

# Non-local Evolutionary Adaptation in Gridplants

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**Abstract**—A simulated model of plant growth and evolution was studied. Plants start out as seeds on a 2-dimensional grid. Plant genomes are modeled as instructions telling a plant where to grow and where to place seeds. Energy is gained by occupying grid space in analogy to collection of light by leaf surface area. At the end of a generation, cells currently occupied by plants are cleared and the seeds dropped by all the plants sprout to become the new plants. Each seed produced has a probability of mutation to the genome it contains. The simulated plants evolve to play a game of competitive exclusion, in which grid space is a limited resource.

This paper tested the hypothesis that the evolved plants would display nonlocal adaptation, i.e. that the plants would not only adapt to their local environment, but would acquire general skill that would enable them to grow competitively against plants that were never a part of their environment. Statistical tests show that populations of plants that have evolved for a larger number of generations are able to occupy more grid space when played against populations of plants evolved for a shorter time. This occurs even if the two competing populations come from entirely different lineages. This improvement in competitive ability continues over the course of the evolution performed in this study, without appearing to reach an equilibrium after which further evolution fails to improve the plants. This suggests that the plants are continually discovering generally useful strategies, rather than adapting only to their local environment.

## I. INTRODUCTION

Orthodox evolutionary biology teaches that organisms develop specialized skills to cope with only their local environments. This view is sensible and consistent with the observation that many organisms are well adapted to their local environment. Cockburn [1] stated

It is widely believed that habitat specialization will arise because a jack of all trades is a master of none.

This view is not universally held, however. Dawkins [2] conjectured that

if, by the medium of a time machine, predators from one era could meet prey from another era, the later, more ‘modern’ animals, whether predators or prey, would run rings around the earlier ones. This is not an experiment that can ever be done...

In other words, genomes would retain adaptive skills that confer advantage over other organisms, even when the latter organisms are long since dead. This is contrary to the view that genomes adapt only to their local environments, which contain only living organisms.

An experiment using biological organisms cannot be done, since the timescale over which evolution operates is far too long. We use an evolutionary algorithm to simulate biological evolution and provide an environment in which experimental parameters may be precisely controlled. This experiment provides evidence in favor of the latter view above, that more evolved organisms will “run circles around” less evolved organisms in a coevolutionary system. Rather than a predator-prey model, we study a model of plant growth. However, the two are special cases of a coevolutionary system, which is an evolutionary system in which the fitness of an one organism depends on other organisms, which are themselves evolving.

This experiment was designed to detect *non-local adaptation*. Non-local adaptation refers to the tendency of evolving organisms to evolve generally useful abilities that allow them to compete in environments different from those in which they evolved. The technique for documenting such non-local adaptation is to place organisms from entirely distinct lineages

into competition and examine the impact of additional evolutionary time. The times from which organisms are drawn for comparison are all well after population average fitnesses cease to increase rapidly. As a result comparisons are between roughly equally fit groups of organisms, according to the fitness function used to drive evolution. Non-local adaptation is related to the *red queen effect* [2]. This effect appears in coevolutionary systems in which the fitness (as measured by reproductive success) of coevolving organisms stays roughly constant across evolutionary time, even though the organisms are becoming increasingly more adapted to each other. The difference between non-local adaptation and the red queen effect is that non-local adaptation postulates that organisms will become increasingly adapted not only to the other organisms with which they are coevolving, but will develop adaptive abilities that will allow them to outperform less evolved organisms in general.

Past studies [3], [4] have shown a form of general adaptation of data structures undergoing evolution in an evolutionary algorithm. These past studies worked with finite state machines playing the iterated prisoner’s dilemma and in populations of simulated robots competitively painting a grid in two colors. In both these studies the organisms gained general skill at competitive tasks rather than adapting only to their local environment.

