A Scalable Cellular Implementation of Parallel Genetic Programming

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Abstract

A new parallel implementation of genetic programming based on the cellular model is presented and compared with both canonical genetic programming and the island model approach. The method adopts a load balancing policy that avoids the unequal utilization of the processors. Experimental results on benchmark problems of different complexity show the superiority of the cellular approach with respect to the canonical sequential implementation and the island model. A theoretical performance analysis reveals the high scalability of the implementation realized and allows to predict the size of the population when the number of processors and their efficiency are fixed.

Keywords: genetic programming, parallel processing, cellular GP model, load

balance, scalability.

1 Introduction

Genetic programming (*GP*) [22, 23, 25] is an extension of genetic algorithms (*GAs*)(and more broadly evolutionary algorithms) that induces computer programs, usually represented as trees. A genetic program system evolves iteratively a population of trees, having variable size, by applying variation operators. Each individual encodes a candidate solution and is associated with a fitness value that measures the goodness-of-fit of that solution. The capability of genetic programming in solving challenging problems, coming from different application domains, has been largely recognized. Many problems have been solved by means of *GP*. For difficult problems, however, in order to find a good solution, GP may require large number of generations by using a population of sufficient size. The choice of population size is determined by the complexity of the problem. It is well known that the evaluating fitness is the dominant time consuming task for *GP* and evolutionary algorithms in general. The necessity of high computational resources, both in terms of memory, to store big populations of trees, and in terms of time, to evaluate the fitness of the individuals in the population, may degrade *GP* performance drastically when applied to large difficult problems. There has been recent increasing interest in realizing high-performance *GP* implementations to extend the number of problems that *GP* can cope with. To this end, different approaches to parallelize *GP* have been studied and proposed [6, 8, 10, 19, 20, 28, 30, 34]. An extensive survey on the subject can be found in [37]. Differently from parallel genetic algorithms [2, 3], for which it has been found experimentally that their behavior is generally better than their sequential counterpart, parallel *GP* implementations produce controversial outcomes [32].

This paper presents a parallel GP implementation, called $CAGE$ (*CellulAr GEnetic programming*), on distributed-memory parallel computers based on the fine-grained cellular model. Preliminary results of the implementation were presented in [12]. $CAGE$ is endowed with a load balancing mechanism that distributes the computational load among the processors equally. Experiments on classical test problems show that the cellular model outperforms both the sequential canonical implementation of GP and the parallel $island$ model. A theoretical study of the performances, based on the $isoefficiency$ function, reveals the high scalability of the system and allows predicting the size of the problem when the number of processors and a given efficiency (the percentage of utilization of processors) are fixed. The main novelties are the following:

- $CAGE$ is the first parallel implementation of GP through the cellular model;
- the cellular implementation yields the same results of parallel genetic algorithms [2, 37], that is, the multi-population case generally needs fewer evaluations to get the same solution quality as a single-population case with the same total number of individuals;
- the very good performances of $CAGE$ run counter to the widespread belief that parallel GP is not suitable for cellular models [37] because of the varying size and complexity of the individuals that makes cellular implementations of GP difficult both in terms of memory and efficiency.

The paper is organized as follows. Section 2 proposes the main parallel models. Section 3 provides an overview of the parallel implementations. Section 4 presents the cellular parallel implementation of GP. Section 5 evaluates the scalability of $CAGE$ by using the isoefficiency function. Section 6 presents the results of the method on some well-known benchmark problems and validates the theoretical performance analysis on two of those problems. Furthermore, the benefits of the proposed load balancing technique are showed. Finally, Section 7 presents a comparison between our cellular model method and some island model implementations of GP.

2 Parallel Genetic Programming

GP belongs to the class of evolutionary algorithms and, as such, shares the same parallelization features of evolutionary techniques. A classification of the approaches for parallelizing GP includes three main models [2, 37]: the *global* model, the *coarse-grained* (*island*) model [26], and the *fine-grained* (*grid*) model [31].

In the global model, the fitness of each individual is evaluated in parallel on different processors. A *master* process manages the population by assigning a subset of individuals to a number of *slave* processes. During the evaluation there is no communication among the processors. At the end of the evaluation the master collects the results and applies the variation operators to generate the new population. This model is easy to implement but a main problem, as observed in [37], can be a load imbalance, which decreases in the utilization of the processors due to presence in the population of trees of different sizes.

The island model divides a population $\mathcal{P}$ of M individuals into N subpopulations D_1, $\ldots, D_N$, called *demes*, of M/N individuals. A standard GP algorithm works on each deme and is responsible for initializing, evaluating, and evolving its own subpopulation. Subpopulations are interconnected according to different *communication topologies* and can exchange information periodically by *migrating* individuals from one subpopulation to another. The number of individuals to migrate (*migration rate*), the number of generations after which migration should occur (*frequency*), the migration topology, and the number of subpopulations are all parameters of the method that must be set.

In the grid model (also called *cellular* [41]) each individual is associated with a spatial location on a low-dimensional grid. The population is considered as a system of active individuals that interact only with their direct neighbors. Different neighborhoods can be defined for the cells. The most common neighborhoods in the two-dimensional case are the 4-neighbor (*von Neumann neighborhood*) consisting of the North, South, East, West neighbors and 8-neighbor (*Moore neighborhood*) consisting of the same neighbors augmented with the diagonal neighbors. In the ideal case, one processor is assigned to each grid point, thus fitness evaluation is performed simultaneously for all the individuals. In practical implementations, however, this is not true because the number of processors generally does not coincide with the number of points on the grid. Selection, reproduction, and mating take place locally within the neighborhood. Information diffuses slowly across the grid, giving rise to the formation of semi-isolated niches of individuals having similar characteristics. The choice of the individual to mate with the central individual and the replacement of the latter with one of the offspring can be accomplished in several ways.

Ref. [37] noted that parallel genetic algorithms are faster than their sequential counterpart and benefit from the multi population approach in two different aspects. First, the problem of premature convergence is reduced thanks to the spatial isolation of the subpopulations that co-evolve independently but promote local search. Second, the same solution quality can be obtained in fewer generations, by using many populations instead of a single population with the same total number of individuals.

The same results, however, have not been obtained for the coarse-grained parallel implementations of GP. In fact, although Koza [1, 24] reported a super-linear speedup for the 5-parity problem, for other problems, Punch [32] found poorer results of convergence with respect to the canonical *GP*. A systematic study on the performances of parallel genetic programming has not been conducted. Punch [32] was the first to analyze the behavior of distributed GP with respect to sequential GP. In the next section, we review the main parallel implementations of GP. Next, after the description of CAGE, we compare the few experimental results available in the literature with our approach.

3 Related Work

The most famous coarse-grained parallel implementation of *GP* is due to Koza and Andre [24, 1]. They used a PC 486 computer as host and a network of 64 transputers as processing nodes. For the *Even-5 parity* problem, they obtained a super-linear speedup using a population of 32000 individuals, 500 on each node and a migration rate of 8% in the four directions of each subpopulation at each generation.

Juillé and Pollack [19, 20] described a parallel implementation of GP on a SIMD system. Each SIMD processor simulated a computer program by using a simple instruction set defined specifically for *GP*. S-expressions were evaluated efficiently, precompiling them in a postfix program. The authors, for few classical problems, reported the execution time for one run and the average execution time for one generation. For $cos 2x$, using a population of 4096 individuals, one per processor, they found a solution after an average of 17.5 generations with an average execution time of 30.48 seconds.

Stoffel and Spector [35] described a high-performance *GP* system (HiGP) based on a virtual stack machine (similar to [20]) that executed GP programs represented as fixed-length strings. HiGP manipulated and generated linear programs instead of tree-structured S-expressions. Each gene in a chromosome corresponded to an operator of the virtual machine. They executed 100 runs for a symbolic regression problem for a maximum of 30 generations and obtained good time performances. Nothing, however, was said about convergence results.

Dracopoulos and Kent [5, 6] described two different implementations of parallel *GP* based on the *Bulk Synchronous Parallel* (BSP) model [39] of parallel computation. The first implementation adopted the master-slave paradigm. A master process performed the standard sequential GP algorithm and the slave processes assisted the master only during the fitness evaluation. The slaves received equal portions of the population from the master, evaluated the fitness of individuals, and returned them back to the master. The second implementation realized the island model. Each process was considered an island and, every 10 generations, the top 10% of individuals were migrated. Two different communication topologies were considered: the ring and the star. The results presented regards only the speedup obtained for the *Artificial Ant Los Altos Hills* problem by running these implementations for 50 generations. The authors experiments showed that the coarse-grained parallel implementation achieved better speedups than the global version. The convergence results of the two approaches were not reported.

Niwa and Iba [28] described a parallel implementation of *GP*, named *Distributed Genetic Programming* (DGP), based on the island model and realized on a MIMD parallel system AP-1000+ consisting of 32 processors. The global population was distributed among the processing nodes, each of which executed a canonical GP on its subpopulation. At every generation, the best individual of a subpopulation was sent asynchronously to its adjacent subpopulations and, for each subpopulation, the worst individual was replaced by this one if the fitness of the received individual was better than the best individual of the current subpopulation. The authors used three different communication topologies: ring type, one-way torus, and two-way torus. Experimental results on three problems (*discovery of trigonometric identities, predicting* *a chaotic time series and Boolean concept formation*) revealed the ring topology as the best. A comparison between *DGP* and *CAGE* is offered in section 7.

