Modeling Selection Intensity for Toroidal Cellular Evolutionary Algorithms

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Abstract. We present quantitative models for the selection pressure of cellular evolutionary algorithms structured in two dimensional regular lattices. We derive models based on probabilistic difference equations for synchronous and several asynchronous cell update policies. Theoretical results are in agreement with experimental values and show that the selection intensity can be controlled by using different update methods.

1 Introduction

Cellular evolutionary algorithms (cEAs) use populations that are structured according to a lattice topology. The structure may be an arbitrary graph, but more commonly it is a one-dimensional or two-dimensional grid. This kind of evolutionary algorithm has become popular because it is easy to implement on parallel hardware. However, what really matters is the model, not its implementation. Thus, in this work we will focus on cEA models and on their properties without worrying about implementation issues.

Several results have appeared on selection pressure and convergence speed in cEAs. Sarma and De Jong performed empirical analyses of the dynamical behavior of cellular genetic algorithms (cGAs) [8, 9], focusing on the effect that the local selection method, the neighborhood size, and neighborhood shape have on the global induced selection pressure. Rudolph and Sprave [7] have shown how cGAs can be modeled by a probabilistic automata network and have provided proofs of complete convergence to a global optimum based on Markov chain analysis for a model including a fitness threshold. Recently, Giacobini *et al.* [2] have successfully modeled the selection pressure curves in cEAs on one-dimensional ring structures, and a preliminary study of two-dimensional, torus-shaped grids has appeared in [1].

Our purpose here is to investigate in detail selection pressure in two-dimensional population structures for two kinds of dynamical systems: synchronous and asynchronous. For that purpose, we model the experimentally observed takeover-time curves with simple difference equations describing the propagation of the best individual under probabilistic conditions.

The paper proceeds as follows. In section 2 we briefly describe synchronous and asynchronous cEAs. Section 3 introduces the concept of takeover time. In sections 4 and 5 we describe our mathematical models for synchronous and asynchronous updates. Theoretical predictions are compared with experimental results in section 6, and section 7 gives our conclusions.

2 Synchronous and Asynchronous cEAs

We consider cEAs defined on a square lattice of finite size $n \times n$. Let us call S the (finite) set of states that a cell (individual) can take up: this is the set of points in the (discrete) search space of the problem. The set N_i is the set of neighbors of a given cell i, and let $|N_i| = N$ be its size. The local transition function $\phi(\cdot)$ can then be defined as:

$$\phi : S^N \rightarrow S$$

which maps the state $s_i \in S$ of a given cell i into another state from S, as a function of the states of the N cells in the neighborhood N_i. The neighborhood we consider in this paper is the so-called von Neumann neighborhood, also called linear5, which is constituted by a central cell and the four first neighbor cells in the directions north, east, south, and west, and $|N_i| = 5$. Thus, the implicit form of the stochastic transition function $\phi(\cdot)$ is:

$$\phi(\cdot) = P\{x_i(t+1) \ \mid \ x_j(t) \in N_i\}$$

where P is the conditional probability that cell x_i will assume at the next time step $t + 1$ a certain value from the set S, given the current (time t) values of the states of all the cells in the neighborhood. We are thus dealing with probabilistic automata, and the set S should be seen as a set of values of a random variable. The probability P will be a function of the particular selection and variation methods; that is, it will depend on the genetic operators. In this paper we model cEAs using two particular selection methods: binary tournament and linear ranking, but the same framework could easily be extended to other selection strategies.

A cEA starts with the cells in a random state and proceeds by successively updating them using evolutionary operators, until a termination condition is met. Updating a cell in a cellular EA means selecting two parents in the individual's neighborhood, applying genetic operators to them, and finally replacing the individual if an offspring has a better fitness (different replacement policies can be used). Cells can be updated *synchronously* or *asynchronously*. In the synchronous case all the cells change their states simultaneously, while in the asynchronous case cells are updated one at a time in some order. There are many ways for sequentially updating the cells of a cEA. We consider four commonly used asynchronous update methods [10]:

- In *fixed line sweep* (LS), the n cells are updated sequentially from left to right and line after line starting from the upper left corner cell.