This study provides an additional example of general adaptation in simulated plants called *gridplants*. It is demonstrated that a population of gridplants that has evolved for a significantly higher number of generations are able to occupy more board space than a less evolved population when the two are placed in the same environment and allowed to grow for a number of generations. The simulations presented here also moved closer to biology in that there is no explicit fitness function. Plants grow and make seeds which later sprout. Fitness is, implicitly, the number of offspring an organism has. When we are making comparisons to detect non-local adaptation the degree to which a given population of simulated plants is dominant is determined by their numbers in the simulated ecosystem.

## II. GRIDPLANTS

### A. Description

Gridplants are simulated models of plants that live on a 2-dimensional toroidal grid. The grid is toroidal in that a cell on the edge of the grid is adjacent

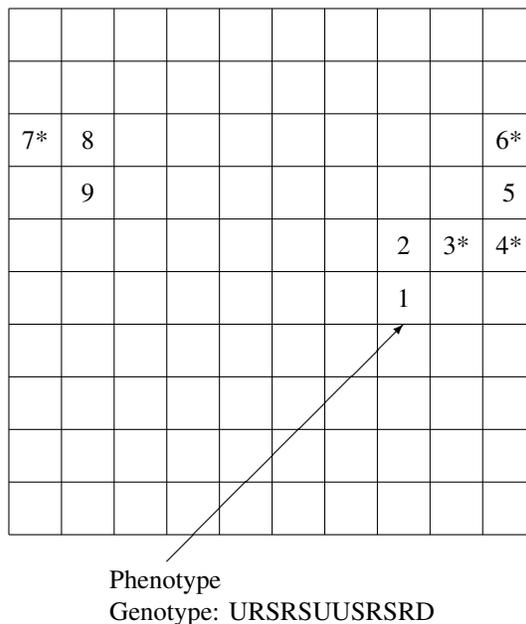


Fig. 1. Example of a gridplant genotype and its corresponding phenotype. The plant starts as a seed in the position marked “1” and grows. Each grid cell occupied contains a number representing the order in which the plant occupied the cell. Cells with a \* had a seed planted at that position.

to the cell on the opposite edge of the grid. Each plant has a genome consisting of a string drawn from the alphabet  $\{U, D, L, R, S\}$ . The characters of the genome represent instructions that direct the plant to grow up (*U*), down (*D*), left (*L*), right (*R*), or to plant a seed (*S*). Since the plant may occupy several grid cells, it has a “tip”, from which growth and seed planting occur. When the plant grows into a new cell, the tip moves into that cell. When the plant drops a seed, the tip stays on the current cell. A plant may not grow to occupy a cell that is already occupied. Fig. 1 shows an example of a gridplant genome and the plant it creates when the genome instructions are followed.

Evolution of the plants consists of a series of generations. At the end of a generation, all plants die, and the cells they occupied become available again. Every seed that was planted, in turn, sprouts to become a new one-cell plant occupying the same cell that the seed did. Each seed has a fixed probability of actually sprouting into a plant (this is termed the *seed survival rate*), and a fixed percentage of the seeds undergo one-point mutation of their genomes (this is the *seed mutation rate*).