Oussaidéne et al. [29, 30] presented a parallel implementation of *GP* on a distributed-memory machine that used the master-slave model. The *Parallel Genetic Programming Scheme* (PGPS) had a master process whose task is to manage the *GP* algorithm, that is, it created the initial population, applied the variation operators, and performed the selection of the individuals for the reproduction phase. The slave processes controlled fitness evaluation, thus they received the parse trees from the master process to evaluate. The trees were packed as strings in a buffer and sent to the slaves. Each slave process unpacked the buffer content and rebuilt the parse tree in memory. In order to distribute the computational load among the processing nodes equally, two different load balancing algorithms (one static and another one dynamic) were used. The dynamic scheduling algorithm gave better speedup results as compared to the static one. PGPS has been applied to the evolution of trading strategies to infer robust trading models [29, 30].

Punch [32] discussed the conflicting results on the use of multiple populations in *GP*, in contrast with the indisputable benefits obtained in genetic algorithms with the same approach. He argued that there are problem-specific factors that affect the multiple-population approach. He presented experiments for the *Ant Santa Fe* and the *royal tree* problem. A comparison between his results and ours is offered in section 7.

Salhi et al. [34] reported a parallel implementation of GP based on a random island model, designed specifically for symbolic regression problems. In such a model, individuals migrate at random. This is possible because two new operators, *import* and *export* are introduced. They have the role of supporting communication among the islands and have associated a probability like the other variation operators. For two symbolic regression problems the authors obtained a superlinear speedup, and for $cos2x$ they obtained a linear speedup. Convergence results were not reported.

Tongchim and Chongstitvatana [38] presented a coarse-grained parallel implementation of GP with asynchronous migration and applied it on a mobile robot navigation problem. They obtained a superlinear speedup by using a population size of 6000 individuals, while migrating the top 5% of individuals of each subpopulation with a frequency depending on the number of processors used.

Fernández et al. [8] presented an experimental study to verify the influence of two parameters, number of subpopulations and size of each population, on the performances of parallel genetic programming. A standard GP tool was suitably modified to allow the coarse-grained parallelization of GP. The tool, described in [7], used communication primitives of the PVM (*Parallel Virtual Machine*) and adopted a client/server model where the server has the task of managing input/output buffers and of choosing the communication topology (that can be dynamically changed), while the clients constitute the subpopulations. The results reported for the Even-5 parity and a regression problem were evaluated with respect to the number of nodes evaluated in a GP tree, called computational effort. For these two problems they found optimal ranges for parameter values. Such values, however, are problem dependent.

An improvement of the tool described in [7] was presented in [10] and consisted of a parallel GP kernel that used MPI (*Message Passing Interface*) message passing system, and a graphical-user interface. The communication between the processes/subpopulations and the master process was synchronous. A new communication topology, the random one, among the subpopulations, was added to the ring and mesh topologies. In the random topology, the master process received a block of individuals and sent them to a randomly chosen subpopulation. This software tool was used in [9] to study the influence of the communication topology and the frequency of migration on the performances of parallel GP. Three test problems were considered: Even-5 parity, Ant Santa Fe and a real world problem. The authors found that the random and ring topology were better than the mesh for the ant problem. For the Even-5 parity, if the population size was large, the grid was the best, while, if the population size was small, the ring and the random were better. With regard to migration, a number of individuals of about 10% the population size, every 5-10 generations, appeared to be the best values for all the problems considered.

4 Parallel implementation of CAGE

This section describes the implementation of $CAGE$ on distributed-memory parallel computers. To parallelize GP, $CAGE$ uses the cellular model. The cellular model is fully distributed with no need of any global control structure and it is naturally suited for implementation on parallel computers. It introduces fundamental changes in the way GP works. In this model, the individuals of the population are located on a specific position in a toroidal two-dimensional grid and the selection and mating operations are performed, cell by cell, only among the individual assigned to a cell and its neighbors. This local reproduction has the effect of introducing an intensive communication among the individuals that could influence negatively the performance of the parallel implementation of GP. Moreover, unlike genetic algorithms, where the size of individuals is fixed, the genetic programs are individuals of varying sizes and shapes. This requires a large amount of local memory and introduces an unbalanced computational load per grid point. Therefore, an efficient representation of the program trees must be adopted and a load balancing algorithm must be employed to maintain the same computational load among the processing nodes.

The best way to overcome the drawbacks associated with the implementation of the cellular model on a general-purpose distributed-memory parallel computer is to use a partitioning technique based on domain decomposition in conjunction with the *Single-Program-Multiple-Data* ($SPMD$) programming model. According to this model, an application on N processing elements (PEs) is composed of N similar processes, each of which operates on a different set of data. For an effective implementation, data should be partitioned such that communication takes place locally and the computation load be balanced among the PEs. This approach increases the granularity of the cellular model, transforming it from a fine-grained model to a coarse-grained model. In fact, instead of assigning only one individual to a processor, the individuals are grouped by *slicing up* the grid and assigning a *slice* of the population to a node.

$CAGE$ implements the cellular GP model using a one-dimensional domain decomposition (in the x direction) of the grid and an explicit message passing to exchange information among the domains. This decomposition is more efficient than a two-dimensional decomposition. In fact, in the two-dimensional decomposition, the number of messages sent is higher, even though the size of the messages is smaller. On the other hand, in one-dimensional decomposition, the number of messages sent is fewer but their size is greater. Considering that generally in a send operation the startup time is much greater than the transfer time, the second approach is more efficient than the first. The concurrent program that implements the architecture of $CAGE$ is composed of a set of identical *slice processes*. No coordinator process is necessary because the computational model is decentralized completely. Each slice process, which contains a portion of elements of the grid, runs on a single PE of the parallel machine and executes the code, shown in figure 1, on each subgrid point, thus updating all the individuals of the subpopulation.

```
1.   Read from a file the configuration parameters
2.   Generate a random sub-population
3.   Evaluate the individuals of the sub-population
4.   while not numGenerations do
5.     update boundary data
6.     for x =1 to width
7.       for y =1 to height
8.         select an individual k (located at position [x',y'])
           neighboring with i (located at position [x,y]);
9.         generate offspring from i and k ;
10.          apply the user-defined replacement policy to update i;
11.          mutate i with probability pmut;
12.          evaluate the individual i;
         end for
       end for
     end while
```

Figure 1: Pseudocode of the slice process.

Each slice process uses the parameters read from a file (step 1) to configure the GP algorithm that must be executed on each subgrid point. The parameters concern the population size, the max depth that the trees can have after the crossover, the parsimony factor, the number of iterations, the number of neighbors of each individual, and the replacement policy. We have implemented three replacement policies: *direct* (the best of the offspring always replaces the current individual), *greedy* (the replacement occurs only if offspring is fitter), and *probabilistic* (the replacement happens according to difference of the fitness between parent and offspring (*simulated annealing*)[11]).

Simulated annealing [21] is a randomized technique for finding a near-optimal approximate solution of difficult combinatorial optimization problems that reflects the annealing process that takes place in nature. A SA algorithm starts with a randomly generated candidate solution. Then, it repeatedly attempts to find a better solution by moving to a neighbor with higher fitness. In order to avoid getting trapped in poor local optima, simulated annealing strategy occasionally allows for *uphill moves* to solutions of lower fitness by using a *temperature parameter* to control the acceptance of the moves. At the beginning, the temperature has a high value and then a cooling schedule reduces its value. The new solution is kept if it has a better fitness than the previous solution, otherwise it is accepted with a probability depending on the current temperature. As the temperature becomes cooler, it is less likely that bad solutions are accepted and that good solutions are discarded. In our implementation, a parameter α, which has a value between 0.95 and 1.0, is chosen to reduce the temperature at each generation and such that the temperature assumes the final value when $NumGenerations$ steps have been executed. The best of the offspring replaces the current individual only if the difference between their fitness is below the current temperature. This deterministic criterion [17] has been shown to be less expensive and performs equivalently as the random technique.

The size of the subpopulation of each slice process is calculated by dividing the population for the number of the processors on which CAGE is executed. Each slice process updates the individuals belonging to its subgrid sequentially. Initially, in each process, a random subpopulation is generated (step 2.) and its fitness is evaluated (step 3.). Then, steps 6-12 are executed for generating the new subpopulation for $numGenerations$ iterations. The variables $width$ and $height$ define the boundaries of the 2D subgrid that is contained in a process. It should be noted that two copies of the data are maintained for calculating the new population. In fact, as each element of the current population is used many times, the current population cannot be overwritten.

Because of the data decomposition, physically neighboring portions of data are allocated to different processes. To improve the performances and to reduce the overhead due to the remote communications, we introduced a local copy of boundary data in each process. This avoids remote communication more than once on the same data. Boundary data are exchanged at each iteration before breeding the new population. In our implementation, the processes form a logical ring and each processor determines its right- and left-neighboring processes. The communication between processes is local since only the outermost individuals need to communicate between the slice processes.

All the communications are performed using the MPI (*Message Passing Interface*) portable message passing system so that $CAGE$ can be executed across different hardware platforms. Since the processes are connected according to a ring architecture and each process has a limited buffer for storing boundary data, we use asynchronous communication in order to avoid processors to idle.