- In *fixed random sweep* (FRS), the next cell to be updated is chosen with uniform probability without replacement; this will produce a certain update sequence $(c_1^j, c_2^k, \ldots, c_n^m)$, where c_q^p means that cell number p is updated at time q and $(j, k, \ldots, m)$ is a permutation of the n cells. The same permutation is then used for all update cycles.
- The *new random sweep* method (NRS) works like FRS, except that a new random cell permutation is used for each sweep through the array.
- In *uniform choice* (UC), the next cell to be updated is chosen at random with uniform probability and with replacement. This corresponds to a binomial distribution for the updating probability.

A *time step* is defined as updating n times sequentially, which corresponds to updating *all* the n cells in the grid for LS, FRS and NRS, and possibly less than n different cells in the uniform choice method, since some cells might be updated more than once.

3 Takeover Time

The *takeover time* is defined as being the time it takes for a single best individual to take over the entire population. It can be estimated experimentally by measuring the propagation of the proportion of the best individual under the effect of selection only, without any variation operator. Shorter takeover times indicate a higher selection pressure, and thus a more exploitative algorithm. By lowering the selection intensity the algorithm becomes more explorative. Theoretical takeover times have been derived by Deb and Goldberg [3] for panmictic populations and for the standard selection methods. These times turn out to be logarithmic in the population size, except in the case of proportional selection, which is a factor of n slower, where n is the population size.

It has been empirically shown in [8] that as we move from a panmictic to a square grid population of the same size with synchronous updating of the cells, the selection pressure induced on the entire population is weaker.

A study on the selection pressure in the case of ring and array topologies in one dimensional cEAs has been done by Rudolph [6]. Abstracting from specific selection methods, he splits the selection procedure into two stages: in the first stage an individual is chosen in the neighborhood of each individual, and then, in the second stage, for each individual it is decided whether the previously chosen individual will replace it in the next time step. Using only replacement methods in which extinction of the best by chance cannot happen, i.e. non-extinctive selection, Rudolph derives the expected takeover times for the two topologies as a function of the population size and the probability that in the selection step the individual with the best fitness is selected in the neighborhood. This study has been followed by Giacobini *et al.* investigation of the asynchronous cases for the ring topology [2].

In the present paper we study in detail the two-dimensional case for both the synchronous and the asynchronous cell update mode. In the next section we introduce quantitative models for the growth of the best individual in the form of difference stochastic equations.

4 Models

Let us consider the random variables $V_i(t) \in \{0,1\}$ indicating the presence in cell $i\,(1 \leq i \leq n)$ of a copy of the best individual ($V_i(t) = 1$) or of a worse one ($V_i(t) = 0$) at time step t, where n is the the population size. The random variable

$$N(t) = \sum_{i=1}^{n} V_i(t)$$

denotes the number of copies of the best individual in the population at time step t. Initially $V_i(1) = 1$ for some individual i, and $V_j(1) = 0$ for all $j \neq i$.

Following Rudolph's definition [6], if the selection mechanism is non-extinctive, the expectation $E[T]$ with $T = \min\{t \geq 1 : N(t) = n\}$ is called the takeover time of the selection method. In the case of spatially structured populations the quantity $E_i[T]$, denoting the takeover time if cell i contains the best individual at time step 1, is termed the takeover time with initial cell i. Assuming a uniformly distributed emergence of the best individual among all cells, the takeover time is therefore given by

$$E[T] = \frac{1}{n} \sum_{i=1}^{n} E_i[T]$$

In the following sections we give the recurrences describing the growth of the random variable $N(t)$ in a cEA with torus topology for the synchronous and the four asynchronous update policies described in Section 2. We consider a non-extinctive selection mechanism that selects the best individual in a given neighborhood with probability $p \in (0,1)$.

