire gene is exchanged during crossover. The exchanged genes are randomly chosen and occupy the same position in the parent chromosomes. Consider the following parent chromosomes:

```
012345678012345678012345678
/aa-abaaa/a*bbaaab/Q*+aaaab
/-*/abbabQ+aQbabaa-Q/Qbaaba
```

Suppose gene 2 was chosen to be exchanged. In this case the following offspring is formed:

```
012345678012345678012345678
/aa-abaaaQ+aQbabaa/Q*+aaaab
/-*/abbab/a*bbaaab-Q/Qbaaba
```

The newly created individuals contain genes from both parents. Note that with this kind of recombination, similar genes can be exchanged but, most of the times, the exchanged genes are very different and new material is introduced in the population.

It is worth noticing that this operator is unable to create new genes: the individuals created are different arrangements of existing genes. In fact, when gene recombination is used as the unique source of genetic variation, more complex problems can only be solved using very large initial populations in order to provide for the necessary diversity of genes. However, the creative power of GEP is based not only in the shuffling of genes or building blocks, but also in the constant creation of new genetic material.

6. Gene expression programming in problem solving: six examples

The suite of problems chosen to illustrate the functioning of this new algorithm is quite varied, including not only problems from different fields (symbolic regression, planning, Boolean concept learning, and cellular automata rules) but also problems of great complexity (cellular automata rules for the density-classification task).

Problems with the kind of complexity exhibited by symbolic regression, sequence induction, block stacking, or the 11-multiplexer, are frequently used when comparisons are made between different evolutionary algorithms [8]. The comparisons are usually made in terms of likelihood of success and in terms of the average number of fitness-function evaluations needed to find a correct solution. Despite the differences between GEP and GP, the performance of these techniques can be easily compared because identical problems can be similarly implemented due to the phenotypic tree representation.

Comparisons are made on five problems and, whenever possible, the performance of GEP and GP is compared in terms of the average number of fitness-functions evaluations (F_z) needed to find a correct program with a certain probability (z). F_z is evaluated by the equation:

$$F_z = G \cdot P \cdot C \cdot R_z \qquad (6.1)$$

where G is the number of generations; P the population size; C the number of fitness cases; and R_z the number of independent runs required to find a correct solution by generation G with $z = 0.99$. R_z is evaluated by the formula:

$$R_z = \frac{\log(1-z)}{\log(1-P_s)}, \text{ and } P_s \neq 1 \qquad (6.2)$$

where P_s is the probability of success; if $P_s = 1$, then $R_z = 1$.

6.1. Symbolic regression

The objective of this problem is the discovery of a symbolic expression that satisfies a set of fitness cases. Consider we are given a sampling of the numerical values from the function

$$y = a^4 + a^3 + a^2 + a \qquad (6.3)$$

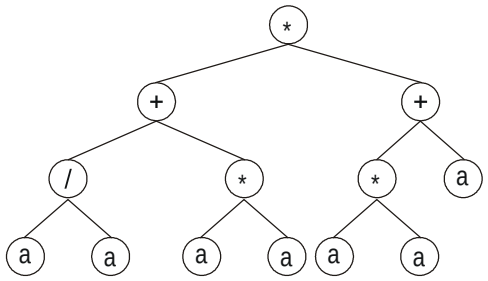
over ten chosen points and we wanted to find a function fitting those values within 0.01 of the correct value.

First, the set of functions F and the set of terminals T must be chosen. In this case F = {+, -, *, /} and T = {a}. Then the structural organisation of chromosomes, namely the length of the head and the number of genes, is chosen. It is advisable to start with short, single-gene chromosomes and then gradually increase h. Figure 6 shows such an analysis for this problem. A p_m equivalent to two point mutations per chromosome and a $p_{1r} = 0.7$ were used in all the experiments in order to simplify the analysis. The set of fitness cases C is shown in Table 1 and the fitness was evaluated by equation 4.1, being $M = 100$. If E equal or less than 0.01, then $E = 0$ and $f = 100$; thus for $C = 10$, $f_{max} = 1000$.

Note that GEP can be useful in searching the most parsimonious solution to a problem. For instance, the chromosome

```
0123456789012
*++/**aaaaaaa
```

with $h = 6$ codes for the ET:



which is equivalent to the target function. Note also that GEP can efficiently evolve solutions using large values of h, i.e. is capable of evolving large and complex sub-ETs. As shown in Figure 6, for each problem there is an optimal chromosome length to efficiently evolve solutions. It is worth noticing that the most compact genomes are not the most efficient. Therefore a certain redundancy is fundamental to efficiently evolve good programs.

In another analysis, the relationship between success rate and P, using an $h = 24$ was studied (Figure 7). These results show the supremacy of a genotype/phenotype representation, as this single-gene system which is equivalent to GP, greatly surpasses that technique [6]. However, GEP is much more complex than a single-gene system because

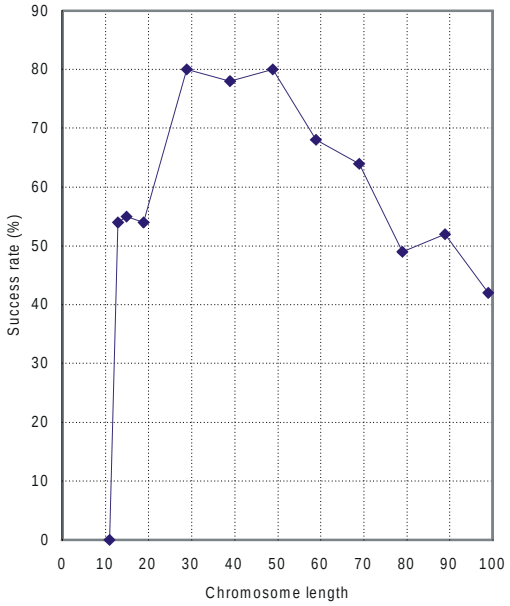


Figure 6. Variation of success rate (P_s) with chromosome length. For this analysis $G = 50$, $P = 30$, and P_s was evaluated over 100 identical runs.