Each generation, in turn, consists of a series of

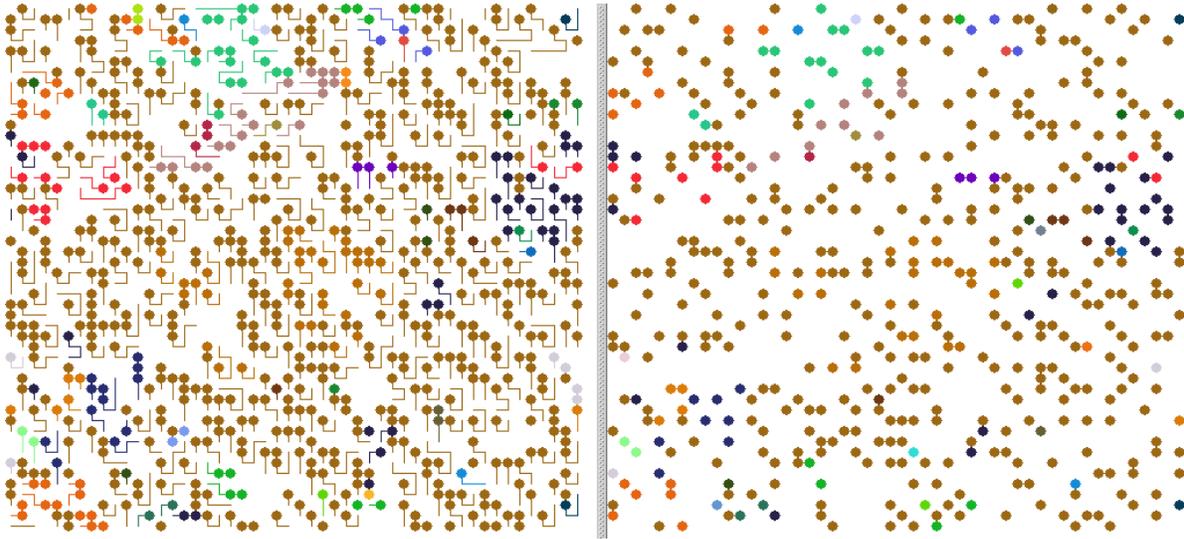


Fig. 2. Two views of a 50 x 50 grid. The cells that the plants occupy are shown on the left. The cell where each plant started is shown with a circle, and its growth is traced out by a line starting at the circle. The seeds planted thus far are shown on the right. Each plant's color (or shade of gray if viewed in grayscale) is determined by its genome, so two different plants with the same genome will have the same color. Since the grid is toroidal, plants that grow past the border appear on the other side of the grid.

iterations, where each plant may execute one action per iteration. In addition to the instructions of the genome (the actions  $U$ ,  $D$ ,  $L$ ,  $R$ , and  $S$ ), the act of reading the genome to determine what instruction to perform next is itself an action, denoted as the action  $READ$ . Each action, including the reading of the genome, costs energy. Plants start out the generation with a fixed amount of energy, and they gain energy at the beginning of each iteration in proportion to the amount of grid space that they occupy. A picture of an example grid in the middle of a generation is shown in fig 2.

Each plant starts the generation occupying a single grid square. The plants are then processed to determine what action they will attempt that iteration. The order in which the plants are processed is random. If this were not the case, for example, if the plants were processed left-to-right, top-to-bottom, in the order in which they appear on the grid, then plants in the upper left corner would be given an unfair advantage in growing, since they would always have first opportunity to occupy cells. Randomization ensures that no plants will be given a growing advantage due to an artifact of the program implementation.

Each plant has an action scheduled for execution at the beginning of each iteration. The scheduled action is  $READ$  on the first iteration and on any

iteration immediately after a growth or seed action was executed. If the plant reads its genome on the last iteration, then its scheduled action is whatever instruction it read from the genome. If the plant does not have enough energy to do execute its current action, it takes no action during the current iteration and uses no energy. If there is sufficient energy to execute the current action, but the current action is impossible, the plant skips that action (so that the next instruction read will be the following), takes no action during the current iteration, and uses no energy. The two impossible actions are

- 1) growing into an already occupied cell
- 2) planting a seed twice in the same location

### B. Formal Specification

The following pseudo-code fully details the process by which plants evolve. `EVOLVE-GRIDPLANTS` is the top-level procedure that is called. It is assumed that the following global variables and procedures are available to all procedures:

- 1) `grid[i, j]` is a grid coordinate, marked as either `OCCUPIED` or `UNOCCUPIED`. The coordinate system is the same as that used to index a matrix:  $(i, j)$  is the  $i^{\text{th}}$  row and  $j^{\text{th}}$  column of the grid (indexing begins at 1).
- 2) `seed-pos[s]` is the  $(i, j)$  position of the seed  $s$  in the grid

- 3) `plant-pos[p]` is the position of the *tip* of the plant  $p$  in the grid
- 4) `energy[p]` is the current energy of the plant  $p$
- 5) `cur-action[p]` is the current pending action to be executed by plant  $p$
- 6) `genome-pos[p]` is a pointer to the current position being read from the genome of  $p$
- 7) `seeds` is a list of all the seeds that have been planted in the current iteration
- 8) `plants` is a list of all the plants currently growing on the grid
- 9) `RAND-INT( $a, b$ )` randomly generates an integer uniformly in the range  $[a, b]$
- 10) `RAND-FLOAT( $a, b$ )` randomly generates a real number uniformly in the range  $[a, b]$
- 11) `LIST-ADD( $L, x$ )` adds object  $x$  to the end of list  $L$ .

