

Dude, Where is My Sex Gene? — Persistence of Sex over Evolutionary Time in Cellular Automata

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Abstract—We created a simple evolutionary system, **F-sexyloop**, on a deterministic twelve-state five-neighbour cellular automaton (CA) where self-reproducing loops have the capability of sex. This work was based on the sexyloop which was transformed by adding two new states and new rules. In the F-sexyloop, the loops can carry a sex gene used to facilitate the transfer of genetic material from a loop to another. This gene is analogous to the F factor plasmid in bacterial conjugation which confers the capacity to act as a donor of genetic material (including the gene itself). Therefore, the sex gene could potentially be maintained in the population during evolution or disappear. We show that in a wide variety of cases, the sex gene persists over evolutionary time and is present in the genomes of the dominant species.

I. INTRODUCTION

THE origin and maintenance of sex in biology is an active area of research with a long history [1-5]. Here we understand ‘sex’ as the transfer of heritable genetic material between individuals [2, 3] (see also discussion in [6]).¹ In Artificial Life the study of self-reproduction goes back to the work of von Neumann on self-reproducing automata implemented in cellular automata [7], but few evolutionary models have supported any bottom-up autonomous capacity for sex (exceptions include Tierra [8] in assembly code programs, and [6] in Cellular Automata; see also Vitányi [9]), and prior to the work presented here no such models, to our knowledge, have investigated evolution and persistence of sexual mechanisms. Such a study takes us beyond the examples of ‘sex as-we-know-it’ in organic biological systems [2-4] toward a more general understanding of ‘sex as-it-could-be’ in other instantiations of living systems. Here we do not address the origins of sex, but its persistence (or not) in evolving populations.

¹ Note that *sex* (the transfer of heritable genetic information) does not require reproduction. Indeed, *reproduction* may be asexual or may involve sex, and in many evolving biological populations, individuals may reproduce either asexually or with sex at different times and conditions, e.g. [1, 4].

In order to investigate the persistence of sex in a population of self-reproducing loops, here we introduce a new simple evolutionary system, based on the sexyloop [6], where sex is only performed using a specific gene. In the sexyloop, a loop was able to transfer its genetic material into another one. But sex was just a particular configuration based on environmental configuration, dependent on CA rules rather than something carried in the genomes of loops. The loops did not have a unique “sex gene” used to create or use this connection. In all living sexually reproducing creatures, such sex genes do exist. So it was natural to modify the sexyloop, by adding a gene in the genome of the loop which would be used only for inducing sexual behaviour, and to study its persistence or extinction in evolving populations. We named the new model F-sexyloop, where F stands for ‘fertility’.

A. Background

Cellular Automata (CAs) are discrete synchronously updated, spatially distributed models of computation in which changes in state at a given location depend only on local conditions (states of neighbours) [7]. Models of self-reproduction have been described in CAs [7, 10, 11] and Darwinian evolution has been exhibited in populations of self-reproducing loops [6, 12, 13]. In the sexyloop [6], we managed to allow the transfer of genes from a loop into another one using a simple mechanism with a minimum number of new states, using a mechanism similar to bacterial conjugation [2, 3].

The sexyloop work was based on Sayama’s evolloop [12] which was transformed by adding a new state and new rules. In the evolloop, all undefined rules create a dissolving state ‘8’. When the tip of a loop’s arm hits another loop on its sides or the corners, a dissolving state appears eventually deleting the “attacked” loop and the attacker’s arm. Like in [6], we mean by “attacker” the loop that will transfer its genetic material into another loop (the “attacked” loop). The use of the term “attacker” in this paper is due to the fact that in our scenario, the donor transmitting heritable information sexually is generally at an evolutionary advantage compared to the recipient as the latter generally loses some part of its genome in such interactions. In the sexyloop, the attacker’s

arm bonds with the attacked loop, creating a bonder state ‘3’ on its sheath (Figs 1 & 2). This junction was only made if the attacker’s arm hit another loop on its side, not on the corners. So when a loop hit another one at a corner, its behaviour was the same as in the evolooop. Once the junction was made, the transfer from the attacker loop into the attacked one could begin. When the genetic material coming in from the attacker has been transferred, then only core cells ‘1’ were present at the junction with the attacker’s arm so an umbilical cord dissolver ‘6’ was created in the attacker’s arm beside the detection sheath. A blocker dissolver ‘9’ was also created to delete the signal blocker. Finally, the umbilical cord dissolver moved back into the attacker arm to retract it and a sheath ‘2’ was created in its previous location. At the same time, the signal blocker, the detection sheath and the blocker dissolver disappear (see [6] for more details).

