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Co-evolving Parallel Random Number Generators

Moshe Sipper[1] and Marco Tomassini[2]

[1] Logic Systems Laboratory, Swiss Federal Institute of Technology, IN-Ecublens, CH-1015 Lausanne, Switzerland. E-mail: Moshe.Sipper@di.epfl.ch
[2] Swiss Scientific Computing Center, Manno, and Logic Systems Laboratory, Swiss Federal Institute of Technology, IN-Ecublens, CH-1015 Lausanne, Switzerland. E-mail: Marco.Tomassini@di.epfl.ch

Abstract. Random numbers are needed in a variety of applications, yet finding good random number generators is a difficult task. In the last decade cellular automata (CA) have been used to generate random numbers. In this paper *non-uniform* CAs are studied, where each cell may contain a *different* rule, in contrast to the original, uniform model. We present the *cellular programming* algorithm for co-evolving non-uniform CAs to perform computations, and apply it to the evolution of random number generators. Our results suggest that good generators can be evolved; these exhibit behavior at least as good as that of previously described CAs, with notable advantages arising from the existence of a "tunable" algorithm for obtaining random number generators.

Keywords: non-uniform cellular automata, random number generators, cellular programming, evolution, co-evolution, parallel computation, artificial life, complex systems.

1 Introduction

Random numbers are needed in a variety of scientific, mathematical, engineering, and industrial applications, including Monte Carlo simulations, sampling, decision theory, game theory, and the imitation of stochastic natural processes. To generate a random sequence on a digital computer, one starts with a fixed length seed, then iteratively applies some transformation to it, progressively extracting as long as possible a random sequence. Such numbers are usually referred to as *pseudo*-random, as distinguished from true random numbers resulting from some natural physical process. In order to demonstrate the efficiency of a proposed generator, it is usually subjected to a battery of empirical and theoretical tests, among which the most well known are those described by [5].

Good random number generators, or randomizers, are hard to come by; indeed, a number of generators which had gained prominence over the years, were ultimately found to be unsatisfactory, some displaying particularly "bad", non-random behavior [11]. In the last decade certain cellular automata (CA) have been shown to act as good random number generators. CAs are dynamical system in which space and time are discrete. They consist of an array of cells, each of which can be in one of a finite number of possible states, updated synchronously in discrete time steps according to a local, identical interaction rule. The state of a cell is determined by the previous states of a surrounding neighborhood of

cells [20]. CAs exhibit three notable features, namely massive parallelism, locality of cellular interactions, and simplicity of basic components (cells), thus lending themselves naturally to fast, efficient hardware implementation.

The model investigated by us is an extension of the CA model, termed *non-uniform cellular automata* [12]. Such automata function in the same way as uniform ones, the only difference being in the cellular rules that need not be identical for all cells. Our main focus is on the *evolution* of non-uniform CAs to perform computational tasks, employing a local, co-evolutionary algorithm, an approach referred to as *cellular programming* [16].

In this paper we apply the cellular programming algorithm to the evolution of random number generators. While a more extensive suite of tests should be conducted, our results suggest that good randomizers can be evolved; these exhibit behavior at least as good as that of previously described CAs, with notable advantages arising from the existence of a "tunable" algorithm for the generation of randomizers (see also [18]). In Section 2 we survey previous work on randomizers and on evolving CAs. The cellular programming algorithm is delineated in Section 3, and applied to the co-evolution of random number generators in Section 4. Finally, our conclusions are presented in Section 5.

2 Previous work

The first work examining the application of CAs to random number generation is that of [21], in which rule 30 is extensively studied for its ability to produce random, temporal bit sequences[3]. Such sequences are obtained by sampling the values that a particular cell attains as a function of time. The cellular space under question is one-dimensional with $k = 2$ and $r = 1$, where k denotes the number of possible states per cell and r denotes the radius of a cell, i.e., the number of neighbors on either side (thus each cell has $2r + 1$ neighbors, including itself). A common method of examining the behavior of one-dimensional CAs is to display a two-dimensional space-time diagram, where the horizontal axis depicts the configuration at a certain time t and the vertical axis depicts successive time steps (e.g., Figure 2). The term 'configuration' refers to an assignment of 1 states to several cells, and 0s otherwise.