$p[i]$  is interpreted to mean the  $i^{\text{th}}$  instruction in the genome of plant  $p$ , so that  $p[\text{genome-pos}[p]]$  indicates the next instruction to be executed by plant  $p$ . If  $p$  is a plant and  $s$  is a seed,  $p \leftarrow s$  is interpreted to mean, “create a plant  $p$  and assign its genome to be that of the seed  $s$ ”.  $s \leftarrow p$  is interpreted to mean, “create a seed  $s$  and assign its genome to be that of the plant  $p$ ”.

Additionally, the following global constants and procedures are assumed to be defined. The particular value for each used in this experiment is given.

- 1)  $w_g = 100$  is the width of the grid in cells
- 2)  $h_g = 100$  is the height of the grid in cells
- 3)  $r_s = 0.9$  is the seed survival rate
- 4)  $r_m = 0.01$  is the seed mutation rate
- 5) `cost[ $a$ ]` is the energy required to execute action  $a$ . In this experiment these constants were:

- a) `cost[READ] = 1`
- b) `cost[U] = 3`
- c) `cost[D] = 3`
- d) `cost[L] = 3`
- e) `cost[R] = 3`
- f) `cost[S] = 10`

- 6)  $E_i = 4$  is the initial energy of each plant
- 7)  $L_s = 40$  is the generation length (number of iterations per generation)
- 8)  $L_g = 20$  is the genome length. In this experiment, the generation length guarantees that the end of the genome will not be reached before the generation is finished, since each execution of a genome instruction requires two iterations (one to read the genome and one to execute the instruction).

- 9) `ENERGY` is a procedure that calculates the energy added to a plant at the beginning of one iteration. In this experiment, if the number of cells a plant  $p$  occupies is  $n$ , then  $\text{ENERGY}(p) = n - 1$ .

Many of these parameters were picked somewhat arbitrarily. The reasoning behind the initial energy and incremental energy function was based on the following observation. Suppose that gridplants are able to plant a seed in the place where they start growing. Suppose then that somehow the grid became completely occupied by seeds. Then no gridplant would have incentive to attempt to grow before planting a seed. Any gridplant that did mutate to a genome that did not plant a seed immediately would die off, because there would be nowhere for it to grow, and it would not pass along its genome.

Hence, in an environment in which the board is fully occupied, the strategy “plant a seed immediately before growing anywhere” is an evolutionarily stable strategy [7]. Intuitively, this means that such a population cannot be invaded by a genome that does not plant a seed immediately before growing anywhere. Hence, there will be no selection pressure on any loci after the first “seed” instruction, and no evolution by natural selection will occur.

In order to prevent this situation, the energy values were set in order to give the gridplants an incentive to grow before planting their first seed. By receiving  $n - 1$  incremental energy each iteration, no gridplant gains energy unless it occupies at least two cells. 4 energy units (the initial energy) is the minimum energy needed to grow from one to two cells (1 to read the genome instruction, 3 to grow in some direction).