We managed to allow genetic transfer by adding just one new state ‘9’ with different functions and the corresponding rules [6]. We then created two versions of sexyloop with different mechanisms: M1 and M2. In the first one, the transfer was made only when the beginning of the signal arrived at the junction. The second mechanism was more flexible. The sexyloop M2 could begin the transfer at any time until the end of the signal arrived at the junction. Sexyloop with these variants resulted in different evolutionary dynamics and generally in more diversity than with evolooop - see [6] for details.

In the present work the capacity for sex is not universal (unlike [6]) but is conferred by a particular gene, which may be absent or present. This is analogous to the F-factor (F for “fertility”) plasmid involved in bacterial conjugation (e.g. in *E. coli* [14, 15]). Depending on whether this factor is present (F^+) or absent (F^-), the bacterium is able to act as a donor of genetic material to other individuals.

B. Sexyloop with sex gene: F-sexyloop

In the F-sexyloop, we kept the capability for the loops to create a junction between an attacker and a receiver (Fig. 1). The bond is created like in the sexyloop. Once the junction is created, the attacker loop must have a sex gene in its genome for transfer of its genetic material to be possible under the local cellular automaton dynamics. If it does not have it, its arm will stay bonded to the attacked loop until one of them dies. In comparison with the sexyloop, we used the state ‘9’ as a sex gene allowing genetic transfer (sex). We added a new state ‘A’ used as a signal blocker, detection sheath and blocker dissolver (like state ‘9’ in the sexyloop), and also a state ‘B’ used as a corrector allowing correction of genetic information during sex (Table 1). Our system uses twelve states in a five-neighbour cellular automaton and 662 rules³.

II. MECHANISMS OF GENETIC TRANSFER

We used the state ‘9’ as a sex gene to transfer genetic material, in the form of a moving signal, from an attacker loop to another loop. When the junction between the attacker and the attacked loop is made, a bonder ‘3’ is created like in the sexyloop (Figs. 1, 3), but it will now only be removed when a ‘9’, present in the signal of the attacker, arrives at the

junction (Fig. 3, left). The signal will then be transferred into the attacked loop. When the ‘9’ arrives in the attacked loop, a signal blocker ‘A’ and a detection sheath ‘A’ are created like in the sexyloop (Fig. 3, left). The blocker erases the genes of the signal coming from the attacked loop (when they arrive at the blocker). Once the attacker loop has transferred its signal, the junction and the arm of the attacker are deleted like in the sexyloop. In the example presented here (Fig. 3, left), the ‘9’ was used to “open the door” by deleting the bonder ‘3’ therefore allowing the signal to move into the attacked loop.

The signal blocker and detection sheath in the attacked loop are also created if the signal of the attacked loop has a ‘9’ that arrives at the junction before the ‘9’ of the attacker, it will create the signal blocker and detection sheath (Fig. 3, right).

Fig. 4 shows two loops linked with a sex junction which was made before and the signal blocker and detection sheath ‘A’ were created by the sex gene coming from the attacked loop (bottom). At steps 1 and 2, the signal coming from the attacker is arriving at the junction while the signal of the attacked loop is being erased by the blocker. At step 3, due the presence of the sex gene the bonder is deleted so the transfer can begin (steps 4 and 5).

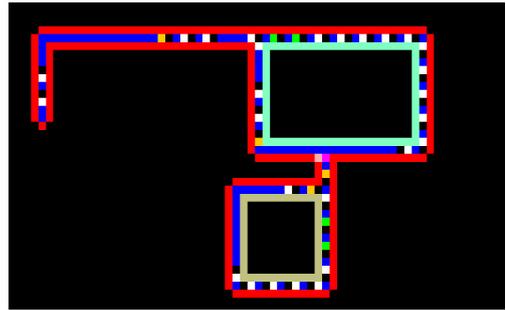


Fig. 1. Sex junction on the side of the attacked loop.