In [21], the uniform rule 30 CA is initialized with a configuration consisting of a single cell in state 1, with all other cells being in state 0; the initially non-zero cell is the site at which the random temporal sequence is generated. Wolfram studied this particular rule extensively, demonstrating its suitability as a high-performance randomizer which can be efficiently implemented in parallel; indeed, this CA is one of the standard generators of the massively parallel Connection Machine CM2. A non-uniform CA randomizer was presented by [3, 4], consisting of two rules, 90 and 150, arranged in a specific order in the grid. The performance of this CA in terms of random number generation was found to be at least as good as that of rule 30, with the added benefit of less costly hardware implementation.

[3] Rule numbers are given in accordance with Wolfram's convention [20], representing the decimal equivalent of the binary number encoding the rule table.

It is interesting in that it combines two rules, both of which are simple linear rules that do not comprise good randomizers, to form an efficient, high-performance generator.

The application of genetic algorithms to the *evolution* of *uniform* cellular automata was initially studied by [10] and recently undertaken by the EVCA (evolving CA) group [9, 8, 7, 2, 1]. They carried out experiments involving one-dimensional CAs with $k = 2$ and $r = 3$; spatially periodic boundary conditions were used, resulting in a circular grid. Mitchell *et al.* studied two computational tasks, namely density and synchronization, employing a genetic algorithm to evolve uniform CAs to perform these tasks. The algorithm uses a randomly generated initial population of CAs with $k = 2$, $r = 3$. Each CA is represented by a bit string, delineating its rule table, containing the output bits for all possible neighborhood configurations (i.e., the bit at position 0 is the state to which neighborhood configuration 0000000 is mapped to and so on until bit 127 corresponding to neighborhood configuration 1111111). The bit string, known as the "genome", is of size $2^{2r+1} = 128$, resulting in a huge search space of size 2^{128}. Each CA in the population was run for a maximum number of M time steps, after which its fitness was evaluated, defined as the fraction of cells in the correct state at the last time step. Using the genetic algorithm highly successful CA rules were found for both the density and the synchronization tasks.

An evolutionary approach for obtaining random number generators was taken by Koza [6], who used genetic programming to evolve a symbolic LISP expression that acts as a rule for a uniform CA (i.e., the expression is inserted into each CA cell, thereby comprising the function according to which the cell's next state is computed). He demonstrated evolved expressions that are equivalent to Wolfram's rule 30. The fitness measure used by Koza is the *entropy* E_h: let k be the number of possible values per sequence position (in our case CA states) and h a subsequence length. E_h (measured in bits) for the set of k^h probabilities of the k^h possible subsequences of length h is given by:

$$E_h = -\sum_{j=1}^{k^h} p_{h_j} \log_2 p_{h_j}$$

where $h_1, h_2, \ldots, h_{k^h}$ are all the possible subsequences of length h (by convention, $\log_2 0 = 0$ when computing entropy). The entropy attains its maximal value when the probabilities of all k^h possible subsequences of length h are equal to $1/k^h$; in our case $k = 2$ and the maximal entropy is $E_h = h$. Koza evolved LISP expressions which act as rules for uniform, one-dimensional CAs. The CAs were run for 4096 time steps and the entropy of the resulting temporal sequence of a designated cell (usually the central one) was taken as the fitness of the particular rule (i.e., LISP expression). In his experiments Koza used a subsequence length of $h = 4$, obtaining rules with an entropy of 3.996. The best rule of each run was re-tested over 65536 time steps, some of which exhibited the maximal entropy value of 4.0.