#### EVOLVE-GRIDPLANTS

```

1   $s \leftarrow$  random seed genome of length  $L_g$ 
2   $seeds \leftarrow \langle s \rangle$  ▷ singleton list of seeds
3   $h \leftarrow$  RAND-INT(1,  $h_g$ )
4   $w \leftarrow$  RAND-INT(1,  $w_g$ )
5   $seed\text{-}pos[s] \leftarrow (h, w)$ 
6  for  $generation \leftarrow 1, 2, \dots$ 
7      do SPROUT
8          for  $i \leftarrow 1$  to  $L_s$ 
9              do GROW

```

## GROW

```
1 randomly permute order of plants
2 for each plant  $p \in plants$ 
3   do energy[ $p$ ]  $\leftarrow$  energy[ $p$ ] + ENERGY( $p$ )
4    $c \leftarrow$  cost[cur-action[ $p$ ]]
5   if energy[ $p$ ]  $\geq c$ 
6     then if EXECUTE-ACTION( $p$ )
7       then energy[ $p$ ]  $\leftarrow$  energy[ $p$ ] -  $c$ 
```

## SPROUT

```
1 for  $i \leftarrow 1$  to  $h_g$ 
2   do for  $j \leftarrow 1$  to  $w_g$ 
3     do grid[ $i, j$ ]  $\leftarrow$  UNOCCUPIED
4    $plants \leftarrow \langle \rangle$   $\triangleright$  empty list of plants
5   for each seed  $s \in seeds$ 
6     do if RAND-FLOAT(0, 1)  $> r_s$ 
7       then  $p \leftarrow s$ 
8         cur-action[ $p$ ]  $\leftarrow$  READ
9         if RAND-FLOAT(0, 1)  $< r_m$ 
10           then MUTATE( $p$ )
11         LIST-ADD( $plants, p$ )
12         plant-pos[ $p$ ]  $\leftarrow$  seed-pos[ $s$ ]
13         grid[plant-pos[ $p$ ]]  $\leftarrow$  OCCUPIED
14         energy[ $p$ ]  $\leftarrow E_i$ 
15         genome-pos[ $p$ ]  $\leftarrow 1$ 
16    $seeds \leftarrow \langle \rangle$   $\triangleright$  empty list of seeds
```

## MUTATE( $p$ )

```
1  $i \leftarrow$  RAND-INT(1,  $L_g$ )
2  $p[i] \leftarrow$  random action from  $\{U, D, L, R, S\}$ 
```

## EXECUTE-ACTION( $p$ )

```
1  $act \leftarrow$  cur-action[ $p$ ]
2 if  $act =$  READ
3   then cur-action[ $p$ ]  $\leftarrow p$ [genome-pos[ $p$ ]]
4   genome-pos[ $p$ ]  $\leftarrow$  genome-pos[ $p$ ] + 1
5   return TRUE
6 elseif  $act = S$ 
7   then cur-action[ $p$ ]  $\leftarrow$  READ
8    $s \leftarrow p$ 
9   seed-pos[ $s$ ]  $\leftarrow$  plant-pos[ $p$ ]
10  LIST-ADD( $seeds, s$ )
11  return TRUE
12 else return EXECUTE-GROWTH-ACTION( $p, act$ )
```

## EXECUTE-GROWTH-ACTION( $p, action$ )

```
1 cur-action[ $p$ ]  $\leftarrow$  READ
2  $(i, j) \leftarrow$  plant-pos[ $p$ ]
3  $\triangleright$  calculate new position, wrapping if necessary
4 if  $action = U$ 
5   then  $(i_n, j_n) \leftarrow ((i - 2) \bmod h_g + 1, j)$ 
6 elseif  $action = D$ 
7   then  $(i_n, j_n) \leftarrow (i, [(j - 2) \bmod w_g + 1])$ 
8 elseif  $action = L$ 
9   then  $(i_n, j_n) \leftarrow (i, [(j - 2) \bmod w_g + 1])$ 
10 elseif  $action = R$ 
11  then  $(i_n, j_n) \leftarrow (i, [j \bmod w_g + 1])$ 
12 if grid[ $i_n, j_n$ ] = UNOCCUPIED
13  then plant-pos[ $p$ ]  $\leftarrow (i_n, j_n)$ 
14  grid[ $i_n, j_n$ ]  $\leftarrow$  OCCUPIED
15  return TRUE
16 else return FALSE
```

## III. EXPERIMENTAL SETUP AND RESULTS

### A. Hypothesis

The plants evolve to play a game of competitive exclusion. In the gridplant environment, grid space is a scarce resource required in order to grow and reproduce. Hence, if a population of gridplants is better than another, the former should be able to occupy more grid space than the latter when growing for a number of generations in the same grid.