Each processor has two send buffers ($SRbuf, SLbuf$) and two receive buffers ($RRbuf$, $RLbuf$). The SRbuf and SLbuf buffers correspond to the outermost (right and left) individuals of the subgrid. The receive buffers are added to the subgrid in order to obtain a bordered grid. The exchange of the boundary data occurs, in each process, by two asynchronous send operations followed by two asynchronous receive operations to the right- and left-neighboring processes. After this, each process waits until the asynchronous operations complete.

Figure 2 shows the pseudocode for this data movement operation.

$CAGE$ uses the standard tool for GP, sgpc1.1, a simple GP in the C language, available freely at [36], to apply the GP algorithm to each grid point. However, in order to meet the

```
MPI_Isend(SRbuf, right);
MPI_Isend(SLbuf, left);
MPI_Irecv(RRbuf, right);
MPI_Irecv(RLbuf, left);
MPI_Waitall();
```

Figure 2: Pseudocode for data movement.

requirements of the cellular *GP* algorithm, a number of modifications were introduced.

We used the same data structure of sgpc1.1 to store a tree in each cell. The structure that stores the population was transformed from a one-dimensional array to a two-dimensional one and we duplicated this structure in order to store the current and the new generated tree. The selection procedure was replaced with one that uses only the neighborhood cells and three replacement policies were added. Crossover is performed between the current tree and the best tree in the neighborhood. Two procedures to *pack* and *unpack* the trees, that must be sent/received to/from the other processes, were added. The pack procedure is used to send the trees of the boundary data to the neighboring processes in a linearized form. We use a breadth-first traversal to linearize the trees of the boundary data into an array. However, before exchanging the array containing the linearized trees, we send another array containing the size of the trees to the neighboring processes in order to allow an optimized allocation of the space in memory of the receiving nodes. Immediately after, the unpack procedure rebuilds the data and stores them in the new processor's private address space.

In many *GP* applications, the size of the trees of the population is very variable and the computational load is completely unbalanced. To equally distribute the computational load among the processing nodes, CAGE introduces an intelligent partitioning of the grid. The

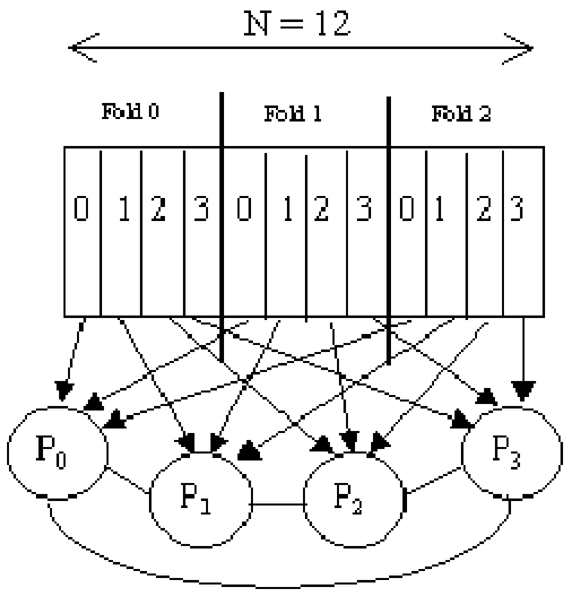


Figure 3: Load balancing strategy: each fold is divided in four strips.

partitioning strategy is a form of block-cyclic decomposition [4]. The idea is to split the grid virtually in a number of folds and assign equal parts of each fold to each of the processors of the multicomputer.

According to this strategy the cells partitioning is static, whereas the number of cells mapped in each partition is dynamic. The grid of cells is first divided into f vertical folds, where f is defined by the user. Each fold is then partitioned into p strips, where p is the number of processors. In this way, each strip contains one or more contiguous columns of the grid.

To better specify the load balancing strategy, we number the slice processes from 0 to p - *1* and the grid columns from 1 to N. The block-cyclic data distribution maps the index of the k^{th} column of the grid onto a process P_i with $0 \leq i \leq p-1$ according to the following formula:

$$k \rightarrow i = \lfloor \frac{(k-1)}{N_c} \rfloor \ mod \ p$$

where $N_c = \frac{N}{fp}$ is the number of columns in each strip.

Figure 3 shows the layout of a grid ($N = 12$) partitioned in three folds ($f = 3$) each one split in four strips ($p = 4$); in this case each strip contains one column and each process P_i has three elements.

This task distribution based on folds requires each process P_i to communicate only with processes P_{i-1} and P_{i+1}, so a simple logical ring connecting all the processors is sufficient to accomplish all the communications. The number of folds and processes should be chosen with caution, since the more strips are used, the bigger the communication overhead among the processing elements becomes.

The next section presents a theoretical performance analysis of CAGE. This analysis allows us to evaluate the performance of CAGE when the population size and the number of processors are increased. Note that the quality of the solution obtained is not related to this kind of analysis.

5 Performance Analysis

In this section, we analyze the performance of our parallel implementation of GP. We first focus on genetic programs in which we do not consider the effects of the load balancing algorithm. Then we extend our model to handle the strategy of load balancing presented in the previous section. Analyzing the performance of a given parallel algorithm/architecture requires a method to evaluate scalability. The *isoefficiency* function [16] is one among many parallel performance metrics that measure scalability. It indicates how the problem size n must grow as the number of processor m increases in order to obtain a given efficiency E. It relates problem size to the number of processors required to maintain the efficiency of a system, and lets us to determine scalability with respect to the number of processors, their speed, and the communication bandwidth of the interconnection network.

We assume that GP works on a population of size $A \times B$ points, where A is the width and B is the height of the grid. Furthermore, s represents the average dimension of the trees of the population. On a sequential machine we can model the computation time T_1 for evolving a population of genetic programs for one generation as:

$$T_1 = t_{as} + AB(t_f + t_{up})$$

where t_f is the average computation time required to perform the evaluation phase at a single grid point; t_{as} is the average time required at each generation to perform some simple operations, such as the increment of the iterations and the zero setting of some variables; t_{up} is the time necessary to update, after one evaluation, the state of each cell of the grid with the new genetic program and the corresponding value of the fitness. So, defining $t'_f = t_f + t_{up}$ we have:

$$T_1 = t_{as} + ABt'_f \qquad (1)$$

The parallel execution time of the GP program on a distributed memory parallel machine with p processors can be modelled by summing up the computation time needed to evaluate the genetic programs on a partition A/p of the grid, the time for packing and unpacking the trees, representing the genetic programs, and the communication time needed to exchange the buffers containing the trees of the boundary data to the neighboring processes. Therefore, the parallel execution time can be estimated as follows:

$$T_p = (t_{as} + \frac{A}{p}Bt'_f) + T_{pack} + T_{unpack} + T_{exc} \qquad (2)$$

where T_{pack} is the time spent to pack each tree from its memory representation into two linearized data structures, containing the size and the nodes of each tree respectively; T_{unpack} is the time necessary to rebuild the equivalent trees in memory of the received data from the neighboring processors, and T_{exc} is the time required to exchange the borders.

The time for packing and unpacking is:

$$T_{pack} + T_{unpack} = Bs(t_1 + t_2) = Bst_{punp} \qquad (3)$$

where t_1 is the time to visit a tree and build the linearized data structures and t_2 is the time to rebuild the tree. Let $t_{punp} = t_1 + t_2$. To take into account the communication time, we consider that each task must exchange with two neighboring tasks the borders of its own portion and receive those of the neighbors for a total of four messages. As we must exchange two data structure (trees and their size), the time required to exchange the borders can be estimated, according to Hockney's model [18], as:

$$T_{exc} = 4(t_s + sBt_b) + 4(t_s + 4Bt_b) = 8t_s + 4Bt_b(4 + s) \qquad (4)$$

where s is the average size of a tree, t_s is the startup time, that is, the time required to initiate the communication, and t_b is the incremental transmission time per byte, which is determined by the physical bandwidth of the communication channel linking the source and destination processors. Therefore we can represent the parallel execution time as:

$$T_p = t_{ap} + B[\frac{A}{p}t'_f + 4t_b(4 + s) + st_{punp}] \qquad (5)$$

where $t_{ap} = 8t_s + t_{as} + \alpha$. The α parameter includes all the times that do not depend on the size of the grid and the communication among processors.