The model investigated in this paper is that of non-uniform CAs, where cellular rules need not be identical for all cells. We have previously applied this model

to the study of artificial life issues, presenting multi-cellular "organisms" that display several interesting behaviors, including reproduction, growth and mobility [12, 15, 13]. In [14, 17] we demonstrated that universal computation can be attained in non-uniform, two-dimensional, 2-state, 5-neighbor CAs, which are not computation-universal in the uniform case. The universal systems we presented are simpler than previous ones and are *quasi*-uniform, meaning that the number of distinct rules is extremely small with respect to rule space size; furthermore, the rules are distributed such that a subset of dominant rules occupies most of the grid. The co-evolution of non-uniform, one-dimensional CAs to perform computations was undertaken in [16, 17], where the cellular programming algorithm was presented; we showed that high performance, non-uniform CAs can be co-evolved not only with radius $r = 3$, as studied by Mitchell *et al.*, but also for smaller radiuses, most notably $r = 1$ which is minimal. It was also found that evolved systems exhibiting high performance are quasi-uniform.

The above account leads us to ask whether good CA randomizers can be co-evolved using cellular programming; the results reported below suggest that indeed this is the case.

3 Cellular programming

We study one-dimensional, 2-state, $r = 1$ non-uniform CAs, in which each cell may contain a different rule; spatially periodic boundary conditions are used, resulting in a circular grid. A cell's rule table is encoded as a bit string, known as the "genome", containing the output bits for all possible neighborhood configurations (see Section 2). Rather than employ a *population* of evolving, uniform CAs, as with genetic algorithm approaches, our algorithm involves a *single*, non-uniform CA of size N, with cell rules initialized at random. Initial configurations are then randomly generated and for each one the CA is run for $M = 4096$ time steps.[4] Each cell's *fitness*, f_i, is accumulated over $C = 300$ initial configurations, where a single run's score equals the entropy E_h of the temporal sequence of cell i. Note that we do not restrict ourselves to one designated cell, but consider all grid cells, thus obtaining N random sequences in parallel, rather than a single one. After every C configurations evolution of rules occurs by applying the genetic operators of crossover and mutation in a completely *local* manner, driven by $nf_i(c)$, the number of fitter neighbors of cell i after c configurations. The pseudo-code of our algorithm is delineated in Figure 1. Crossover between two rules is performed by selecting at random (with uniform probability) a single crossover point and creating a new rule by combining the first rule's bit string before the crossover point with the second rule's bit string from this point onward. Mutation is applied to the bit string of a rule with probability 0.001 per bit.

There are two main differences between our evolutionary algorithm and a standard genetic algorithm: (a) A standard genetic algorithm involves a popu-

[4] A standard, 48-bit, linear congruential algorithm proved sufficient for the generation of random initial configurations.

```
for each cell i in CA do in parallel
    initialize rule table of cell i
    f_i = 0 { fitness value }
end parallel for
c = 0 { initial configurations counter }
while not done do
    generate a random initial configuration
    run CA on initial configuration for M time steps
    for each cell i do in parallel
        f_i = f_i + entropy E_h of the temporal sequence of cell i
    end parallel for
    c = c + 1
    if c mod C = 0 then { evolve every C configurations}
        for each cell i do in parallel
            compute nf_i(c) { number of fitter neighbors }
            if nf_i(c) = 0 then rule i is left unchanged
            else if nf_i(c) = 1 then replace rule i with the fitter neighboring rule,
                                     followed by mutation
            else if nf_i(c) = 2 then replace rule i with the crossover of the two fitter
                                     neighboring rules, followed by mutation
            else if nf_i(c) > 2 then replace rule i with the crossover of two randomly
                                     chosen fitter neighboring rules, followed by mutation
                                     (this case can occur if the cellular radius, r, > 1)
            end if
            f_i = 0
        end parallel for
    end if
end while
```

Fig. 1. Pseudo-code of the cellular programming algorithm.