The hypothesis tested was that the evolved gridplants display *non-local adaptation*. This means that evolution imparts on gridplants general ability to compete with other plants, even if the other plants were not part of the environment in which the gridplants were evolved.

If the hypothesis is true, then a population of gridplants that has evolved for a significantly higher number of generations should be able to occupy more board space than a less evolved population when the two are placed in the same environment and allowed to grow for a number of generations. The following two sections detail the statistical tests that tested this hypothesis.

### B. Cooperative Test and Results

The pairwise test between two plant populations is as follows. Given two populations  $p_i$  and  $p_j$ , randomly seed 5% of a grid with seeds chosen uniformly at random from  $p_i$  and 5% of the grid with seeds chosen uniformly at random from  $p_j$ . Run for 50 generations *without mutation*. Turning off mutation ensures that the plants do not continue to

introduce new genetic material into the population that may distort the test results, since we wish to know how adept the plants were *at the generation the population represents*. At the end of 50 generations, record how many cells were occupied by descendants of population  $p_i$  and how many cells were occupied by descendants of population  $p_j$ . These two numbers will serve as the basic statistic of a single pairwise test. This section is called “Cooperative Test and Results” because of the cooperative nature of the test: when a population is tested, many of its members are sampled. Therefore, if a population comes out of one of these tests with more cells occupied than its opponents, it may be because interactions between different members of the population (cooperation) are required in order for the population to grow effectively. The next section discusses what was done to test for this effect.

30 populations of gridplants were evolved for 100000 generations according to the rules specified in the previous section. Each population was saved at generations 10,100,1000,10000, and 100000.

For each possible pair  $(g_i, g_j)$  of sampled generations  $g_i$  and  $g_j$  ( $g_i, g_j \in \{10, 100, 1000, 10000, 100000\}$ ), all 30 populations evolved to  $g_i$  generations were tested against all 30 populations evolved to  $g_j$  generations as described above. Each of the 900 pairwise tests gives an order pair  $(n_i, n_j)$ , where  $n_i$  is the number of cells occupied by the population evolved to  $g_i$  generations, and  $n_j$  is the number of cells occupied by the population evolved to  $g_j$  generations. All 900 pairwise tests can thus be represented by two matrices  $M_i$  and  $M_j$ . Entry  $(m, n)$  of matrix  $M_i$  represents how many cells were occupied by the  $m^{\text{th}}$  population that was evolved to  $g_i$  generations when that population was tested against the  $n^{\text{th}}$  population that was evolved to  $g_j$  generations. Entry  $(m, n)$  of matrix  $M_j$  represents how many cells the latter population ( $n^{\text{th}}$  population evolved to generation  $g_j$ ) occupied at the end of that test.

For each possible pair of generations  $g_i, g_j$ , such that  $g_i \leq g_j$ , two such matrices were generated. What was needed was a way to test, given two matrices  $M_i$  and  $M_j$ , whether the populations evolved to generation  $g_i$  were significantly worse than the populations evolved to  $g_j$  generations. Matrix  $M_i$  represents the number of cells occupied by the first population against all its opponents, and matrix  $M_j$  represents the number of cells occupied by its opponents during

these tests. Hence, a test that the entries of  $M_i$  are significantly smaller than those of  $M_j$  is required.

However, the 900 entries in each matrix cannot be treated as statistically independent. This is because each row of a matrix held one population constant while it was being tested against 30 other populations. Hence there will be dependence between numbers in the same row (or the same column) that is absent between entries from different rows (or different columns). To correct for this, the rows of each matrix  $M_i$  and  $M_j$  were averaged to give two 30-element vectors  $v_i$  and  $v_j$ . Entry  $m$  of  $v_i$  then represents the *average* number of cells occupied by the  $m^{\text{th}}$  population evolved to  $g_i$  generations when it was tested against *all* of its opponents. Entry  $m$  of  $v_j$  represents the average number of cells occupied by that population’s opponents in those tests. The entries of these two vectors were then treated as independently sampled, paired data.