GEP chromosomes can encode more than one gene.

Suppose we could not find a solution after the analysis of Figure 7. Then we could increase the number of genes, and choose a function to link them. For instance, we could choose an $h = 6$ and then increase the number of genes gradually. Figure 8 shows how the success rate for this problem depends on the number of genes. In this analysis, the p_m was equivalent to two point mutations per chromosome, $p_{1r} = 0.2$, $p_{2r} = 0.5$, $p_{gr} = 0.1$, $p_{is} = 0.1$, $p_{ris} = 0.1$, $p_{gt} = 0.1$, and three transposons (both IS and RIS elements) of lengths 1, 2 and 3 were used. Note that GEP can cope very well with an excess of genes: the success rate for the 10-genic system is still very high (47%).

In Figure 9 another important relationship is shown: how the success rate depends on evolutionary time (G). In contrast to GP where 51 generations are the norm, for after that nothing much can possibly be discovered [4], in GEP, populations can adapt and evolve indefinitely because new material is constantly being introduced in the genetic pool.

Finally, suppose that the multigenic system with sub-ETs linked by addition could not evolve a satisfactory solution. Then we could choose another linking function, for instance multiplication. This process is repeated until a good solution has been found.

Table 1.
Set of fitness cases for the symbolic regression problem.

a	f(a)
2.81	952.425
6	1554
7.043	2866.55
8	4680
10	11110
11.38	18386
12	22620
14	41370
15	54240
20	168420

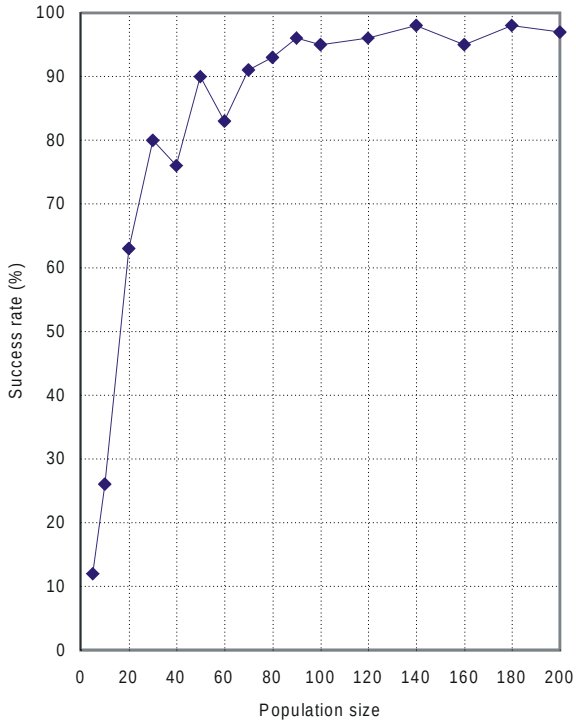


Figure 7. Variation of success rate (P_s) with population size (P). For this analysis $G = 50$, and a medium value of $h = 24$ was used. P_s was evaluated over 100 identical runs.

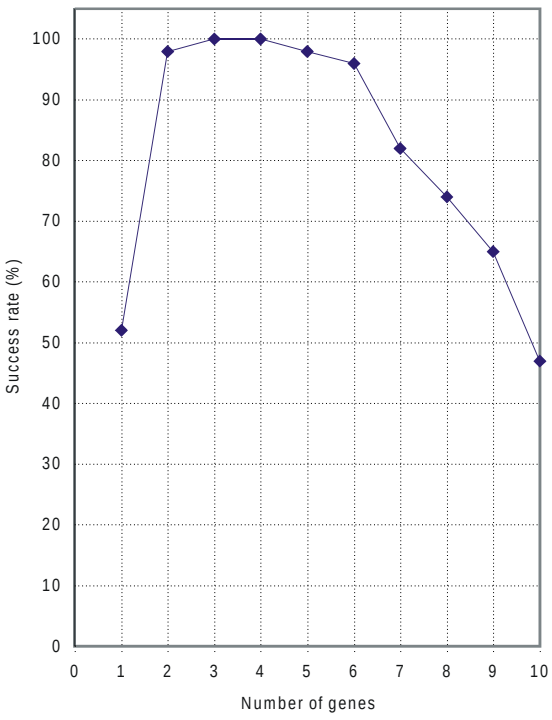


Figure 8. Variation of success rate (P_s) with the number of genes. For this analysis $G = 50$, $P = 30$ and $h = 6$. P_s was evaluated over 100 identical runs.

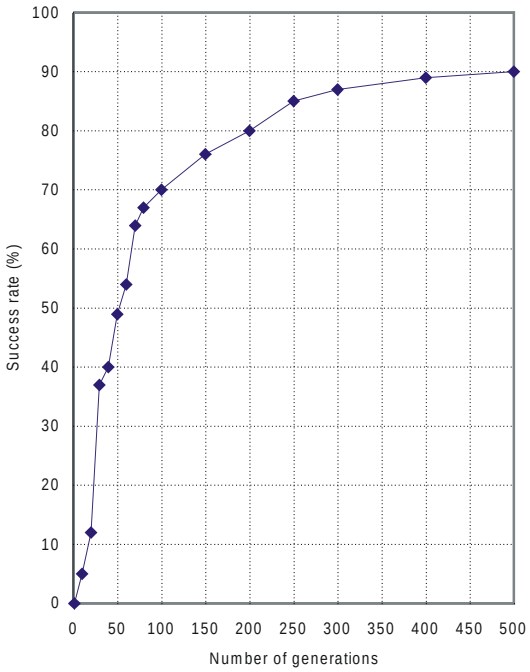


Figure 9. Variation of success rate (P_s) with the number of generations (G). For this analysis $P = 30$ and a medium value of $h = 39$ was used. P_s was evaluated over 100 identical runs.