TABLE I
ROLES OF THE NEW STATES USED IN THE F-SEXYLOOP

State	Name	Functions
9	Sex gene	Delete the bonder ‘3’ allowing transfer. Create the blocker and detection sheath ‘A’.
A	Signal blocker	Stop a signal from being conducted in the loop.
	Detection sheath	Detects the end of the transfer.
	Blocker dissolver	Delete the signal blocker.
B	Error corrector	Correct genetic error made during transfer

In both cases presented above, the signal coming from the attacker is transferred into the attacked loop when the signal of the attacked loop is not present at the junction. If that happens, both signals should merge without any problems, although generally with most of the attacked loop’s genome being overwritten. Unfortunately, some errors can be created during the process. To be valid, the signal must be composed of genes ‘4’, ‘7’ or ‘9’ and each one of them should be encapsulated between a ‘1’ and a ‘0’. When a loop transfers

its genes into another one and both signals merge, this encapsulation can be broken so the genome is not valid anymore and the loop is destroyed. To prevent this, we added a new state ‘B’, created by the sex gene ‘9’, which detects when the transfer is generating an error. When an error occurs, the sex gene ‘9’ becomes a ‘B’ and will stay at a fixed position in the loop until a gene ‘7’ comes in. Then, the ‘B’ becomes a ‘9’ replacing the ‘7’ (Fig. 7).

III. EXPERIMENTS

We performed two series of tests to see if the sex gene would persist in evolution or disappear. We did ten simulations in two different environments, one of size 500 x 500 and a bigger one of size 1000 x 1000. For each run, two loops of the same species² were placed randomly, but not overlapping or directly adjacent to one another, in the environment. One loop had a sex gene in its genome (Fig. 2) and the other one did not. The goal of this study was to see if the sex gene could actually propagate into the population of loops that did not have this gene.

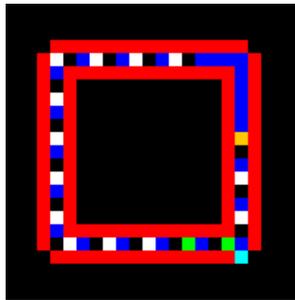


Fig. 2. Ancestor used of species 13 (13 genes ‘7’ in white) having one sex gene (orange) placed at the beginning of the signal.

IV. RESULTS

The results show that in the smaller world, the dominant species at the end of most runs had a sex gene in their genome. In 6 of 10 runs in 500 x 500 scenario, the sex gene persisted throughout the 50,000 timesteps of the run (with between 21% to 88% carrying it), and in over 53-88% of the population in most of those runs. In 4 of these 10 runs, the sex gene was lost by around half-way through the run. In 10 of 10 runs in 1000 x 1000 scenarios, the sex gene persisted - here in 60% to 96% of the final population, except for one run with 32% where it was still rising in prevalence at the end. In either scenario, the sex gene usually persisted in a large fraction of the loops (represented in over 68% of the final population in 4 of the ten 500 x 500 runs, over 67% of the final population in 8 of the ten 1000 x 1000 runs). Although in some stages of the experimental runs the sex gene was present in 100% of individuals, interactions and collisions continued to create individuals not carrying the

² As in [12] and [6], the “species” of an individual loop is given formally by the number of 7’s in its genome (which determines the loop’s size). It is *not* related to the so-called ‘biological species’ concept, but is only used here as an indication of genetic diversity in the population, since a population with many species (in this sense) will have at least as many different genomes present.

³ For sexyloop and F-sexyloop rules and data on more experiments, see: <http://homepages.feis.herts.ac.uk/~nehaniv/sexyloop/>

gene. Even if only one loop had the sex gene at the beginning, it was passed from generations to generations and transferred to other species during evolution. Fig. 5 (left) shows the percentage of loops with a sex gene in the population averaged over ten runs. We can clearly see that the sex gene does not disappear in time. Fig. 6 (left) shows the percentage for one run. We can see that at the end of the run, almost all loops living in the environment have a sex gene. Examining Fig. 8, we can see that they belong to the species 5. These loops are actually the smallest sized viable loops that can contain a sex gene. Surprisingly, these loops can have sex but it might be ‘harmful’ in the long term. In fact, if one of them transfers its genes into another one, the sex connection can never be deleted and they will remain joined together until another loop kills them due to a collision (although the recipient may continue to produce offspring during this time). The problem is that these loops have a signal that “overfills” them, meaning that there are no gaps “1” after the signal. The signal forms a complete loop. As the mechanism used to dissolve the arm works by detecting gaps after the signal, it will never be used. But even if sex might have become harmful at the end, the sex gene is still persistent in the population and is not removed by further evolution³.