5 Torus Structure

Sarma and De Jong [8] proposed a simple quantitative model for the study of the selection pressure curves for cEAs. They assumed that the diffusion of the best individual in the artificial evolution of a torus-structured population would follow a logistic curve. As suggested by Gorges-Schleuter in [4], in the artificial evolution of locally interacting, spatially structured populations, the assumption of a logistic growth doesn't hold anymore, if the local neighborhood is small enough. In fact, for a torus structure we have a quadratic growth. We complete here her analysis which holds for deterministic unrestricted growth, extending it to finite-size synchronously and asynchronously updated spatial populations using probabilistic selection.

As derived in [1], for a structured population let us consider the limiting case, which represents an upper bound on growth rate, in which the selection mechanism is deterministic, and a cell always chooses its best neighbor for updating.

In the case of a population of size n disposed on a torus grid of size $\sqrt{n} \times \sqrt{n}$ (assuming $\sqrt{n}$ odd) and the von Neumann neighborhood structure, the number of copies of the best individual can be described by the following recurrence:

$$\begin{cases} N(0) = 1 \\ N(t) = N(t-1) + 4t & , \ for\ 0 \leq t \leq \frac{\sqrt{n}-1}{2} \\ N(t) = N(t-1) + 4(\sqrt{n} - t) \ , & for\ t > \frac{\sqrt{n}-1}{2} \end{cases}$$

This growth is described by a convex quadratic equation followed by a concave one, as the two closed forms of the recurrence clearly show:

$$\begin{cases} N(t) = 2t^2 + 2t + 1 & , \ for\ 0 \leq t \leq \frac{\sqrt{n}-1}{2} \\ N(t) = -2t^2 + 2(2\sqrt{n} - 1)t + 2\sqrt{n} - n \ , & for\ t > \frac{\sqrt{n}-1}{2} \end{cases}$$

The described case of a deterministic growth of the number of copies of the best individual is shown in figure 1 in the case of a population of 81 individuals disposed on a 9 × 9 torus structure.

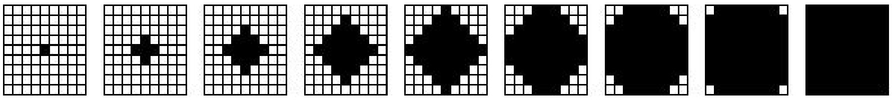


Fig. 1. Example of a deterministic growth of $N(t)$ for a population of 81 individuals on a 9 × 9 torus structure

Thus, a more accurate model should take into account a non-exponential quadratic growth followed by a quadratic saturation (crowding effect).

In the following sub-sections we will present models for the synchronous and the four asynchronous updates. To keep the models mathematically simple and understandable, some approximations have been made. We will see that the resulting recurrences still fit the experimental curves quite well.

In the limiting case the time t in the recurrences determines the measure of the half diagonal of the 45 degrees rotated square (see figure 1) containing the $N(t)$ copies of the best individual. Since we want to model probabilistic selection mechanisms, we can approximate the measures of the side s and the half diagonal d of the 45 degrees rotated square in the following way:

$$s = \sqrt{N(t)}, \quad d = \frac{\sqrt{N(t)}}{\sqrt{2}}$$

5.1 Synchronous Takeover Time

Let us consider the growth of such a region with a selection mechanism of probabilities p_1, p_2, p_3, p_4 and p_5 of selecting the best individual when there are respectively 1, 2, 3, 4 and 5 copies of it in the neighborhhod.