As I have said, GEP chromosomes can be easily modified in order to encode the linking function as well. In this case, for each problem the ideal linking function would be found in the process of adaptation.

Consider for instance a multigenic system composed of 3 genes linked by addition. As shown in Figure 8, the success rate has in this case the maximum value of 100%. Figure 10 shows the progression of average fitness of the population and the fitness of the best individual for run 0 of the experiment summarised in Table 2, column 1. In this run, a correct solution was found in generation 11 (the sub-ETs are linked by addition):

```
012345678901201234567890120123456789012
**-*a+aaaaaaa++**a*aaaaaaa*+-a/aaaaaaaa
```

Mathematically it corresponds to the target function (the contribution of each sub-ET is indicated in brackets):

$$y = (a^4) + (a^3 + a^2 + a) + (0) = a^4 + a^3 + a^2 + a$$

The detailed analysis of this program shows that some of the actions are redundant for the problem at hand, like the addition of zero or multiplication by 1. However, the existence of these unnecessary clusters or even pseudogenes like gene 3 is important to the evolution of

Table 2.
Parameters for the symbolic regression (SR), sequence induction (SI), block stacking (BS), and 11-multiplexer (11-M) problems.

	SR	SI	BS	11-M
Number of runs	100	100	100	100
Number of generations	50	100	100	400
Population size	30	50	30	250
Number of fitness cases	10	10	10	160
Head length	6	6	4	1
Number of genes	3	7	3	27
Chromosome length	39	91	27	27
Mutation rate	0.051	0.022	0.074	0.074
1-Point recombination rate	0.2	0.7	0.1	0.7
2-Point recombination rate	0.5	0.1	--	--
Gene recombination rate	0.1	0.1	0.7	--
IS transposition rate	0,1	0,1	0,1	--
IS elements length	1,2,3	1,2,3	1	--
RIS transposition rate	0.1	0.1	0.1	--
RIS elements length	1,2,3	1,2,3	1	--
Gene transposition rate	0.1	0.1	--	--
Selection range	100	100	--	--
Absolute error	0.01	0.0	--	--
Success rate	1	0.79	0.7	0.57

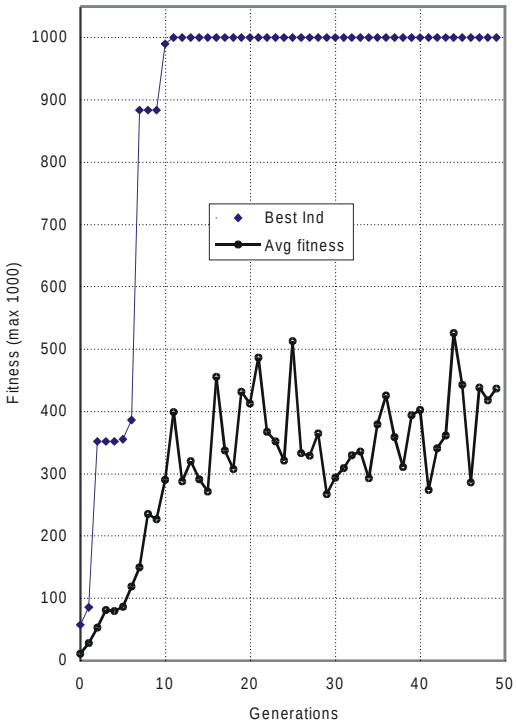


Figure 10. Progression of average fitness of the population and the fitness of the best individual for run 0 of the experiment summarised in Table 2, column 1.

more fit individuals (compare, in Figures 6 and 8, the success rate of a compact, single-genic system with $h = 6$ with other less compact systems).

The comparison of F_z values obtained by GEP and GP [6] for this problem (Table 3, column 1) shows that GEP surpasses GP in 374 times, more than two orders of magnitude.

6.2. Sequence induction

The problem of sequence induction is a special case of symbolic regression where the domain of the independent variable consists of the non-negative integers. However, the sequence chosen is more complicated than the expression used in symbolic regression, as different coefficients were used.

In the sequence 1, 15, 129, 547, 1593, 3711, 7465, 13539, 22737, 35983, 54321,..., the n^{th} (N) term is

$$N = 5a_n^4 + 4a_n^3 + 3a_n^2 + 2a_n + 1 \qquad (6.4)$$

where a_n consists of the non-negative integers 0, 1, 2, 3,....

For this problem F = {+, -, *, /} and T = {a}. The set of fitness cases C is shown in Table 4 and the fitness was evaluated by equation 4.1, being $M = 100$. Thus, if the 10 fitness cases were computed exactly, $f_{max} = 1000$.