The overhead function T_0 of a parallel system represents the total sum of all overhead incurred by the p processors during the parallel execution of the algorithm and it depends on the problem size. In our case T_0 is given by:

$$T_0 = pT_p - T_1 \cong p(t_{ap} + 4Bt_b(4 + s) + Bst_{punp}) \qquad (6)$$

under the really plausible hypothesis that t_{as} is negligible with respect to the total time. The speedup on p processors can be evaluated as $S = \frac{T_1}{T_p}$ and the efficiency as $E = \frac{S}{p}$. Using the expressions 1 and 5, the speedup and the efficiency can be expressed respectively as:

$$S = \frac{T_1}{T_p} = \frac{t_{as} + ABt'_f}{t_{ap} + B[\frac{A}{p}t'_f + 4t_b(4+s) + st_{punp}]} \qquad (7)$$

$$E = \frac{S}{p} = \frac{t_{as} + ABt'_f}{ABt'_f + p[4Bt_b(4+s) + sBt_{punp} + t_{ap}]} \qquad (8)$$

For scalable parallel systems, the problem size T_s must grow to keep the efficiency fixed, as p increases. To maintain efficiency to fixed value (between 0 and 1), the following relation must be satisfied:

$$AB = \frac{1}{t'_f}kT_0 \qquad (9)$$

(6) where $k = \frac{E}{1-E}$ is a constant depending on the efficiency to be maintained. From expression (1) and (6) we obtain:

$$ABt'_f \cong kp(t_{ap} + 4Bt_b(4+s) + Bst_{punp}) \qquad (10)$$

The isoefficiency function is determined by abstracting the problem size as a function of p, through algebraic manipulations in the equation (9). In our case, examining the equation (10), we can notice that doubling the number of processors, we must double the width of the grid, in order to maintain the efficiency to a constant value. The isoefficiency function for our system is therefore $\Theta(p)$. Since the amount of computation increases linearly with respect to p in order to keep the efficiency constant, our implementation is highly scalable. From equation (7) we deduce that for a fixed problem size, the speedup saturates at:

$$\frac{t_{as} + ABt'_f}{t_{ap} + B[4t_b(4+s) + st_{punp}]} \qquad (11)$$

when increasing to infinity the number p of processors. Moreover, from equation (10) we can estimate the size of the problem that we should allocate on p processors to obtain a fixed value of efficiency. For example, to have an efficiency of 90% on 24 processors, A should be:

$$A \cong \frac{9 * 24(t_{ap} + 4Bt_b(4+s) + Bst_{punp})}{Bt'_f} \qquad (12)$$

The previous analysis does not consider the effects of the load balancing strategy. Now we modify the model in order to include the load balancing strategy. The main changes of the model concern the estimation of the time to pack and unpack the trees in the equation (3) and the time T_{exc}, required to exchange the borders in the equation (4). In fact, we now do not have to exchange only the border data regarding a contiguous portion of the grid (A/p) but the border data of all the strips allocated on a generic process. Considering that the number of strips mapped on a process is equal to the number of folds f, the equations (3) and (4) will be modified as follows:

$$T_{pack} + T_{unpack} = fBst_{punp} \qquad (13)$$

$$T_{exc} = 4(t_s + sfBt_b) + 4(t_s + 4fBt_b) = 8t_s + 4fBt_b(4+s) \qquad (14)$$

Using this expression we obtain for the overhead function T_0 the following expression:

$$T_0 = p * T_p - T_s \cong p(t_{ap} + 4Bt_b(4+s) + Bst_{punp}) \qquad (15)$$

that used in the expression 9 shows as our implementation is still scalable.

6 Results

This section presents experimental and theoretical results of our cellular parallel implementation on some well-known test problems. Furthermore, the benefits of the load balancing technique introduced in section 4 are shown. The parallel implementation was realized on a CRAY T3E parallel machine with 256 processors based on DEC Alpha processor with 128 Mbytes of memory. We used sgpc1.1 [36] as the sequential implementation of genetic programming.

6.1 Experimental Analysis

This subsection presents a detailed description of each test problem. The convergence results obtained with *CAGE* when the *greedy* replacement policy was adopted are compared with sequential *GP*. We also present the convergence behavior of *CAGE* when the *direct*, *greedy*, and *probabilistic* replacement policies were used and the influence of the population size on the convergence of the method. The parameters of the method are shown in table 1 and functions and terminal symbols for each problem are described in table 2. Each problem was run 20 times for 100 generations. For all the experiments, we used the *Moore* neighborhood and a population size of 3200, except for *Symbolic Regression.* For this problem, the size of the population was 800 individuals.

Symbolic Regression ([22] par. 7.3). The *symbolic regression* problem consists in searching for a non-trivial mathematical expression that, given a set of values x_i for the independent variable(s), always assumes the corresponding value y_i for the dependent variable(s) of a given mathematical function. In the first experiment, the target function was the polynomial $x^4 + x^3 + x^2 + x$. A sample of 20 data points (x_i, y_i) was generated by randomly choosing the values of the independent variable x in the interval [-1,1].

Table 1: CAGE Parameters

Maximum number of generations	100
Probability of crossover	0.8
Probability of choosing internal points for crossover	0.1
Probability of mutation	0.1
Probability of reproduction	0.1
Generative Method for initial random population	Ramped
Maximum depth for a new tree	6
Max depth for a tree after crossover	17
Max depth of a tree for mutation	4
Parsimony factor	0.0

Table 2: Terminal symbols and functions for each problem.

Problem Name	**Terminal symbols**	**Functions**
Symbolic Regression	{X }	{ +, -, *,%, sin, cos, exp,rlog}
Discovery of trig. id.	{X,1.0}	{+, -, *,%, sin}
Symbolic Integration	{X }	{ +, -, *,%, sin, cos, exp,rlog}
Even-4 parity	$\{d_0, d_1, d_2, d_3\}$	{AND, OR, NAND, NOR}
Even-5 parity	$\{d_0, d_1, d_2, d_3, d_4\}$	{AND, OR, NAND, NOR}
Ant(Santa Fe)	{Forward, Right, Left}	{IfFoodAhead,Prog2, Prog3}
Royal Tree	{X }	{A,B,C,D,E }

Discovery of trigonometric identities. ([22] par. 10.1) In the second experiment, our aim was to discover a trigonometric identity for $cos2x$. 20 values x_i of the independent variable x were chosen randomly in the interval [0,2π] and the corresponding value $y_i = cos2x_i$ computed. The 20 pairs (x_i, y_i) constituted the fitness cases. The fitness was then computed as the sum of the absolute value of the difference between y_i and the value generated by the program on x_i.

Symbolic Integration. ([22] par. 10.5) The symbolic integration problem consists in searching for a symbolic mathematical expression that is the integral of a given curve. In this experiment the curve was $cosx + 2x + 1$ so the genetic program had to obtain $sinx + x^2 + x$, given 50 pairs (x_i, y_i) in the interval [0,2π].

For these three problems it can be useful to adopt the *hits criterion* suggested by Koza ([22] p. 163), which consists in accepting that the numerical value returned by the S-expression differs from the correct value within a small tolerance (e.g. 0.01). Actually, for symbolic integration, this tolerance value is essential to find a solution since the integral is approximated with trapezoids, thus we adopted the criterion for this experiment. With regard to the other two, we show the results with and without the hits criterion.

Even-4 parity. ([22] par. 20.4) The *Even-4 parity* problem consists in deciding the parity of a set of 4 bits. A Boolean function receives 4 Boolean variables and it returns TRUE only if an even number of variables is true. Thus the goal function to discover is $f(x_1, x_2, x_3, x_4)$ $= x_1x_2x_3x_4 \vee \overline{x_1}x_2\overline{x_3}x_4 \vee \overline{x_1}x_2x_3\overline{x_4} \vee x_1\overline{x_2}\overline{x_3}x_4 \vee x_1\overline{x_2}x_3\overline{x_4} \vee x_1x_2\overline{x_3}\overline{x_4} \vee \overline{x_1}\ \overline{x_2}\ \overline{x_3}\ \overline{x_4}$. The fitness cases explored were the 2^4 combinations of the variables. The fitness was the sum of the Hamming distances between the goal function and the solution found.

Even-5 parity. ([22] par. 20.5) The *Even-5 parity* problem consists in deciding the parity of a set of 5 bits. The 2^5 combinations of the 5 Boolean variables constituted the fitness cases and the fitness was the same as Even-4 parity problem.

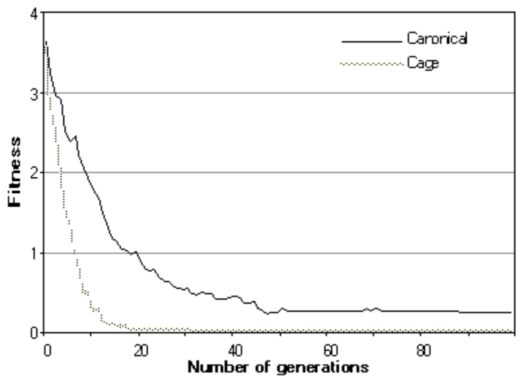
Ant Santa Fe. ([22] par. 7.2) The *artificial ant* problem consists in finding the best list of moves that an ant can execute on a 32×32 matrix in order to eat all the pieces of food put on the grid. In this experiment we used the *Santa Fe trail* that contains 89 food particles. The fitness function was obtained by diminishing the number of food particles by one every time the ant arrived in a cell containing food. The ant can see the food only if it is in the cell ahead in its same direction ($IfFoodAhead$ move); otherwise it can move randomly ($left$ or $right$) for two ($Progn2$) or three ($Progn3$) moves.

Royal Tree. The *royal tree* problem was invented by Punch et al. [33] with the aim of having at disposal a benchmark problem for testing the effectiveness of GP, analogously to the *royal road problems* defined by Holland for genetic algorithms [27]. This problem consists of a single base function that can be specialized to obtain the desired level of difficulty and it has a unique solution tree. A series of functions, a, b, c, etc., with increasing arity is defined. An a function has arity 1, a b function has arity 2, and so on. A perfect tree is defined for each function. A level-e tree has depth 5 and 326 nodes. A score for each subtree id defined and the raw fitness is the score of the root. This score is computed by summing the weighted scores of its direct children. We run the experiments on a level-e royal tree.