Additionally, each diagonal entry of each matrix was set to zeroed before computing the average. This was done because the test is searching for the ability of a more evolved population to beat a less evolved population *that it has never seen before*. Entry  $(m, m)$  of a matrix represents how well a more evolved population plays against its own ancestors, and so these entries were simply not counted in the tests.

The generation samples chosen (10, 100, 1000, 10000, 100000) were based on early observations that the effect was apparently convex in nature. In other words, more evolution always allowed a population to develop more adaptive ability, but the more evolved a population  $p$  already was, the more additional evolution was required to evolve a population better than  $p$ . For example, a population evolved to 1000 generations could beat a population evolved to 100 generations, but a population evolved to 2000 generations performed no better than the population evolved to 1000 generations. However, evolving a population all the way to 10000 generations allowed it to beat a population evolved to 1000 generations. Note that this does *not* mean that a population evolved for more generations will always beat a population evolved for less generations, for two reasons. First, the more evolved a population is, the more additional evolution is required to beat it. One would not suspect that 10100 generations of evolution gives an advantage over 10000 generations of evolution, though 100 generations of evolution is certainly better than 0 generations of evolution. Secondly, for example,

even a population evolved for 1000 generations will occasionally beat a population evolved for 10000 generations. The purpose of the statistical tests was to detect a general trend in increased general adaptive ability, even if individual lineages occasionally fall backwards.

TABLE I  
COOPERATIVE TESTS BETWEEN POPULATIONS: WILCOXON SIGNED RANK TEST BETWEEN EACH POSSIBLE PAIR OF GENERATIONS. IN EACH CASE, THE  $p$ -VALUE IN ROW  $i$ , COLUMN  $j$  REPRESENTS THE PROBABILITY OF THE NULL HYPOTHESIS THAT THE POPULATIONS EVOLVED TO THE GENERATION SHOWN IN COLUMN  $j$  WERE NOT SIGNIFICANTLY DIFFERENT FROM THE POPULATIONS EVOLVED TO THE GENERATION SHOWN IN ROW  $i$ .

	10	100	1000	10000	100000
10	0.975387	0.010444	0.000002	0.000002	0.000002
100		0.909931	0.000002	0.000002	0.000002
1000			0.877403	0.000028	0.000005
10000				0.643517	0.001287
100000					0.544006

Given a pair of generations  $g_i$  and  $g_j$ , such that  $g_i \leq g_j$ , a Wilcoxon signed rank test (see [5] for a detailed explanation of this test) was performed between the two vectors  $v_i$  and  $v_j$ . This test was chosen because it is robust to dependencies in the sampled data and non-normality in the data distributions, both of which were present in the collected data. The signed rank test returns a  $p$ -value representing the probability that the medians of the two vectors are the same. Thus a low  $p$ -value (less than 0.1%, for instance) indicates that the medians were significantly different. The results for each pair of generations are shown in table I. In all cases, it was confirmed that the median was higher for the more evolved population, since the test only reports the probability that they are *different*. Thus, none of the low  $p$ -values result from more evolved populations *losing* to less evolved ones. As the table shows, populations evolved to the same number of generations have no advantage over one another. However, in every single case of *the particular generations sampled* in which more evolved populations were tested against less evolved populations, the more evolved populations were found to be significantly better with high probability. This does not necessarily indicate, however, that all populations evolved for

more generations are significantly better, only that the particular generations sampled display this effect.

### C. Individual Test and Results

As mentioned in the previous section, the performance of a population may be dependent on the interactions between its members. In other words, the adaptation displayed in the previous tests may be stored in the individual genomes or in the interactions between different plants in the population. This was tested in the following way. The pairwise test described above was modified so that instead of seeding 5% of the grid with plants sampled randomly from a population, a single plant was sampled randomly from the population, and copies of this plant were used to fill 5% of the grid. The same was done for the other population. Since each population was tested 30 times, more than one genome from that population had the opportunity to be tested. However, in any single pairwise test between two populations, exactly one genome from each population was represented. Therefore, if interactions between different genomes was required in order for a more evolved population to perform well, the statistical tests of these individual results should show no improvement in more evolved populations.