Figure 11 shows the progression of average fitness of the population and the fitness of the best individual for run 0 of the experiment summarised in Table 2, column 2. In this run, a perfect solution was found in generation 24 (the sub-ETs are linked by addition):

```
0123456789001012345678900101234567890010123456789001...
**++–aaaaaaa*+/+a*aaaaaaa*+*+*+aaaaaaa*-***+aaaaaaa...

...012345678900101234567890010123456789001
...*a/+a-aaaaaaa-+-/**aaaaaaa**+a*+aaaaaaa
```

Mathematically it corresponds to the target sequence (the contribution of each sub-ET is indicated in brackets):

$$y = (0) + (3a^2) + (2a^4 + 4a^3) + (0) + (a) + (1 + a) + (3a^4)$$

As shown in column 2 of Table 2, the probability of success for this problem is 0.79. The comparison of F_z values obtained by GEP and GP for this problem [6] (Table 3, column 2) shows that GEP surpasses GP in 98.6 times. It should be emphasised, though, that GEP not only is capable of solving this kind of problems much more efficiently than GP, but does so without using the *ephemeral random constant R*, which consists of a set of chosen numbers (terminals) that greatly hinders the usefulness of the technique. For instance, for this sequence the R chosen ranged over the integers 0, 1, 2, and 3 [6]. The advantages of GEP are obvious because, first, in real life applications we never know beforehand what kind of constants are needed and, second, the number of elements in the terminal set is much smaller, reducing the complexity of the problem.

Table 3.
Comparison of GEP with GP in symbolic regression, sequence induction, and block stacking problems.

	Symbolic regression		Sequence induction		Block stacking	
	GEP	GP [6]	GEP	GP [6]	GEP	GP [8]
G	50	51	100	51	100	51
P	30	500	50	500	30	500
C	10	20	10	20	10	167
Ps	1	0.35	0.79	0.15	0.7	0.767
Rz	1	11	3	29	4	4
Fz	15,000	5,610,000	150,000	14,790,000	120,000	17,034,000

Table 4.
Set of fitness cases for the sequence induction problem.

a	N
1	15
2	129
3	547
4	1593
5	3711
6	7465
7	13539
8	22737
9	35983
10	54321

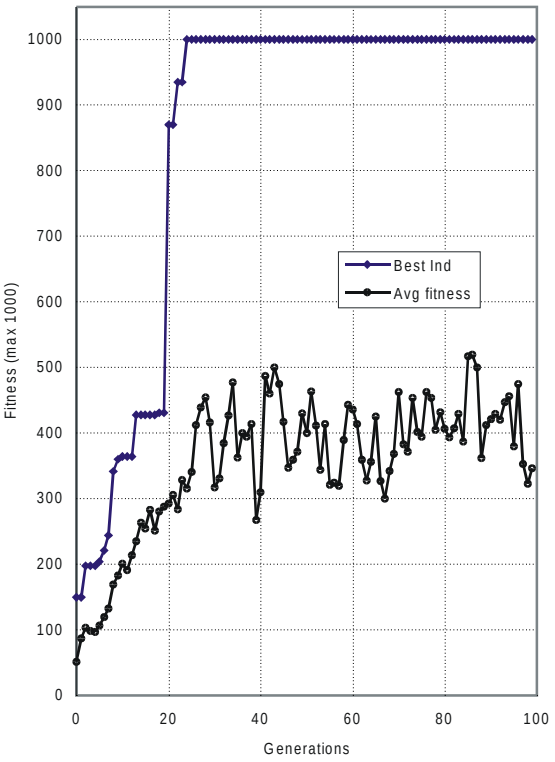


Figure 11. Progression of average fitness of the population and the fitness of the best individual for run 0 of the experiment summarised in Table 2, column 2.

6.3. Block stacking

In block stacking, the goal is to find a plan that takes any initial configuration of blocks randomly distributed between the stack and the table and place them in the stack in the correct order. In this case, the blocks are the letters of the word "universal". (Although the word "universal" was used as illustration, in this version the blocks being stacked may have identical labels like, for instance, in the word "individual".)

The functions and terminals used for this problem consisted of a set of actions and sensors, being F = {C, R, N, A} (*move to stack*, *remove from stack*, *not*, and *do until true*, respectively), where the first three take one argument and 'A' takes two arguments. In this version, the 'A' loops are processed at the beginning, are solved in a particular order (from bottom to top and from left to right), the action argument is executed at least once despite the state of the predicate argument and each loop is executed only once, timing out after 20 iterations. The set of terminals consisted of 3 sensors {u, t, p} (*current stack*, *top correct block*, and *next needed block*, respectively). In this version, 't' refers only to the block on the top of the stack and whether it is correct or not; if the stack is empty or has some blocks, all of them correctly stacked, the sensor returns *True*, otherwise returns *False*; and 'p' refers obviously to the next needed block immediately after 't'.

A multigenic system composed of 3 genes of length 9 was used in this problem. The linking of the sub-ETs consisted of the sequential execution of each sub-ET or sub-plan. For instance, if the first sub-ET empties all the stacks, the next sub-ET may proceed to fill them, etc. The fitness was determined against 10 fitness cases (initial configurations of blocks). For each generation, an empty stack plus nine initial configurations with one to nine letters in the stack were randomly generated. The empty stack was used to prevent the untimely termination of runs, as a fitness point was attributed to each empty stack (see below). However, GEP is capable of efficiently solving this problem using uniquely 10 random initial configurations (results not shown).

The fitness function was as follows: for each empty stack one fitness point was attributed, for each partially and correctly packed stack (i.e., with 1 to 8 letters in the case of the word "universal") two fitness points were attributed, and for each completely and correctly stacked word 3 fitness points were attributed. Thus, the maximum fitness was 30. The idea was to make the population of programs hierarchically evolve solutions toward a perfect plan. And, in fact, usually the first useful plan discovered empties all the stacks, then some programs learn how to partially fill those empty stacks, and finally a perfect plan is discovered that fills the stacks completely and correctly (see Figure 12).