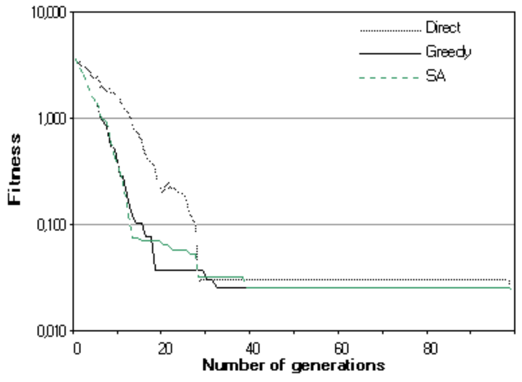
These two last problems are known to be purposely difficult for distributed GP. Next, for each of the above problems, experimental results are reported and discussed. Besides the figures that show the convergence results, we adopted the same method of Punch [32] to present the results of the experiments as the number of $Wins$ and $Losses$ obtained by running canonical GP and CAGE for 20 times. The wins are denoted as $W : (x, y)$, where x represents the number of optimal solutions found before 100 generations and y the average generation in which the optimal solution was found. The losses are denoted as $L : (q, r, s)$, where q is the number of losses (no optimal solution found before 100 generations) r is the average best-of-run fitness, and s is the average generation when the best-of-run occurred. Tables 3 and 4 summarize all the experiments.

Figure 4 shows the results for symbolic regression. In particular, in figure 4(a) the comparison between the convergence of canonical sequential GP and CAGE is presented. CAGE reaches a good fitness value more rapidly than canonical GP and it obtains the exact solution in 18 out of the 20 runs at, approximately, the 11th generation, while canonical GP finds the solution in 11 runs at the 42th generation. If we introduce the hits criterion (0.01), the results do not change for either method. This behavior is expected since when the methods fail, the average fitness is 0.25 for CAGE, and 0.52 for canonical GP. Figure 4(b) shows the CAGE behavior when the three replacement policies are used. The greedy and probabilistic policies are similar. In figures 4(b) and (c) a logarithmic scale is used for a better view of the fitness values. Figure 4(c) shows the influence of the population size on the convergence of the method. It is clear that the bigger is the population the faster is the convergence.

Figure 5 shows the results for the discovery of trigonometric identities. For this problem (figure 5(a)) canonical GP is not able to find any solution before 100 generations. The best value found is 0.32 at about the 45th generation. CAGE finds the exact solution in 7 runs and reaches a value of 0.0029, when it does not find it, at approximately the 83th generation. If we adopt the *hits criterion*, canonical GP again fails for all the 20 runs while CAGE succeeds for all the 20 runs at approximately the 21th generation. Notice that all the figures regards the experiments without the hits criterion. Figure 5(b) shows the CAGE behavior when the three replacement policies are used. The greedy approach is the best. Figure 5(c) shows the



(*a*)



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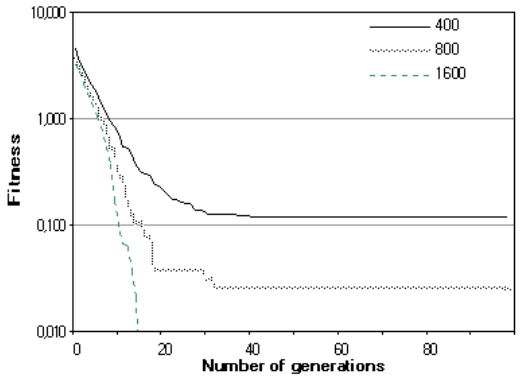

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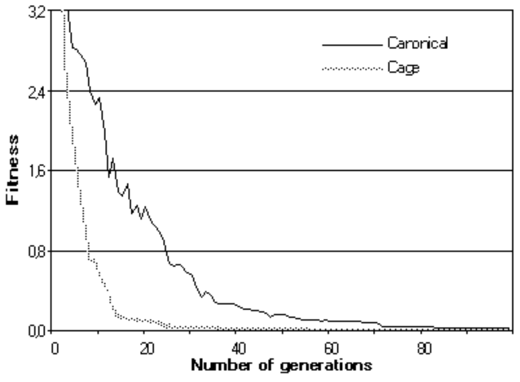
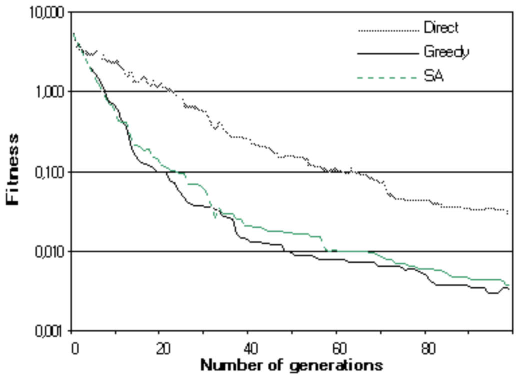
Figure 4: Experimental results for symbolic regression: (a) comparison between Canonical GP and CAGE, (b) convergence for different replacement policies and (c) convergence for different population sizes.



(a)



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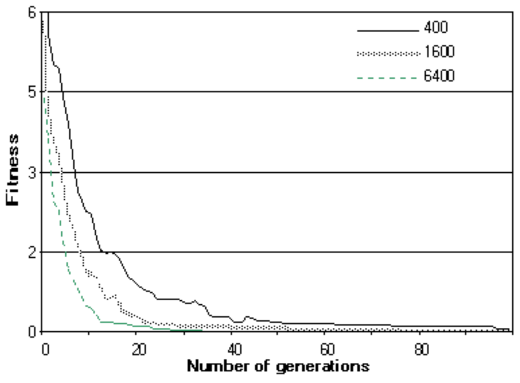

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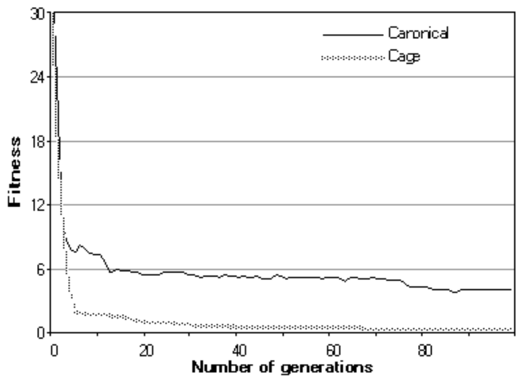
Figure 5: Experimental results for discovery of trigonometric identities: (a) comparison between Canonical GP and CAGE, (b) convergence for different replacement policies and (c) convergence for different population sizes.

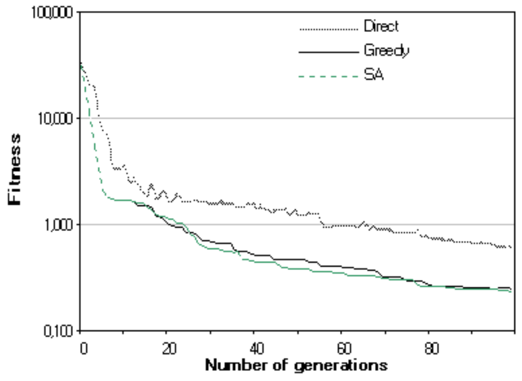
convergence of the method with different population sizes. As the figure shows, with 6400 individuals the convergence is much faster and the fitness has an average value of 0.001 at about the 95th generation. Figures 5(b) and (c) also use a logarithmic scale.

Figure 6 shows the results for symbolic integration. In figure 6(a) the comparison between the convergence of canonical sequential GP and CAGE is presented. CAGE in about 5 generations reaches a fitness value that canonical GP is not able to find in 100 generations. Furthermore canonical GP finds the solution only in one run at the 93th generation with an average fitness value of 3.7, while CAGE obtains the solution in 7 runs at about the 69th generation. When CAGE does not reach the exact solution, it has an average fitness value of 0.45 generation at the 74th generation.

Figures 7 and 8 reports the results for Even-4 and Even-5 problems. It is well known that this family of problems is very difficult. Koza [22] (p.532) states that when Even-5 was run with a population of 4000 individuals for 51 generations no solution was found after 20 runs. It was necessary to double the population to have a solution at the eighth run. With our parameters, canonical GP could not find any solution for both Even-4 and Even-5. CAGE, on the contrary, obtained the solution in 17 out of 20 runs for Even-4 and it was successful in two runs for Even-5. This behavior is evident from the figures 7(a) and 8(a). Canonical GP obtained a fitness value that is far from the solution and it was not able to appreciably improve it before the 100th generation. CAGE did not find the solution in only two cases for Even-4. For Even-5 it obtained the solution in two runs but, when it failed to find it, the average best-of-run fitness was very low. Figure 8(c) shows the convergence improvement when populations of increasing sizes are used. For instance, when CAGE ran with a population of 6400 individuals, at the 100th generation the average fitness wass 1.77, while with 1600 individuals it was 3.10.