lation of evolving, uniform CAs; all CAs are *ranked* according to fitness, with crossover occurring between *any* two CA rules. Thus, while the CA runs in accordance with a local rule, evolution proceeds in a *global* manner. In contrast, our algorithm proceeds *locally* in the sense that each cell has access only to its locale, not only during the run but also during the evolutionary phase, and no global fitness ranking is performed. (b) The standard genetic algorithm involves a population of *independent* problem solutions; each CA is run independently, after which genetic operators are applied to produce a new population. In contrast, our CA *co-evolves* since each cell's fitness depends upon its evolving neighbors. This latter point comprises a prime difference between our algorithm and parallel genetic algorithms, which have attracted attention over the past few years [19]. Some of the proposed models resemble our system in that they are massively parallel and local; however, the co-evolutionary aspect is missing.

4 Results

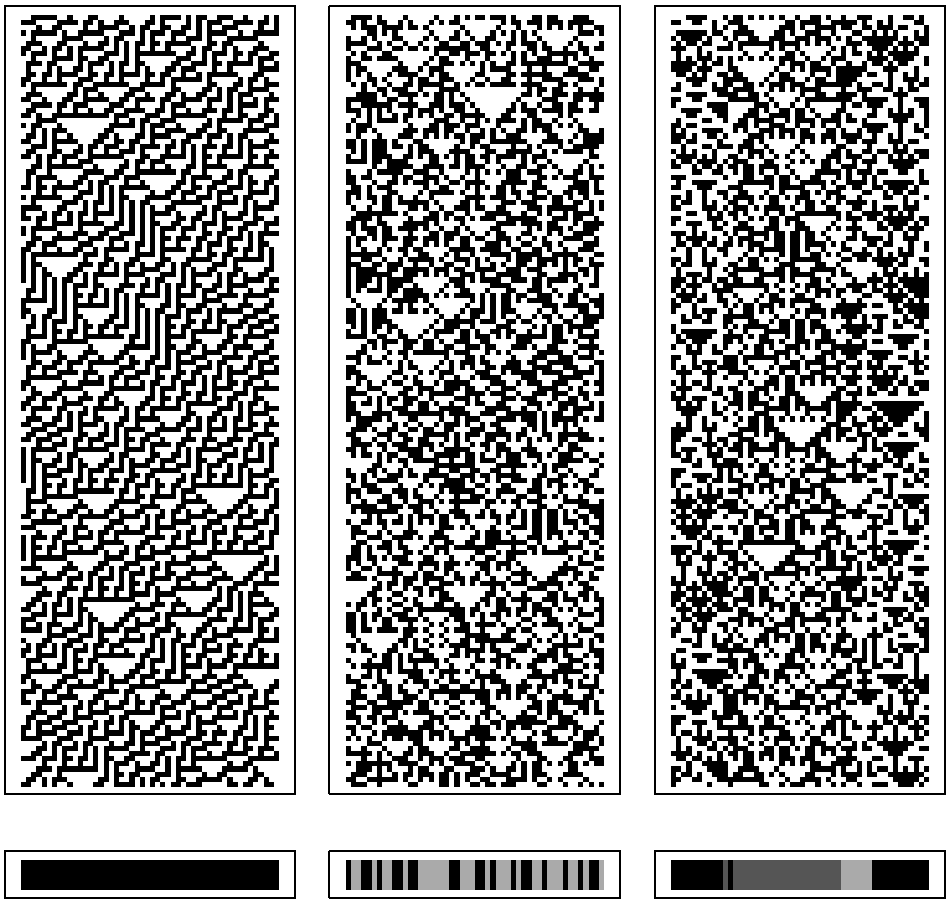
In this section we describe results of applying the cellular programming algorithm to the evolution of random number generators. In our simulations we observed that the average cellular entropy taken over all grid cells is initially low (usually in the range $[0.2, 0.5]$), ultimately evolving to a maximum of 3.997, when using a subsequence size of $h = 4$ (i.e., the entropy is computed by considering the occurrence probabilities of 16 possible subsequences, using a "sliding window" of length 4).