Figure 12 shows the progression of average fitness of the population and the fitness of the best individual for run 2 of the experiment summarised in Table 2, column 3. In this run, a perfect plan was found in generation 50:

```
012345678012345678012345678
ARCuptppuApNCptuutNtpRppptp
```

Note that the first sub-plan removes all the blocks and stacks a correct letter; the second sub-plan correctly stacks all the remaining letters; and the last sub-plan does nothing. It should be emphasised that the plans with maximum fitness evolved are in fact perfect, universal plans: each generation they are tested against 9 randomly generated initial configurations, more than sufficient to allow the algorithm to generalise the problem (as shown in Figure 12, once reached, the maximum fitness is maintained). Indeed, with the fitness function and the kind of fitness cases used, all plans with maximum fitness are universal plans.

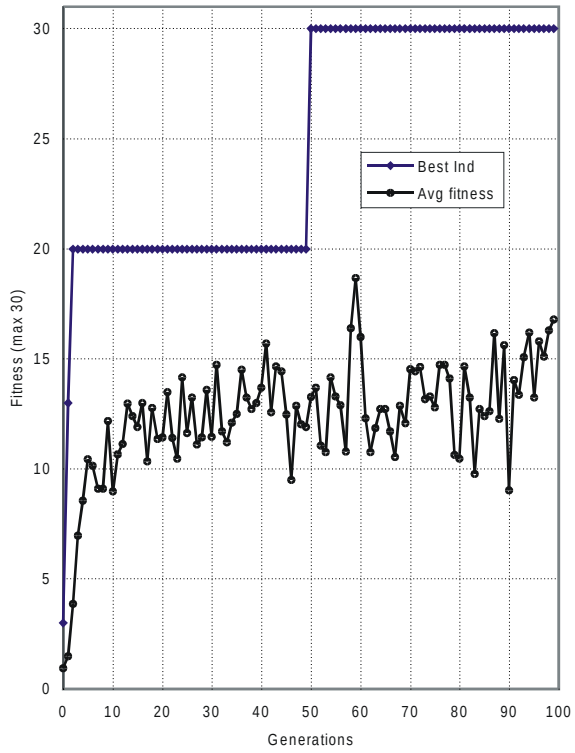


Figure 12. Progression of average fitness of the population and the fitness of the best individual for run 2 of the experiment summarised in Table 2, column 3.

As shown in the third column of Table 2, the probability of success for this problem is 0.70. The comparison of F_z values obtained by GEP and GP for this problem (Table 3, column 3) shows that GEP surpasses GP in 142 times, more than two orders of magnitude. It is worth noticing that GP uses 167 fitness cases, cleverly constructed to cover the various classes of possible initial configurations, whereas GEP uses 9 (out of 10) random initial configurations. Indeed, in real life applications not always is possible to predict the kind of cases that would make the system discover a solution. So, algorithms capable of generalising well in face of random fitness cases are more advantageous.

6.4. Evolving cellular automata rules for the density - classification problem

Cellular automata (CA) have been studied widely as they are idealized versions of massively parallel, decentralized computing systems capable of emergent behaviors. These complex behaviors result from the simultaneous execution of simple rules at multiple local sites. In the density-classification task, a simple rule involving a small neighborhood and operating simultaneously in all the cells of a one-dimensional cellular automaton, should be capable of making the CA converge into a state of all 1's if the initial configuration (IC) has a higher density of 1's, or into a state of all 0's if the IC has a higher density of 0's.

The ability of GAs to evolve CA rules for the density-classification problem was intensively investigated [9, 10, 11, 12], but the rules discovered by the GA performed poorly and were far from approaching the accuracy of the GKL rule, a human-written rule. GP was also used to evolve rules for the density-classification task [13], and a rule was discovered that surpassed the GKL rule and other human-written rules.

In this section is shown how GEP was successfully applied to this difficult problem. The rules evolved by GEP have accuracy levels of 82.513% and 82.55%, thus exceed all human-written rules and the rule evolved by GP.

6.4.1. The density-classification task

The simplest CA is a wrap-around array of N binary-state cells, where each cell is connected to r neighbors from both sides. The state of each cell is updated by a defined rule. The rule is applied simultaneously in all the cells, and the process is iterated for t time steps.

In the most frequently studied version of this problem, $N = 149$ and the neighborhood is 7 (the central cell is represented by 'u'; the $r = 3$ cells to the left are represented by 'c', 'b', and 'a'; the $r = 3$ cells to the right are represented by '1', '2', and '3'). Thus the size of the rule space to search for this problem is the huge number of 2^{128}. Figure 13 shows a CA with $N = 11$ and the updated state for the cellular automaton 'u' upon application of a certain transition rule.

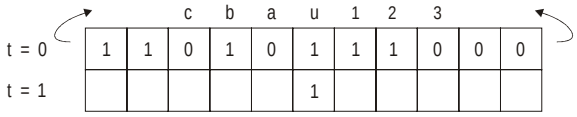


Figure 13. A one-dimensional, binary-state, $r = 3$ cellular automaton with $N = 11$. The arrows represent the periodic boundary conditions. The updated state is shown only for the central cell. The symbols used to represent the neighborhood are also shown.

The task of density-classification consists of correctly determining whether ICs contain a majority of 1's or a majority of 0's, by making the system converge, respectively, to an all 1's state (black or 'on' cells in a space-time diagram), and to a state of all 0's (white or 'off' cells). Being the density of an IC a function of N arguments, the actions of local cells with limited information and communication must be co-ordinated with one another to correctly classify the ICs. Indeed, to find rules that perform well is a challenge, and several algorithms were used to evolve better rules [10, 12, 13, 14]. The best rules with performances of 86.0% (coevolution 2) and 85.1% (coevolution 1) were discovered using a coevolutionary approach between GA evolved rules and ICs [14]. However, the aim of this section is to compare the performance of GEP with the other genetic algorithms (GAs and GP) when applied to a difficult problem. And, in fact, GEP could evolve better rules than the GP rule, using computational resources that are more than four orders of magnitude smaller than those used by GP.