(a)



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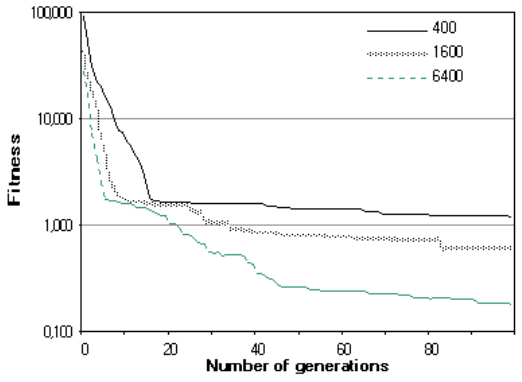

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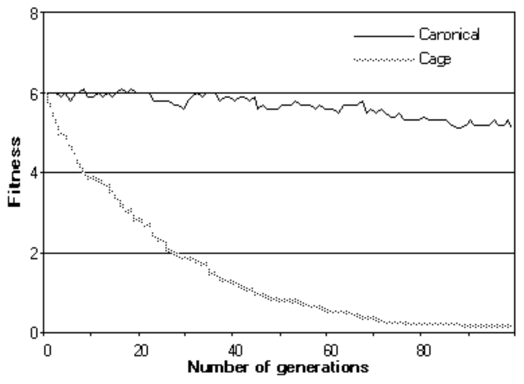
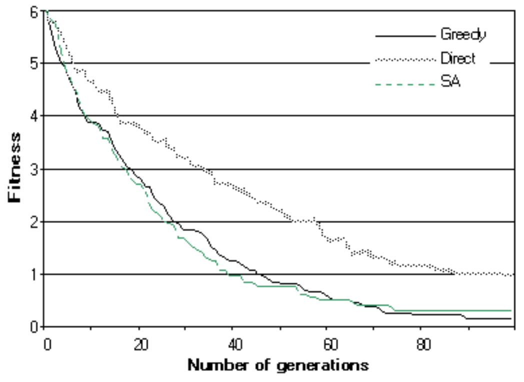
Figure 6: Experimental results for symbolic integration: (a) comparison between Canonical GP and CAGE, (b) convergence for different replacement policies and (c) convergence for different population sizes.



(*a*)



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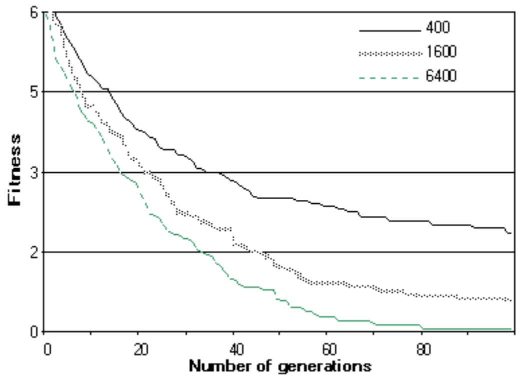

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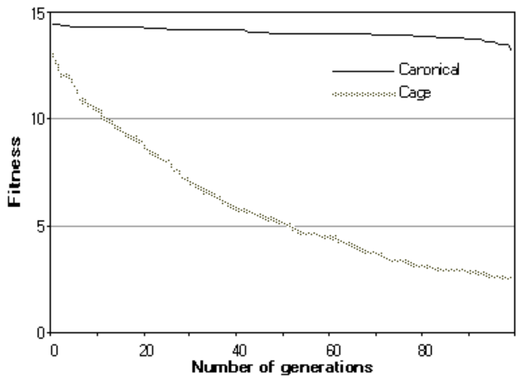
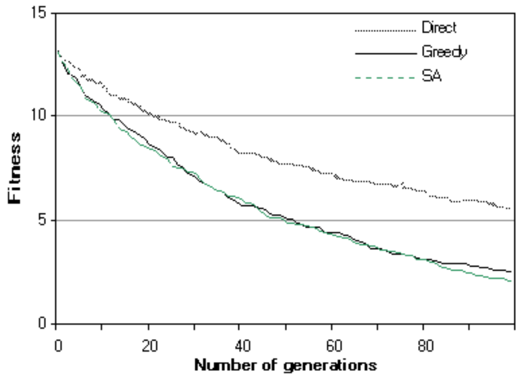
Figure 7: Experimental results for Even-4 parity: (a) comparison between Canonical GP and CAGE, (b) convergence for different replacement policies and (c) convergence for different population sizes.



(a)



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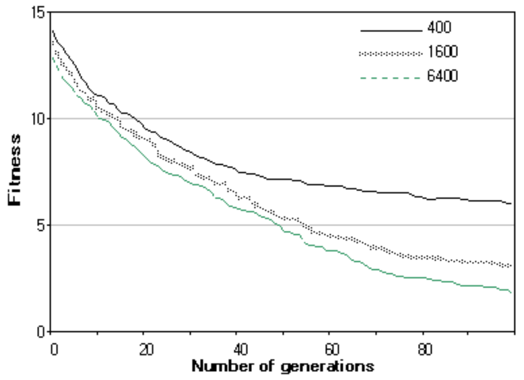
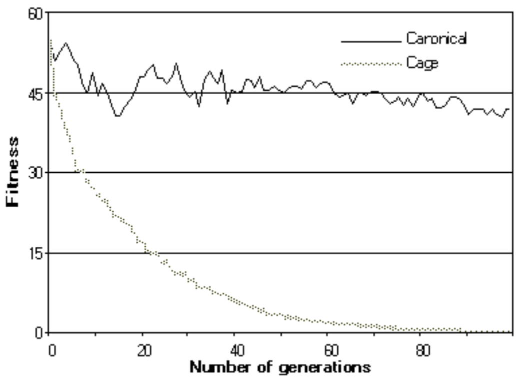
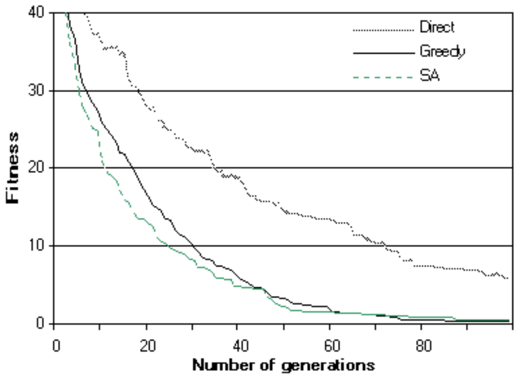


(c)

Figure 8: Experimental results for Even-5 parity: (a) comparison between Canonical GP and CAGE, (b) convergence for different replacement policies and (c) convergence for different population sizes.



(*a*)



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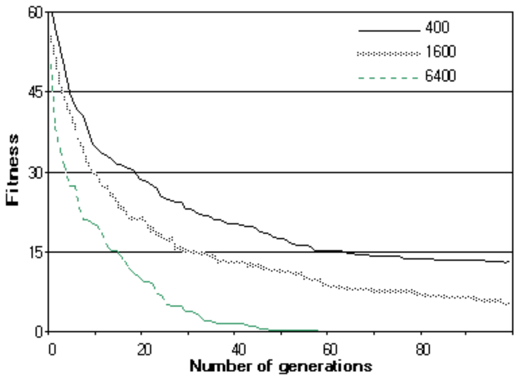

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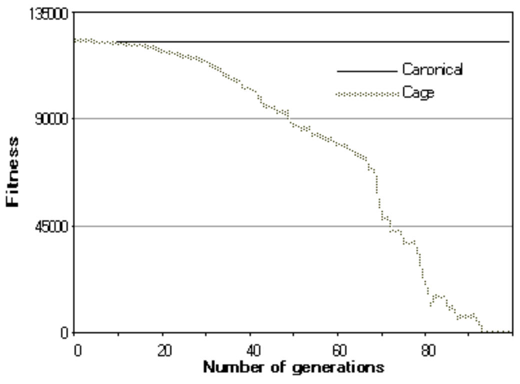
Figure 9: Experimental results for Ant Santa Fe: (a) comparison between Canonical GP and CAGE, (b) convergence for different replacement policies and (c) convergence for different population sizes.



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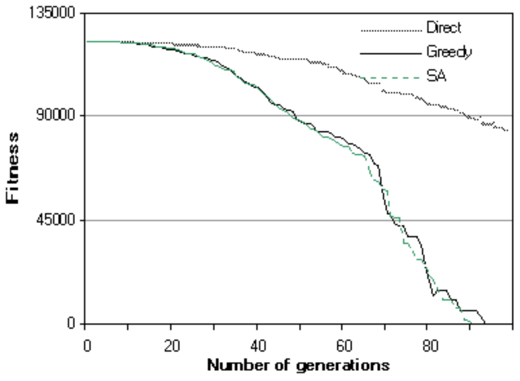

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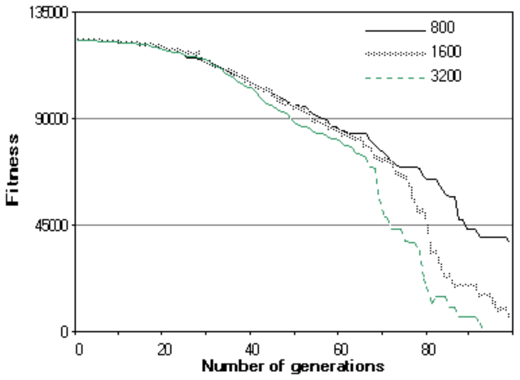

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Figure 10: Experimental results for Royal Tree: (a) comparison between Canonical GP and CAGE, (b) convergence for different replacement policies and (c) convergence for different population sizes.

Table 3: Results for Canonical GP

	Canonical GP			
Problem Name	**Wins**	**Losses**	**Mean**	**Deviation**
Symbolic Regression	W:(11,42.18)	L:(9,0.54,44.78)	0.24	0.27
Discovery of trig. id.	W:(0)	L:(20,0.32,44.60)	0.32	0.19
Symbolic Integration	W:(1,93)	L:(19,3.76,46.95)	3.57	2.50
Even-4 parity	W:(0)	L:(20,4.65,40.15)	4.65	0.71
Even-5 parity	W:(0)	L:(20,12.55,50.95)	12.55	0.52
Ant(Santa Fe)	W:(2,62.50)	L:(18,27.50,35.72)	24.75	10.49
Royal Tree	W:(0)	L:(20,122763,45.65)	122763	24.40

In figure 9 the convergence results of $CAGE$ with respect to canonical GP are shown for the Ant Santa Fe problem. The figure clearly points out that, after 100 generations, canonical GP is far from the solution, while $CAGE$ failed only once in finding the solution. By doubling the population the convergence is much faster and $CAGE$ always succeeded before an average of 55 generations. Also for the Royal tree problem (figure 10(a)) canonical GP always failed, while $CAGE$ obtains the solution for all the 20 runs at, approximately, the 78th generation. Figure 10(c) shows the convergence when 800, 1600 and 3200 individuals are used and it clearly points out that, by increasing the population size, the method has a better convergence.