We performed several such experiments using $h = 4$ and $h = 7$; the evolved, non-uniform CAs attained average fitness values (entropy) of 3.997 and 6.978, respectively. We then re-tested our best CAs over $M = 65536$ times steps (as in [6]), obtaining entropy values of 3.9998 and 6.999, respectively. Interestingly, when we performed this test with $h = 7$ for CAs which were evolved using $h = 4$, high entropy was displayed as for CAs which were originally evolved with $h = 7$. The entropy results are comparable to those of [6] as well as to the rule 30 CA of [21] and the non-uniform, rules $\{90, 150\}$ CA of [3, 4]. Note that while our fitness measure is local, the evolved entropy results reported above represent the average of *all* grid cells; thus, we obtain N random sequences rather than a single one. Figure 2 demonstrates the operation of three CAs discussed above: rule 30, rules $\{90, 150\}$, and a co-evolved CA. Note that the co-evolved CA is quasi-uniform (Section 2), as evident by observing the rules map; this map depicts the distribution of rules by assigning a unique color to each distinct rule.

We next subjected our evolved CAs to a number of additional tests, including chi-square (χ^2), serial correlation coefficient and a Monte Carlo simulation for calculating the value of π; these are well known tests described in detail in [5]. In order to apply the tests we generated sequences of $100,000$ random bytes in the following manner: the CA of size $N = 50$ is run for 500 time steps, thus generating 50 random temporal bit sequences of length 500. These are concatenated to form one long sequence of length $25,000$ bits; this procedure is then repeated 32 times, thus obtaining a sequence of length $800,000$ bits, which are grouped into $100,000$ bytes.

Table 1 shows the test results of four random number generators[5]: two co-evolved CAs (one of which is that demonstrated in Figure 2c), rule 30 CA, and the rules $\{90, 150\}$ CA. We note that for all generators the entropy, serial correlation coefficient and simulated π values are satisfactory. However, the chi-square test, which is one of the most significant ones [5], reveals a different picture. Knuth suggests that at least three sequences from a generator be subjected to the chi-square test and if a majority (i.e., at least two out of three) pass then the generator is considered to have passed (with respect to chi-square). We note that the two co-evolved CAs attain good results for the chi-square test, with the other two CAs trailing behind. It is noteworthy that our co-evolved CAs attain good results on a number of tests, while the fitness measure used during

[5] The tests were conducted using a public domain software written by J. Walker, available at `http://www.fourmilab.ch/random/`.



(a) (b) (c)

Fig. 2. One-dimensional random number generators: Operation of three CAs. Grid size is $N = 50$, radius is $r = 1$. White squares represent cells in state 0, black squares represent cells in state 1. The pattern of configurations is shown through time (which increases down the page); the initial configurations were generated by randomly setting the state of each grid cell to 0 or 1 with uniform probability. Top figures depict space-time diagrams, bottom figures depict rule maps. (a) Rule 30 CA. (b) Rules $\{90, 150\}$ CA. Rules map: light gray represents rule 90, black represents rule 150. (c) A co-evolved, non-uniform CA, consisting of three rules: rule 165 (22 cells), rule 90 (22 cells), rule 150 (6 cells). Rules map: black represents rule 165, dark gray represents rule 90, light gray represents rule 150.

evolution is entropy alone. The relatively low result obtained by the rule 30 CA may be due to the fact that we considered N random sequences generated in parallel, rather than the single one considered by Wolfram (see Section 2). The rules {90,150} CA results may probably be somewhat improved (as perhaps our own results) by using "site spacing" and "time spacing" [3, 4].

5 Conclusions

We presented the cellular programming algorithm for co-evolving non-uniform CAs, and applied it to the problem of generating random number generators. While a more extensive suite of tests should be conducted, it seems safe to say at this point that our co-evolved generators are at least as good as the best available CA randomizers (see also [18]).