6.4.2. Two GEP discovered rules

In one experiment F = {A, O, N, I} ('A' represents the Boolean function AND, 'O' represents OR, 'N' represents NOT, and 'I' stands for IF) and T = {c, b, a, u, 1, 2, 3}. The parameters used per run are shown in Table 5, column 1. The fitness was evaluated against a set of 25 unbiased ICs (fitness cases). In this case, the fitness is a function of the number of ICs *i* for which the system stabilises correctly to a configuration of all 0's or 1's after 2x*N* time steps, and it was designed in order to privilege individuals capable of correctly classifying ICs both with a majority of 1's and 0's. Thus, if the system converged, in all cases, indiscriminately to a configuration of 1's or 0's, only one fitness point was attributed; if, in some cases, the system correctly converged either to a configuration of 0's or 1's, $f = 2$; in addition, rules converging to an alternated pattern of all 1's and all 0's configurations were eliminated, as they are easily discovered and invade the populations impeding the discovery of good rules; and finally, when an individual program could correctly classify ICs both with majorities of 1's and 0's, a bonus equal to the number of ICs, *C*, was added to the number of correctly classified ICs, being in this case $f = i + C$. For instance, if a program correctly classified two ICs, one with a majority of 1's and another with a majority of 0's, it receives 2+25=27 fitness points.

In this experiment a total of 7 runs were made. In generation 27 of run 5, an individual evolved with fitness 44:

```
012345678901234567890123456789012345678901234567890123456789012345678901
0AIIAucONObAbIANIb1u23u3a12aacb3bc21aa2baabc3bccuc13
```

Note that the ORF ends at position 28. This program has an accuracy of 0.82513 tested over 100,000 unbiased ICs in a 149x298 lattice, thus better than the 0.824 of the GP rule tested in a 149x320 lattice [14, 13]. The rule table of this rule (GEP_1 rule) is shown in Table 6. Figure 14 shows three space-time diagrams for this new rule.

As a comparison, the GP technique used populations of 51,200 individuals and 1000 ICs for 51 generations [13], thus a total of 51,200 x 1000 x 51 = 2,611,200,000 fitness evaluations were made, whereas GEP only made 30 x 25 x 50 = 37,500 fitness evaluations. Therefore GEP outperforms GP in more than 4 orders of magnitude (69,632 times). And as John Holland said in his book *Emergence: from chaos to order*, "In the sciences, three orders of magnitude is enough to call for a new science." Indeed, in nature, the creation of an indivisible whole, consisting of a genotype and a phenotype, originated life.

Table 5.
Parameters for the density-classification task.

	GEP_1	GEP_2
Number of generations	50	50
Population size	30	50
Number of ICs	25	100
Head length	17	4
Number of genes	1	3
Chromosome length	52	39
Mutation rate	0.038	0.051
1-Point recombination rate	0.5	0.7
IS transposition rate	0.2	--
IS elements length	1,2,3	--
RIS transposition rate	0.1	--
RIS elements length	1,2,3	--

In another experiment a rule slightly better than GEP_1, with an accuracy of 0.8255, was obtained. Again, its performance was determined over 100,000 unbiased ICs in a 149x298 lattice. In this case F = {I, M} ('I' stands for IF, and 'M' represents the majority function with 3 arguments), and T was obviously the same. In this case, a total of 100 unbiased ICs and three-genic chromosomes with sub-ETs linked by the Boolean function IF were used. The parameters used per run are shown in the second column of Table 5.

The fitness function was slightly modified by introducing a ranking system, where individuals capable of correctly classifying between [2; 3/4 *C*] of the ICs received one bonus equal to *C*; if correctly classified between]3/4 *C*; 17/20 *C*] ICs received 2 bonus; and if correctly classified more than 17/20 *C* ICs received 3 bonus. Also, in this experiment, individuals capable of correctly classifying only one kind of situation, although not indiscriminately, were differentiated and had a fitness of *i*.

Table 6.
Description of the two new rules (GEP_1 and GEP_2) discovered using gene expression programming for the density-classification problem. The GP rule is also shown. The output bits are given in lexicographic order starting with 0000000 and finishing with 1111111.

GEP_1	00010001	00000000	01010101	00000000	00010001	00001111	01010101	00001111
	00010001	11111111	01010101	11111111	00010001	11111111	01010101	11111111
GEP_2	00000000	01010101	00000000	01110111	00000000	01010101	00000000	01110111
	00001111	01010101	00001111	01110111	11111111	01010101	11111111	01110111
GP rule	00000101	00000000	01010101	00000101	00000101	00000000	01010101	00000101
	01010101	11111111	01010101	11111111	01010101	11111111	01010101	11111111