For all the seven problems $CAGE$ outperformed canonical GP. This result allows us to state that the parallel cellular genetic programming implementation, analogously to parallel genetic algorithms [37], needed fewer evaluations to get the same solution quality than for the single population case with the same total number of individuals.

Table 4: Results of CAGE

	CAGE			
Problem Name	**Wins**	**Losses**	**Mean**	**Deviation**
Symbolic Regression	W:(18,10.83)	L:(2,0.25,31.00)	0.025	0.076
Discovery of trig. id.	W:(7,18.43)	L:(13,0.0026,76.15)	0.002	0.002
Symbolic Integration	W:(7,69.43)	L:(13,0.45,74.15)	0.30	0.44
Even-4 parity	W:(17,60.12)	L:(3,1.0,35.67)	0.15	0.36
Even-5 parity	W:(2,96.5)	L:(18,2.72,82.22)	2.45	1.43
Ant(Santa Fe)	W:(19,55.10)	L:(1,9.0,71.0)	0.45	1.96
Royal Tree	W:(20,77.70)	L:(0)	0	0

6.2 Experimental performance evaluation

To illustrate the use of our scalability prediction technique and to assess its accuracy, we present two examples: the Even-4 parity problem and the Ant problem. For both problems we considered a population of 128x13 cells.

Table 5 shows, for the Even-4 parity problem, the estimated values of the parameters necessary to evaluate the parallel execution time T_p for different number of processors using equation (2). The t'_f value was estimated by measuring its computational cost for different problem sizes (i.e. changing the A value) and then using the Matlab toolkit to automatically calculate the least-squares fit of the equation that defines t'_f with the experimental data. Likewise, we estimated t_{punp}. t_{ap} was estimated by measuring its computational cost for different number of processors and then calculating the least-squares fit of the equation that defines t_{ap} with the experimental data. The t_s and t_b values for the CRAY T3E machine were estimated as already done in a previous work for a Meiko CS-2 machine [14]. The average size s of the trees was

Table 5: Even-4 parity problem parameters (Cray T3E)

Parameter	**Value(μsec)**
t'_f	921
t_{punp}	52.6
t_{ap}	11
t_s	15
t_b	0.00300

18.35 nodes. Table 6 shows the measured and predicted execution times, and the relative error associated with each prediction for the Even-4 problem.

For the Ant problem, the average size s of the trees was 19.84 nodes and the values of the constants to evaluate T_p are shown in table 7. Table 8 shows the measured and predicted execution times, and the relative error associated with each prediction for the Ant problem.

The results described in tables 6 and 8 show a good agreement between the model and the experiments. In fact, for the Even-4 problem the measured times were, on average, 6% off the predicted and, on average, 7% off for the Ant problem. The relative error is smaller in the second example because the computation component of the model dominates. Since it is the most accurately estimated model term, the prediction becomes increasingly accurate with larger problems. A more accurate prediction model is obtainable using a refined model of communication cost [15].

From equation 8, we calculate that the value of the speedup is bound to 122.02 for the Even-4 problem and to 64.9 for the Ant problem. The lower value of speedup for the Ant problem is due to the much larger communication/computation ratio. In fact, the average computation

Table 6: Cray T3E execution time predictions for 100 iterations (Even-4 parity problem)

Num. procs	**Num. individuals per node**	**Measured (sec)**	**Predicted (sec)**	**Relative Error (percent)**
1	1664	-	-	-
2	832	-	-	-
4	416	41.706	39.518	5.09
8	208	22.593	20.425	9.60
16	104	11.262	10.847	3.69
32	52	6.556	6.057	7.60
64	26	3.844	3.663	4.71

time, required to perform the evaluation phase at a single grid point in the Ant problem, is about the half of the time required for the Even-4 problem. We can obtain a better value of speedup increasing the granularity, that is, allocating a larger number of cells for node. We can use formula 7 to calculate the exact size of A to increase the speedup. For example, from this formula, we obtain a size of A equal to 1135 to have an efficiency of 90% on 64 processors. The model can be helpful to calculate the correct size of the population of the GP in order to obtain a given efficiency for a specific architecture. Furthermore, we can determinate, for a specific population, the optimal number of processors that allow reaching a specific efficiency.

6.3 Evaluation of the load balancing strategy

This subsection briefly presents some results concerning the load balancing strategy proposed in section 4. Before implementing the strategy we have analyzed the size of the trees of the

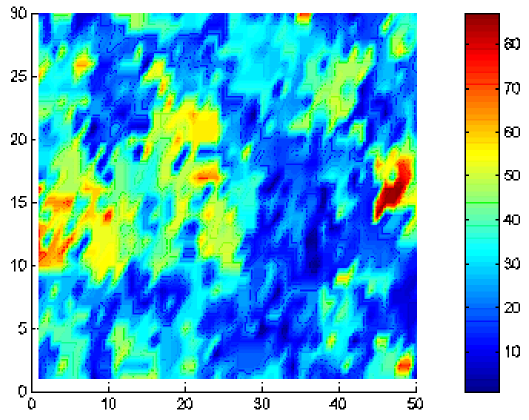
Table 7: Ant problem parameters (Cray T3E)

Parameter	**Value(μsec)**
$t'f$	530
t_{punp}	52.6
t_{ap}	11
t_s	15
t_b	0.00300

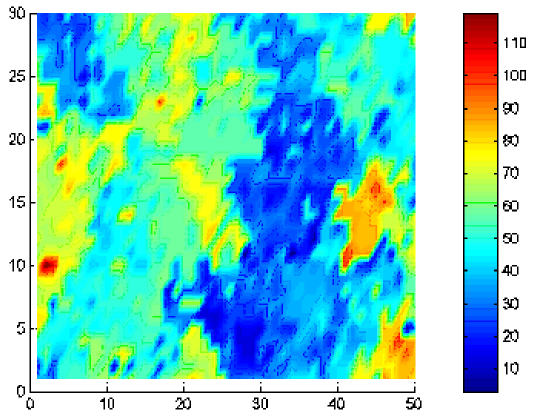
population for different problems and iterations. Figure 11 shows a snapshot of the size of the trees for different iterations (namely 10th, 20th, 30th and 40th) for the Even-4 problem, using a 50 x 30 grid. The size of the trees is very variable and the computational load is completely unbalanced. This behavior is similar for many of the problems used in our analysis. We have implemented and tested the load balancing strategy for all the problems of our test suite. A complete description of the results is presented in [13]. 20 % improvement on average has been obtained for the most of the problems. This result confirms the importance of a load balancing strategy for parallel GP implementations in order to avoid an inefficient utilization of the processors. Note that all the experiments presented in the previous subsection were obtained without load balancing.

7 Comparison with the island model

This section compares the results presented by Niwa and Iba [28], those reported by Punch [32], and by Fernández et al. [8], with those obtained by *CAGE*. To compare our method with these



(a)



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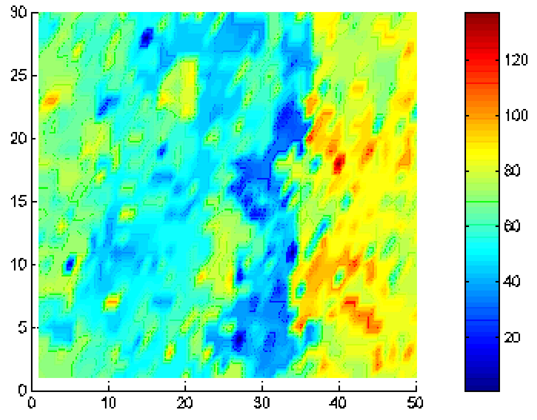

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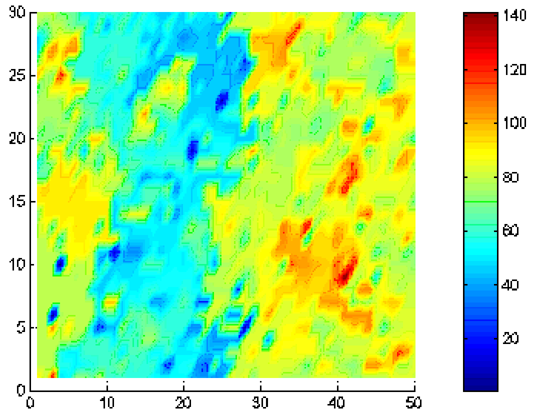


(d)

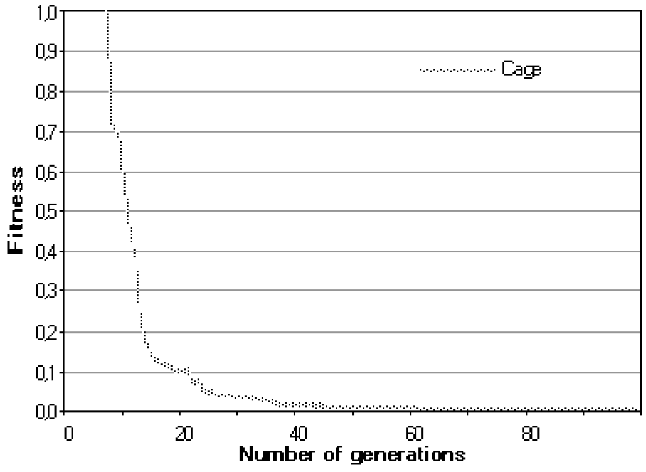
Figure 11: Snapshot of the size of the trees at the 10th (a), 20th (b), 30th (c) and 40th (d) generation for Even-4. Different colors denote different sizes.