The evolved CAs are quasi-uniform, involving only $2-3$ rules; while rules 90 and 150 have been observed (e.g., Figure 2c), other rules have also emerged[6]. This can be advantageous from a hardware point of view since some rules lend themselves more easily to implementation using basic logic gates [3, 4]. It might also be possible to add restrictions to the evolutionary process, e.g., by pre-specifying rules for some cells, in order to further facilitate hardware implementation. Another possible modification of the evolutionary process is the incorporation of statistical measures of randomness into the fitness function (and not just as an aftermath benchmark). These possible extensions could lead to the automatic generation of high-performance, random number generators meeting specific user demands.

Evolving, non-uniform CAs hold potential for studying phenomena of interest in areas such as complex systems, artificial life and parallel computation. This work has shed light on the possibility of using such CAs as random number generators, and demonstrated the feasibility of their evolution.

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[6] One common feature of all evolved rules is the fraction of output 1 bits in the rule tables, which is exactly 0.5.

Test	co-evolved CA (1)	co-evolved CA (2)	rule 30 CA	rules {90,150} CA
Chi-square	50.00%	50.00%	90.00%	50.00%
	50.00%	75.00%	10.00%	5.00%
	90.00%	95.00%	97.50%	10.00%
	25.00%	50.00%	0.01%	75.00%
	50.00%	75.00%	95.00%	97.50%
	25.00%	75.00%	97.50%	25.00%
	75.00%	75.00%	50.00%	25.00%
	10.00%	25.00%	5.00%	25.00%
	50.00%	50.00%	25.00%	95.00%
	90.00%	90.00%	25.00%	75.00%
(% success)	100%	90%	50%	70%
Serial correlation coefficient	0.001849	-0.003904	0.000523	0.006464
	-0.003855	0.002275	-0.001752	-0.000714
	0.001923	0.000480	0.001561	0.002054
	-0.000111	-0.002366	0.004775	-0.004812
	-0.000596	0.001942	0.002137	-0.000751
Entropy	7.998185	7.998074	7.998406	7.998209
	7.998214	7.998352	7.997887	7.997877
	7.998376	7.998446	7.998487	7.997928
	7.997998	7.998060	7.997329	7.998422
	7.998079	7.998293	7.998444	7.998507
Monte Carlo π	3.12448 (0.54%)	3.12832 (0.42%)	3.13488 (0.21%)	3.12512 (0.52%)
	3.14080 (0.03%)	3.13120 (0.33%)	3.14816 (0.21%)	3.14016 (0.05%)
	3.13584 (0.18%)	3.12208 (0.62%)	3.15168 (0.32%)	3.14992 (0.27%)
	3.12752 (0.45%)	3.12640 (0.48%)	3.13008 (0.37%)	3.15392 (0.39%)
	3.14672 (0.16%)	3.13776 (0.12%)	3.12912 (0.40%)	3.11696 (0.78%)

Table 1. Results of tests. Each entry represents the test result for a sequence of $100,000$ bytes generated by the corresponding randomizer (see text). 10 sequences were generated by each randomizer; the table lists the chi-square test results for all 10 sequences and the first 5 results for the other tests. CA Grid size is $N = 50$. Co-evolved CA (1) consists of three rules: rule 165 (22 cells), rule 90 (22 cells), and rule 150 (6 cells); co-evolved CA (2) consists of two rules: rule 165 (45 cells) and rule 225 (5 cells). Interpretation of the listed values is as follows (for a full explanation see [5]): (i) For the chi-square test "good" results are between $10\% - 90\%$, with extremities on both sides (i.e., $< 10\%$ and $> 90\%$) representing non-satisfactory random sequences. The percentage of sequences passing the chi-square test is also listed in the table. (ii) The serial correlation coefficient should be close to zero. (iii) Entropy should be close to 8. (iv) The random number sequence is used in a Monte Carlo computation of the value of π; the final value is shown along with the error percentage in parenthesis.

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