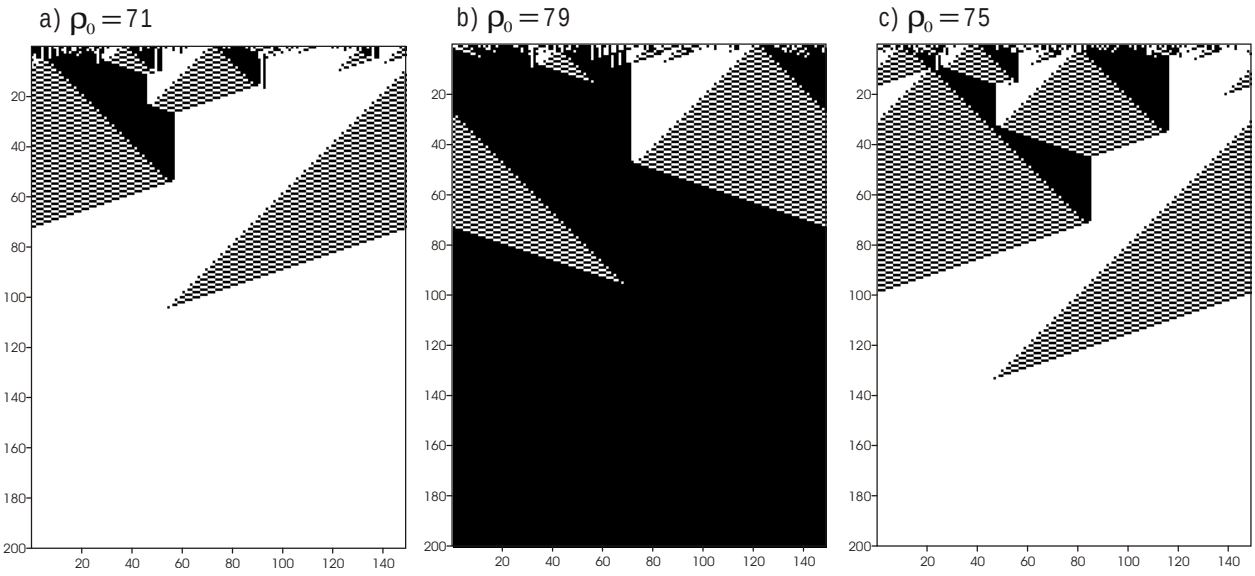


Figure 14. Three space-time diagrams describing the evolution of CA states for the GEP_1 rule. The number of 1's in the IC (ρ_0) is shown above each diagram. In **a)** and **b)** the CA correctly converged to a uniform pattern; in **c)** it converged wrongly to a uniform pattern.

By generation 43 of run 10, an individual evolved with fitness 393:

```
012345678901201234567890120123456789012
MIuua1113b21cMIM3au3b2233bM1MIacc1cb1aa
```

Its rule table is shown in Table 6. Figure 15 shows three space-time diagrams for this new rule (GEP_2). Again, in this case the comparison with GP shows that GEP outperforms GP in 10,444 times.

6.5. Boolean concept learning

The GP rule and the 11-multiplexer are, respectively, Boolean functions of seven and 11 activities. Whereas the solution for the 11-multiplexer is a well known Boolean function, the solution of the GP rule is practically unknown, as the program evolved by GP [13] is so complicated that it is impossible to know what the program really does.

In this section is shown how GEP can be efficiently applied to evolve Boolean expressions of several arguments. Furthermore, the structural organisation of the chromosomes used to evolve solutions for the 11-multiplexer is an example of a very simple organisation that can be used to efficiently solve certain problems. For example, this organisation (one-element genes linked by IF) was successfully used to evolve CA rules for the density-classification problem, discovering better rules than the GKL rule (results not shown).

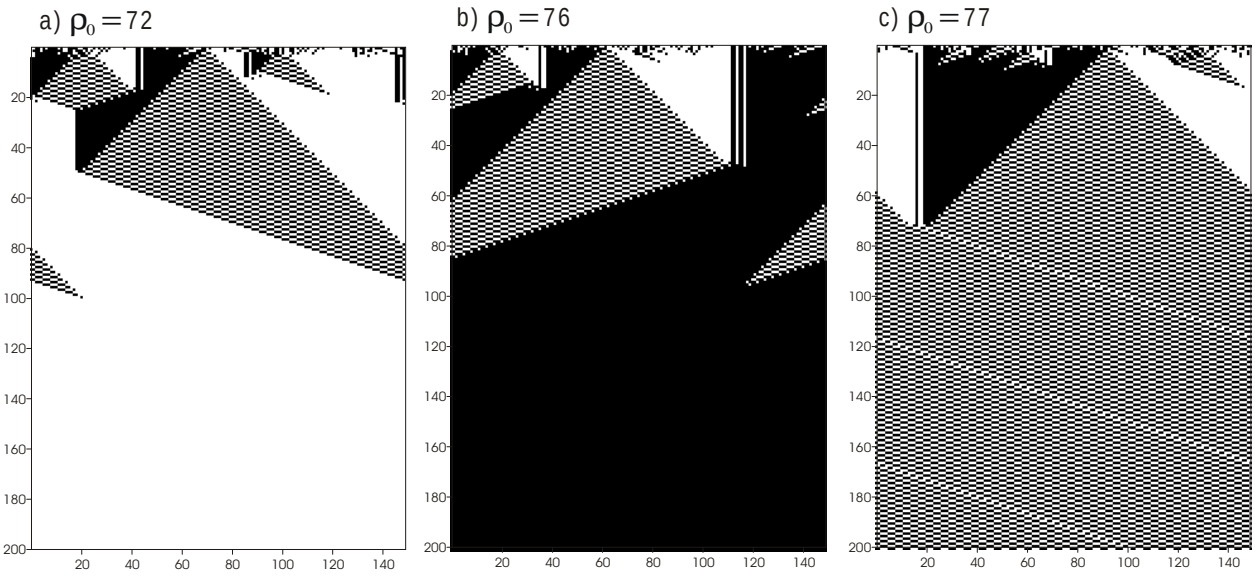


Figure 15. Three space-time diagrams describing the evolution of CA states for the GEP_2 rule. The number of 1's in the IC (ρ_0) is shown above each diagram. In **a)** and **b)** the CA converges, respectively, to the correct configuration of all 0's and all 1's; in **c)** the CA could not converge to a uniform pattern.