Table 8: Cray T3E execution time predictions for 100 iterations (Ant problem)

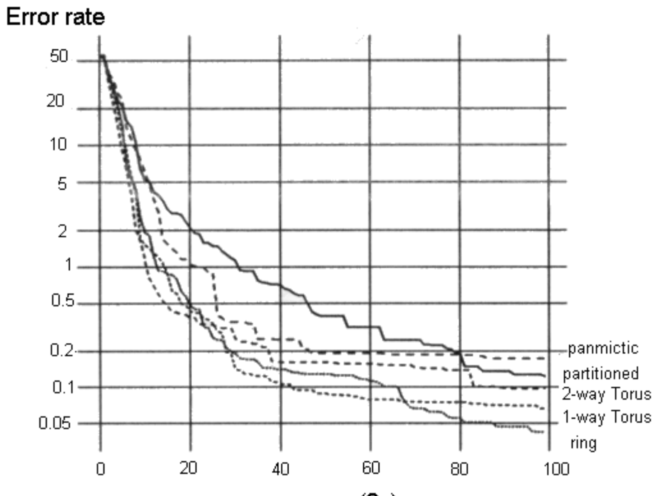
Num. procs	**Num. individuals per node**	**Measured (sec)**	**Predicted (sec)**	**Relative Error (percent)**
1	1664	-	-	-
2	832	44.222	45.491	-2.87
4	416	25.029	23.430	6.39
8	208	12.753	12.400	2.76
16	104	6.891	6.885	0.08
32	52	4.805	4.128	14.10
64	26	2.404	2.749	-14.35

other island-model implementations, we ran CAGE with the same parameters of each approach. However, since we did not run their software, a number of details could be different and influence the quality of the results. For example, Punch used the *lilgp* package [33], while Fernández et al. used the GPC++ package [40].

Figures 12(a) and (b) report the results obtained by *CAGE* and by Niwa and Iba [28] for the discovery of trigonometric identities problem. In figure 12(a), for a better view of the results, the fitness is displayed when it assumes values between 0 and 1. Figure 12(b) was obtained by scanning the figure in [28]. With regard to this problem, the better implementation Niwa and Iba obtained (ring topology) gives a fitness value of 0.5 at the 20th generation, of 0.2 at about the 30th, and 0.1 at about the 62th. CAGE, instead, obtained a fitness value of 0.5 at the 10th generation, of 0.2 at about the 15th, and 0.1 at the 20th. We do not know how many wins and losses they had.

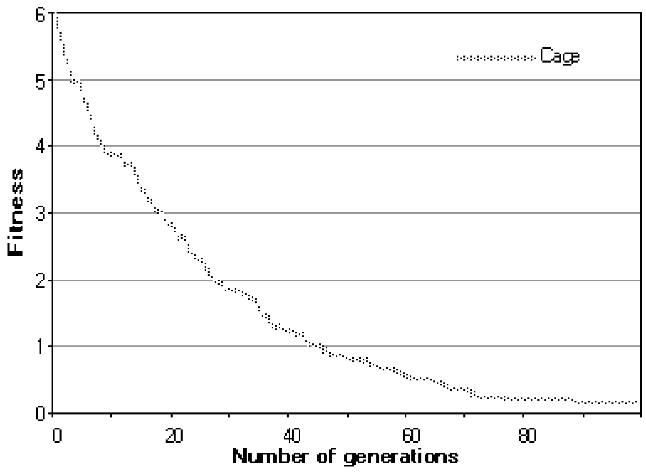


(*a*)

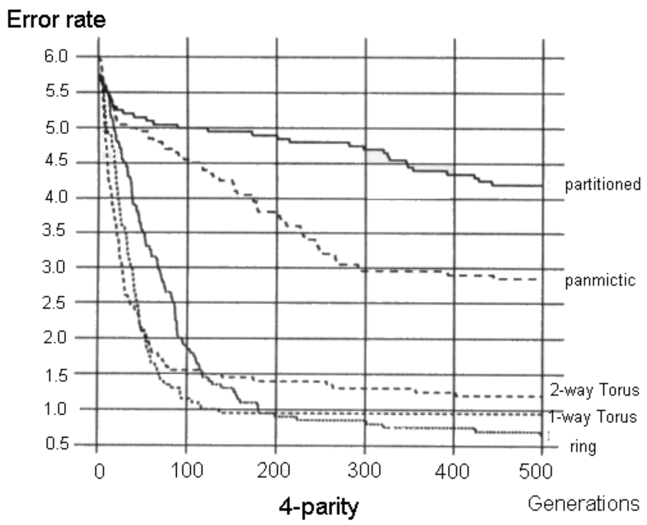


(*b*)

Figure 12: Experimental results for cos2x: (a) CAGE and (b) Niwa and Iba.



(*a*)



(*b*)

Figure 13: Experimental results for even-4 parity problem: (a) CAGE and (b) Niwa and Iba.

Table 9: wins and losses

	Punch		CAGE	
Problem Name	**Wins**	**Losses**	**Wins**	**Losses**
Ant(Santa Fe)	W:(7,240)	L:(9,73,181)	W:(13,94)	L:(3, 28.00, 50.00)
Royal Tree	W:(0)	L:(16,10005,338)	W:(15,119)	L:(1, 98304, 129)

Figures 13(a) and (b) show the results obtained by *CAGE* and by Niwa and Iba [28] for the Even-4 parity problem. For this problem, Niwa and Iba do not always find the correct Boolean function not even after 500 generations. CAGE fails in only three runs before 100 generations with an average best-of-run fitness of 1 at the average generation 36 when the best-of-run occurred. Unfortunately we do not have these kind of details with regard to the implementation of Niwa and Iba. At the 100th generation, their average fitness value is about 1.1.

To compare our results with those of Punch [32], we computed the wins and losses for the ant and royal tree problems by running *CAGE* the same number of times (16) as Punch reported, the same population size (1000) and for 500 generations. Punch obtained the best result for the ant problem by using a ring of 5 populations with proportional selection and no mutation, while for the royal tree with over selection and no mutation. Table 9 compares these results with CAGE's and it confirms the better performances of *CAGE* with respect to the island approach. The single-population results that Punch obtained by using the *GP* tool *lilgp* [33] are better than the multi-population results for these two problems. The best results of his canonical GP are $W:(10,109)$ and $L:(6,73,300)$ for the ant problem and $W:(8,233)$, $L:(8,9064,159)$ for the royal tree problem. Even compared with these results, CAGE performed better.

Finally we compared CAGE results for the Even-5 parity problem with those obtained by

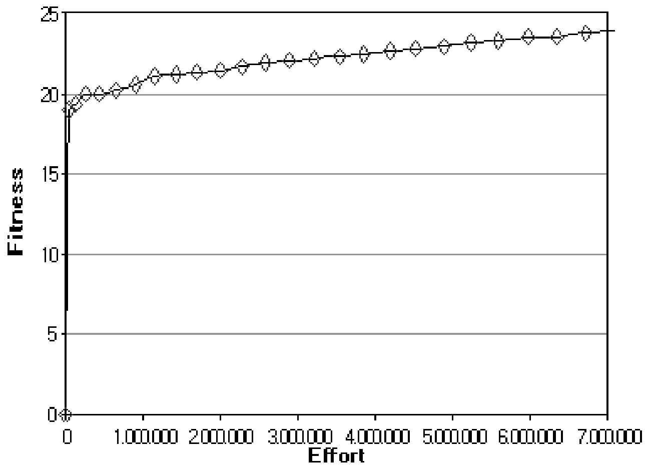


Figure 14: Effort computed for the Even-5 parity problem.

Fernández et al. [8], which introduced the *computational effort* as a measure to compare results of the same problem. The *computational effort* is the number of nodes that are evaluated in a GP tree. Let N and I be the number of times an experiment has been executed and the number of individuals of the population, respectively. Furthermore let AVG_LENGTH be the average number of nodes per individual. Then the required effort in a particular generation is $I \times N \times AVG\_LENGTH$. Figure 14 shows the effort required by CAGE. An effort equal to 7 million is required to reach a fitness value of about 24. In [8], with the same effort, the fitness value is about 11. Thus CAGE requires fewer evaluations.

8 Conclusions

A fine-grained parallel implementation of *GP* through cellular model on distributed-memory parallel computers, has been presented. Experimental results showed very good performances of the proposed approach. The experimental study on a variety of benchmark problems has substantiated the validity of the cellular implementation over both the island model and the sequential single-population approach. The implementation of a load balancing strategy allows CAGE a very good utilization of the computing resources. Finally, a theoretical performance analysis based on the isoefficiency function permitted us to classify *CAGE* as a highly scalable system and to predict execution time, speedup, and efficiency.

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