Assuming that the region containing the copies of the best individual expands keeping the shape of a 45 degrees rotated square, we can model the growth of $N(t)$ with the following recurrence:

$$\begin{cases} N(0) = 1 \\ N(t) = N(t-1) + 4p_2\frac{\sqrt{N(t-1)}}{\sqrt{2}} & , \quad for\ N(t) \le \frac{n}{2} \\ N(t) = N(t-1) + 4p_2\sqrt{n - N(t-1)} & , \quad for\ N(t) > \frac{n}{2} \end{cases}$$

5.2 Asynchronous Fixed Line Sweep Takeover Time

This update method, that is meaningful in a ring topology, in the case of a toroidal topology can be criticized. In fact, there is no biological parallel for this update mechanism. A precise model for such update would be very complicated, since it is difficult to approximate the shape of the region containing the copies of the best individual. We have therefore decided, to keep the model simple and understandable, to roughly approximate the shape of the region with a square stretched to the south-east direction, growing with probability p_1 on the north-east side, p_2 on the south-east side, and p_1 in the south direction.

Let us suppose that in any line the cells containing a copy of the best individual at time step t have index r to s. In the next time step, the cell $r-1$ will contain a copy of the best individual with probability p, while the cells $s+j$ (with $j = 1, \ldots, n-s$) will contain a copy of the best individual with probability p^j. The number of copies of the best individual in the considered line in the next time step is

$$p + \sum_{i=1}^{\sqrt{n}-j} p^i$$

For large n we can approximate this quantity by the limit $(2p - p^2)/(1-p)$. Therefore, we can model the growth of $N(t)$ with the following recurrence:

$$\begin{cases} N(0) = 1 \\ N(t) = N(t-1) + \left(\frac{2p_2-p_2^2}{1-p_2} + 2\frac{2p_1-p_1^2}{1-p_1}\right)\sqrt{N(t-1)} & , \quad for\ N(t) \le \frac{n}{2} \\ N(t) = N(t-1) + \left(\frac{2p_2-p_2^2}{1-p_2} + 2\frac{2p_1-p_1^2}{1-p_1}\right)\sqrt{n - N(t-1)} & , \quad for\ N(t) > \frac{n}{2} \end{cases}$$

5.3 Asynchronous Fixed and New Random Sweep Takeover Time

The behaviors of fixed random sweep and new random sweep averaged over all possible permutations of grid individuals are equivalent. We therefore give only one model describing the growth of the random variable $N(t)$ for both policies.

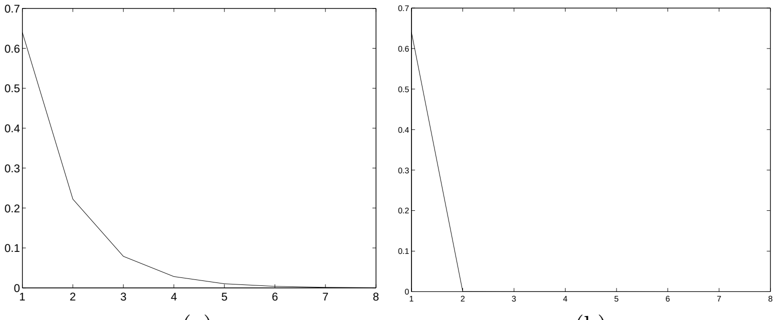
In a time step the probability of one individual on the border of the region being taken over by the best is p_2, while an individual at distance 2 from the region can be replaced by the best if one or two of its neighbors have already been replaced during the sweep. One of its neighbors is replaced if

- only one neighbor comes before in the sweep (and it has been replaced)
- two neighbors come before in the sweep but just one has been replaced

Two of its neighbors are replaced if both come before in the sweep and both have been replaced. The average probability of an individual of being before another in a sweep is 1/2, therefore an individual at distance 2 from the region is replaced with probability

$$2\left(\frac{1}{2}\left(1-\frac{1}{2}\right)p_2p_1\right)+2\left(\frac{1}{2}\frac{1}{2}p_2(1-p_2)p_2\right)+\frac{1}{2}\frac{1}{2}p_2^2p_2 = p_2p_1+\frac{1}{4}(p_2-2p_1)p_2^2$$

At distance 3 or more the same reasoning can be done, but we have decided to model the growth up to distance 2 because, as it can been seen in figure 2, the probability at distances ≥ 3 become very small.