6.5.1. The GP rule problem

For this problem F = { N, A, O, X, D, R, I, M} (representing, respectively: NOT, AND, OR, XOR, NAND, NOR, IF, and Majority, being the first a function of one argument, the second through fifth are functions of two arguments, and the last two are functions of three arguments), and T = {c, b, a, u, 1, 2, 3}. The rule table (2^7=128 fitness cases) is shown in Table 6 and the fitness was evaluated by equation 4.2. Thus, f_{max} = 128.

Three different solutions were discovered in one experiment:

```
MA3OOAMOAuOMRa1cc3cubcc2cu11ba2aacb331ua122uu1
X3RRMIMODIAIAAI3cauuc313bub2uc33ca12u233c22bcb
MMOIOcXOMa3AXAu3cc112ucbb3331uac3cu3auubuu2ab1
```

The careful analysis of these programs shows that the GP rule is, like the GKL rule, a function of five arguments: c, a, u, 1, and 3.

6.5.2. The 11-multiplexer problem

The task of the 11-bit Boolean multiplexer is to decode a 3 binary address (000, 001, 010, 011, 100, 101, 110, 111) and return the value of the correspondent data register (d_0, d_1, d_2, d_3, d_4, d_5, d_6, d_7). Thus, the Boolean 11-multiplexer is a function of 11 arguments: three, a_0 to a_2, determine the address, and eight, d_0 to d_7, determine the answer. As GEP uses single character chromosomes, T = {a, b, c, 1, 2, 3, 4, 5, 6, 7, 8} which correspond, respectively, to {a_0, a_1, a_2, d_0, d_1, d_2, d_3, d_4, d_5, d_6, d_7}.

There are 2^{11} = 2048 possible combinations for the 11 arguments of the Boolean 11-multiplexer function. For this problem a random sampling of the 2048 combinations was used as the fitness cases for evaluating fitness. The fitness cases were assembled by address, and for each address a sub-set of 20 random combinations was used each generation. Therefore, a total of 160 random fitness cases were used each generation as the adaptation environment. In this case, the fitness of a program is the number of fitness cases for which the Boolean value returned is correct, plus a bonus of 180 fitness points for each sub-set of combinations solved correctly as a whole. Therefore, a total of 200 fitness points was attributed for each correctly decoded address, being the maximum fitness 1600. The idea was to make the algorithm decode one address at a time. And, in fact, the individuals learn to decode first one address, then another, until the last one (see Figure 16).

To solve this problem, multigenic chromosomes composed of 27 genes were used, each gene consisting only of one terminal. Thus, no functions were used to generate the chromosomes, although the sub-ETs were posttranslationally linked by IF.

The parameters used per run are shown in column 4 of Table 2. The first correct solution in this experiment was found in generation 390 of run 1 (the characters are linked 3 by 3, forming an ET with depth 4, composed of 40 nodes, being the first 14 nodes IFs, and the remaining nodes, the chromosome characters; see K-expression 3.12 and Figure 5):

```
3652bb5bbba4c87c43bcca62a51
```

which is a universal solution for the 11-multiplexer. Figure 16 shows the progression of average fitness of the population and the fitness of the best individual for run 1 of the experiment summarised in Table 2, column 4.

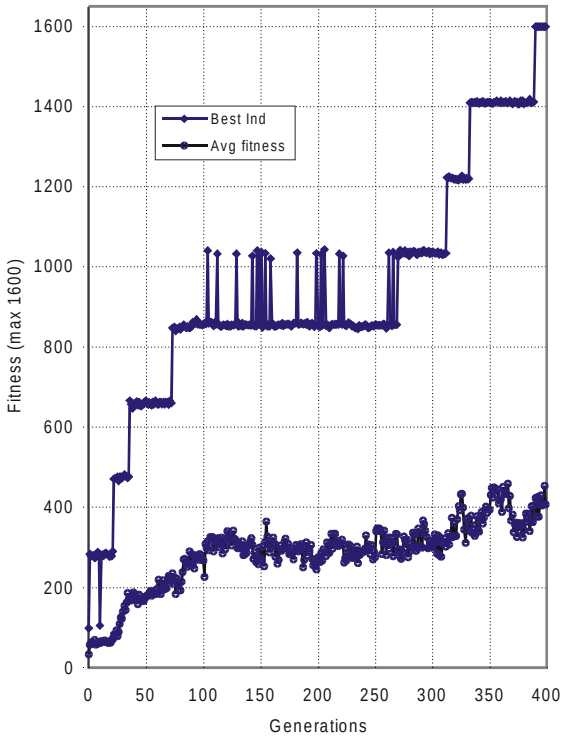


Figure 16. Progression of average fitness of the population and the fitness of the best individual for run 1 of the experiment summarised in Table 2, column 4.

As shown in the fourth column of Table 2, GEP solves the 11-multiplexer with a success rate of 0.57. It's worth noticing that GP could not solve the 11-multiplexer with a population size 500 for 51 generations [8], and could only solve it using 4,000 individuals [6].

7. Conclusions

The details of implementation of GEP were thoroughly explained allowing other researchers to implement this new algorithm. Furthermore, the problems chosen to illustrate the functioning of GEP show that the new paradigm can be used to solve several problems from different fields with the advantage of running efficiently in a personal computer. The new concept behind the linear chromosomes and the ETs enabled GEP to considerably outperform GP: more than two orders of magnitude in symbolic regression, sequence induction, and block stacking, and more than four orders of magnitude in the density-classification problem. Therefore, GEP offers new possibilities to solve more com-

plex technological and scientific problems. Also important and original is the multigenic organisation of GEP chromosomes, which makes GEP a truly hierarchical discovery technique. And finally, GEP algorithms represent nature more faithfully, therefore can be used as computer models of natural evolutionary processes.

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