We had similar results using the bigger environment. Fig. 5 (right) shows the percentage of loops with a sex gene in the population averaged over ten runs. We can clearly see again that the sex gene did not disappear and most of the loops have it. Fig. 6 (right) shows the percentage for one run. We notice that at the end of the run, almost all loops living in the environment have a sex gene. From Fig. 9, we can see that they belong to the species 5 like in the previous experiments.

V. DISCUSSION

We have seen that on average, the sex gene persisted in time during the evolutionary process. Moreover, the prevalence of the sex gene in evolving populations tended to be high. This effect was stronger as environment size increased. Perhaps this trend was due to fewer interactions between asexual and sex-gene carrying subpopulations until population size was large, so that local ‘chance events’ were less likely to influence global evolutionary dynamics. In most of the experiments, the loops that dominated at the end of the runs carried the sex gene and were of species 5. These loops are the smallest viable loops that could contain a sex gene. But surprisingly, sex could be harmful for these loops. In fact, if one of them transfers its genes into another one, the sex connection could never be deleted and they would remain joined together until a collision with another loop destroys one of them. It would be very interesting to know why the sex gene was kept during the whole run and finally became quite useless and even harmful. A possible reason could be that, while sex was very useful during most of the evolutionary process, increasing diversity and accelerating evolution, nevertheless in the small evolved loops no variability could be generated that would eliminate the sex gene: any collisions or interactions that might eliminate the sex gene would almost certainly lead to death of the

reproducing loops involved. Thus, as the loops became smaller and smaller, the sex gene was kept and it became difficult to ‘mutate’ the genome and delete this gene. Another (non-exclusive) reason could be that there was no high selection pressure on having the sex gene so it was kept even it became not really useful.

We have to emphasize the fact that when a loop connects to another one and does not have a sex gene, it will stay stuck until another loop kills it. Therefore, there is a high selection pressure to have sex, intrinsic to the system. A natural next step would be the development of a null model that would make it possible to distinguish between random drift and selection for or against the sex gene. It would be very interesting to see whether sex persists when we limit this pressure by dissolving the arm of a loop that connects to another one but does not have a sex gene.

Nevertheless runs without the sex gene have loops able to reproduce and evolve but in a much smaller numbers: we did experiments using the same environments (500 x 500 and 1000 x 1000) using only one loop without a sex gene (F⁻-sexyloop), and we saw that loops evolved and the dominant species at the end of the runs were of species 4 like in the evolop [12] but actively reproducing viable loops were much fewer in number since many loops became ‘stuck’ in collision. Details on such a comparison of these evolutionary dynamics with those of F⁺-sexyloop will be presented elsewhere³. We also ran experiments starting with only one loop having a sex gene (F⁺-sexyloop) and we observed that loops from the dominant species at the end of the runs all had the sex gene and were of species 5.

Different variations of this system can be created. For example, we could suppress the use of the state ‘B’, so sex would be more harmful to the recipient. We could also make the sex gene ‘9’ act as a ‘7’ so it could grow the arm of a loop. Finally, we could cancel the creation of a blocker ‘A’ when the ‘9’ comes from the attacked loop and still use the state ‘B’ so more variation could be generated in the genome.

We noticed in this system that more ‘debris’ - non-quiescent states that were not part of any reproducing individual loop - was created in the F⁻-sexyloop than in the sexyloop. This might create an additional pressure on the loops to evolve. The prevalence of debris may possibly have been due to new rules introduced to make the sex mechanism more stable.

VI. CONCLUSION

We presented in this paper a new evolutionary system created in a 2D cellular automata. This work was based on the sexyloop where sex was shown to accelerate evolution and increase diversity in a population of self reproducing loops [6]. Sex here is a unidirectional transfer of genetic material (possibly resulting in some recombination rather than equal contributions from members of two genders which would also be interesting to study). We modified the sexyloop by adding new states and rules, so loops could transfer their genes only if they had a sex gene in their genome. We have shown that in most of the experiments, the sex gene persisted in time during the evolutionary process

and was also established in dominant species. However, sex may have hitched-hike on selection pressure for ability to detach when loops interact, so further work is needed to understand the evolutionary dynamics of sex in this and other artificial systems. Also, substantially longer simulation runs would be necessary to establish that the sex genes are really maintained in the long term within the population.