(a) (b)

Fig. 2. Probability of an individual being replaced by a copy of the best individual (y axis) with respect to distance (x axis) from the region formed by copies of the best for asynchronous (a) Fixed Random Sweep and (b) Uniform Choice.

Thus, we can model the growth of $N(t)$ with the following recurrence:

$$\begin{cases} N(0)=1 \\ N(t)=N(t-1)+4\left(p_2p_1+\frac{1}{4}(p_2-2p_1)p_2^2\right)\left(\sqrt{N(t-1)}-1\right)+4p_1, \\ \hfill for\ N(t)\leq\frac{n}{2} \\ N(t)=N(t-1)+4\left(p_2p_1+\frac{1}{4}(p_2-2p_1)p_2^2\right)\left(\sqrt{n-N(t-1)}-1\right)+8p_3, \\ \hfill for\ N(t)>\frac{n}{2} \end{cases}$$

5.4 Asynchronous Uniform Choice Takeover Time

The ways in which an individual can be replaced in a time step for this update case are the same as for fixed and new random sweep (see above). In the present case, the average probability of an individual coming before another in a time step is $1/n$, therefore an individual at distance 2 from the region is replaced with probability

$$\frac{1}{n}p_2p_1 + \frac{1}{n^2}(p_2 - 2p_1)p_2^2$$

The probability is already very small at distance 2 (see figure 2). Thus, in our model we only take into account individuals at distance 1 from the region.

In terms of time steps, the growth of $N(t)$ can be modeled with the following recurrence:

$$\begin{cases} N(0) = 1 \\ N(t) = N(t-1) + 4p_2\sqrt{N(t-1)} & , \quad for\ N(t) \leq \frac{n}{2} \\ N(t) = N(t-1) + 4p_2(\sqrt{n - N(t-1)} - 1) + 8p_3 & , \quad for\ N(t) > \frac{n}{2} \end{cases}$$

6 Empirical Results

Since cEAs are good candidates for using selection methods that are easily extensible to small local pools, we use binary tournament and linear ranking in our experiments. Fitness-proportionate selection could also be used but it suffers from stochastic errors in small populations, and it is more difficult to model since it requires knowledge of the fitness distribution. The cEA structure has torus topology of size 32 × 32 with von Neumann neighborhood. Only the selection operator is active: for each cell it selects one individual in the cell neighborhood, and the selected individual replaces the old individual only if it has a better fitness.

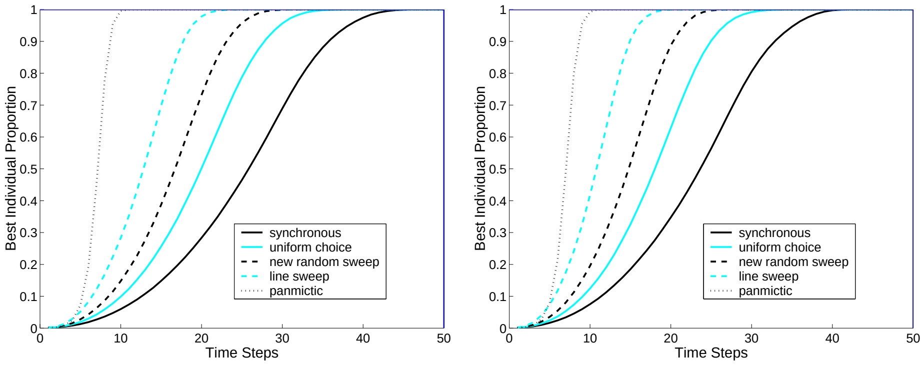
6.1 Binary Tournament Selection

We have used the binary tournament selection mechanism described by Rudolph [6]: two individuals are randomly chosen with replacement in the neighborhood of a given cell, and the one with the better fitness is selected for the replacement phase.