TABLE II  
INDIVIDUAL TESTS BETWEEN POPULATIONS: WILCOXON SIGNED RANK TEST BETWEEN EACH POSSIBLE PAIR OF GENERATIONS. IN EACH CASE, THE  $p$ -VALUE IN ROW  $i$ , COLUMN  $j$  REPRESENTS THE PROBABILITY OF THE NULL HYPOTHESIS THAT THE POPULATIONS EVOLVED TO THE GENERATION SHOWN IN COLUMN  $j$  WERE NOT SIGNIFICANTLY DIFFERENT FROM THE POPULATIONS EVOLVED TO THE GENERATION SHOWN IN ROW  $i$ .

	10	100	1000	10000	100000
10	0.909931	0.025637	0.000002	0.000002	0.000002
100		0.643517	0.000002	0.000002	0.000002
1000			0.926255	0.000020	0.000004
10000				0.614315	0.001036
100000					0.958990

This was not the case, however. As table II shows, the same pattern appears that was shown in the cooperative tests. More evolved genomes were significantly better than less evolved genomes with high probability, even when tested in isolation from the rest of their populations.

#### IV. CONCLUSIONS

The task the gridplants were performing was competitive in nature. This experiment was not designed to test the gridplants' ability to occupy board space in the absence of competition. It only took a few dozen generations starting from a single seed for the plants to occupy the entire board. The competitive nature of the task is what makes this an interesting, and theoretically difficult, problem to study. The gridplant genomes stand to benefit most not only by occupying board space and planting seeds, but by growing in such a way as to grow cooperatively with gridplants to which they are related, and to block the growth of gridplants unrelated to themselves. Thus the ability simply to grow is not what is being studied here, but rather the adaptive ability to survive and proliferate in the presence of other gridplants vying for the same territory.

With this notion of adaptation in mind, this work tested the hypothesis that gridplants adapt non-locally. For every possible pair of generations  $g_i, g_j \in \{10, 100, 1000, 10000, 100000\}$  such that  $g_i < g_j$ , populations evolved to  $g_j$  generations performed significantly better than populations evolved to  $g_i$  generations, even though the performance was measured against gridplants from entirely different lineages. This lends evidence to the hypothesis that evolution was able to impart non-local adaptive skill on the gridplants.

This result held even when the pairwise tests sampled a single individual. This shows that the continual adaptation built up by evolution was packed into a single 20-character genome. At some point, since the length of the genome is finite, this adaptation must halt due to the finite number of possible genomes. However, it is not known how long evolution would take before hitting a wall beyond which additional evolution would not help.

Preliminary tests show that it may be possible to control how long it takes before evolution no longer builds adaptation by adjusting the mutation rate. For example, when the previous tests were run with a mutation rate of 0.1 instead of 0.01, the effect appeared between every pair of generations except for 10000 and 100000. In other words, evolving from generation 10000 to generation 100000 did not enable the more evolved populations to beat the less evolved ones, when the mutation rate was 10 times higher. This may be a result of "forgetting" (i.e. the high mutation rate erased the strategies that may have been

able to beat the less evolved populations).

Note that the parameters controlling the simulation (instruction costs, energy per timestep, etc.) were held constant across each lineage tested. Hence, when the claim is made that the tests occur between two populations that were never a part of the same environment, this refers to the fact that the lineages never interacted; the "environment" in this case defined by the other gridplants that are in the grid. However, a stronger form of non-local adaptation could be shown if gridplants evolved according to one set of parameters were able to outperform less evolved gridplants, even if the test occurred in an environment (as defined by the simulation parameters) identical to that in which the less evolved gridplants arose but "foreign" to the more evolved gridplants. This would be similar to the biological concept of an invasive species [8].

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