Figure 3 shows the growth curves of the best individual for the panmictic, the synchronous and three asynchronous update methods. In all cases the same set of parameters has been used. The mean curves for the two asynchronous methods, fixed and new random sweep, show a very similar behavior, so we have decided to plot only the new random sweep results. The graph shows that the asynchronous update methods give an emergent selection pressure greater than that of the synchronous case, growing from the uniform choice to the line sweep, with the fixed random sweep in between.

The numerical values of the mean takeover times for the five update methods, together with their standard deviations are shown in Table 1, where it can be seen that the fixed random sweep and new random sweep methods give results that are statistically indistinguishable.

Since we use a von Neumann neighborhood, the probabilities p_1, p_2 and p_3 of selecting the best individual when there are respectively 1, 2 and 3 copies



(a) (b)

Fig. 3. Takeover times with (a) binary tournament selection, and (b) linear ranking. Mean values over 100 runs. The vertical axis represents the number of copies $N(t)$ of the best individual in each population as a function of the time step t.

	Synchro	LS	FRS	NRS	UC
Mean Takeover Time	44.06	21.8	27.21	28.26	35.73
Standard Deviation	1.6746	1.7581	1.5654	1.8996	2.4489

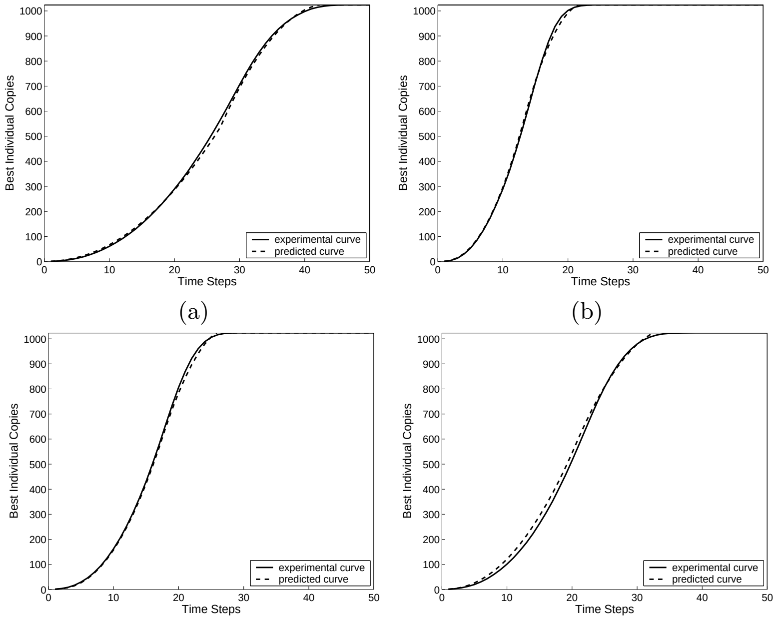
Table 1. Mean takeover time and standard deviation of the binary tournament selection for the five update methods. Mean values over 50 independent runs.

of it in the neighborhhod are respectively 9/25, 6/25 and 21/25. Using these probabilities in the models, we calculated the theoretical growth curves. Figure 4 shows the predicted and the experimental curves for the five update methods.

6.2 Linear Ranking Selection

We have used a standard linear ranking selection mechanism. The five individuals in the neighborhood of a considered cell are ranked according to their fitnesses: each individual then has probability $2(s-i)/(s(s-1))$ to be selected for the replacement phase, where s is the number of cells in the neighborhood ($s = 5$ in our case) and i is its rank in the neighborhood.

Figure 3 shows the growth curves of the best individual for the panmictic, the synchronous and three asynchronous update methods, using the same parameter set in all cases. We can observe in the linear ranking case the same behavior that emerged in the binary tournament case: the mean curves for the two asynchronous updates, fixed and new random sweep, show a very similar behavior. We have therefore decided to plot only the new random sweep results. The graph shows that the asynchronous update methods give an emergent selection pressure greater than that of synchronous one, growing from the uniform choice to the line sweep, with the fixed renadom sweep in between. The numerical values of the mean takeover times for the five update methods, together with



(a) (b) (c) (d)

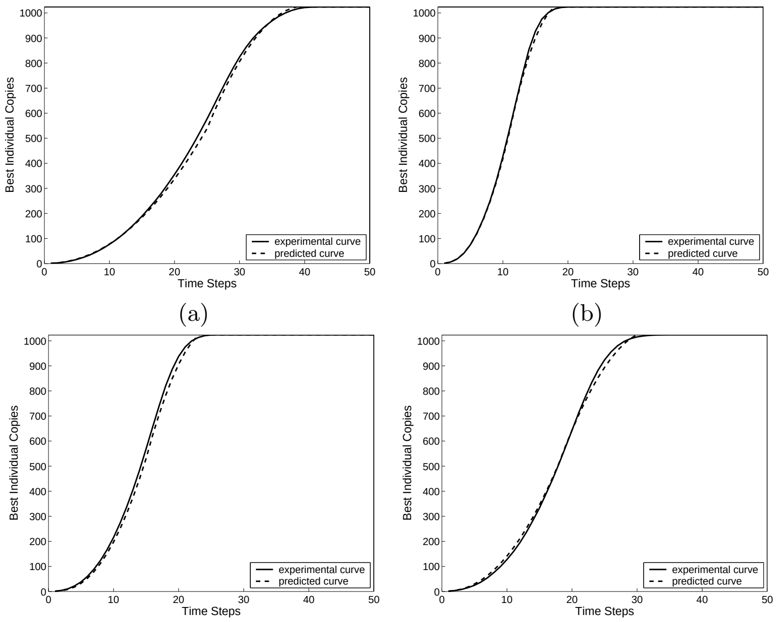
Fig. 4. Comparison of the experimental takeover time curves (full) with the model (dashed) in the case of binary tournament selection for four update methods: synchronous (a), asynchronous line sweep (b), asynchronous fixed random sweep (c), uniform choice (d).

their standard deviations are shown in Table 2. Again, the results show that the two random sweep methods are statistically equivalent.

	Synchro	LS	FRS	NRS	UC
Mean Takeover Time	40.68	18.2	23.96	24.89	32.16
Standard Deviation	1.2703	1.633	1.4766	1.4626	2.3856

Table 2. Mean takeover time and standard deviation of the linear ranking selection for the five update methods. Mean values over 50 independent runs.

Since we use a von Neumann neighborhood, the probabilities p_1, p_2 and p_3 of selecting the best individual when there are respectively 1, 2 and 3 copies of it in the neighborhhod are respectively 2/5, 7/10 and 9/10. Using these probabilities in the models, we calculated the theoretical growth curves. Figure 5 shows the predicted and the experimental curves for the five update methods. The agreement between theory and experiment is very good.



(a) (b) (c) (d)

Fig. 5. Comparison of the experimental takeover time curves (full) with the model (dashed) in the case of linear ranking selection for four update methods: synchronous (a), asynchronous line sweep (b), asynchronous fixed random sweep (c), uniform choice (d).

7 Conclusions and Future Work

We have presented quantitative models describing the growth of a single best individual in cellular evolutionary algorithms structured as a torus with von Neumann neighborhood. New results have been obtained for synchronous and some asynchronous cell update policies. The models are given as probabilistic recurrence equations. We have studied two types of selection mechanisms that are commonly used in cEAs: binary tournament and linear ranking. With these selection methods, our results show that there is a good agreement between theory and experiment; in particular, we confirmed that asynchronous cell update methods give rise to different global selection intensity. This should allow the control of selection pressure in an easy and principled way, without using *ad hoc* parameters.

In the future, we intend to extend this type of analysis to larger neighborhoods, and to more complex topologies such as general graph structures, including random graphs. Moreover, we intend to investigate Markov chain modeling of our system and the relationships that may exist with probabilistic particle systems such as voter models [5].

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