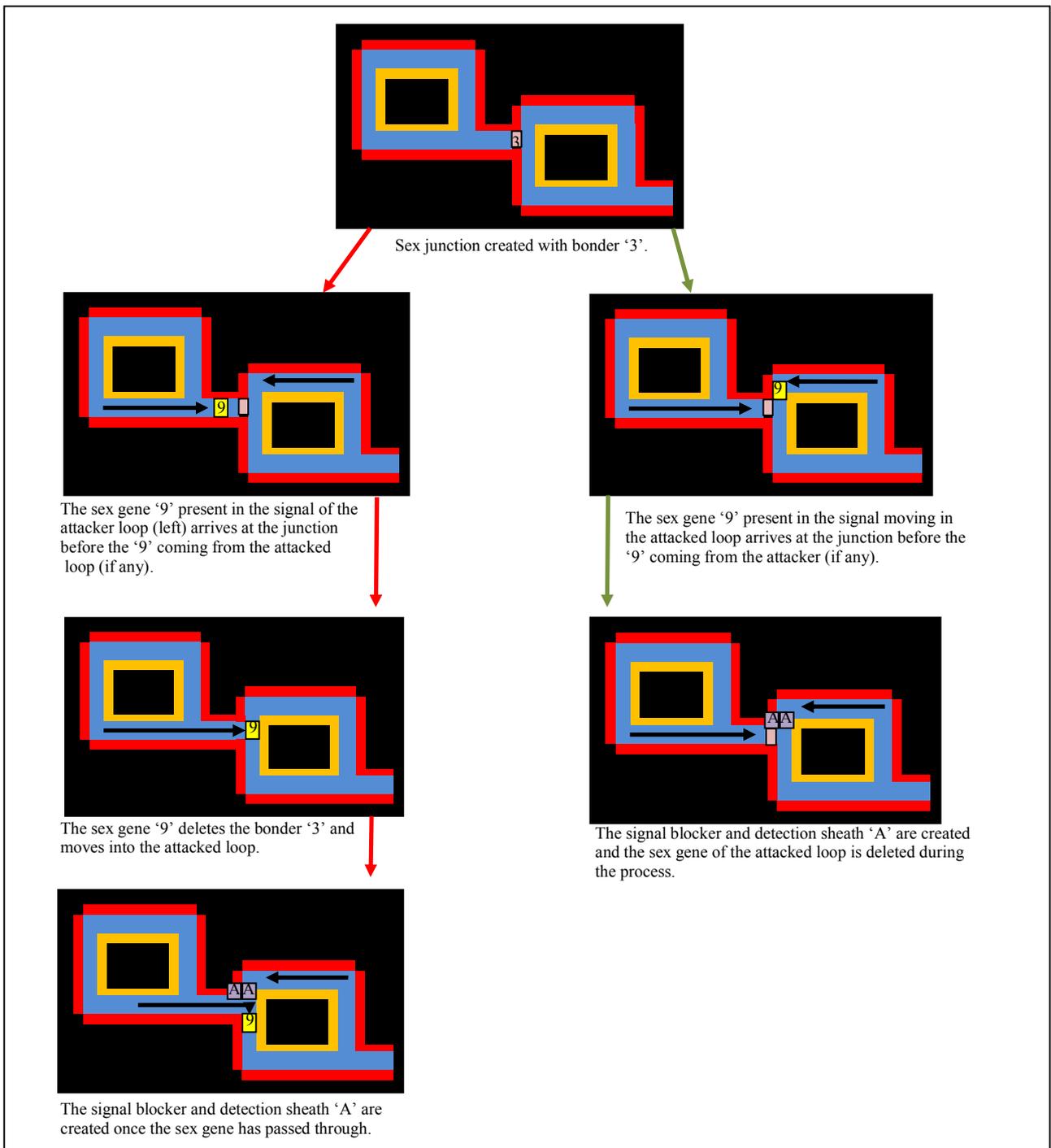


Fig. 3. Simplified schematic illustration of two possible courses of sexual interaction both resulting in the creation of a signal blocker and a detection sheath. The black arrows inside the loops represent the moving signals (genomes). The left pathway shows a case when the sex gene from the attacker loop arrives at the junction before the sex gene of the attacked loop (if any); the right pathway shows the case when the sex gene of the attacked loop arrives first.

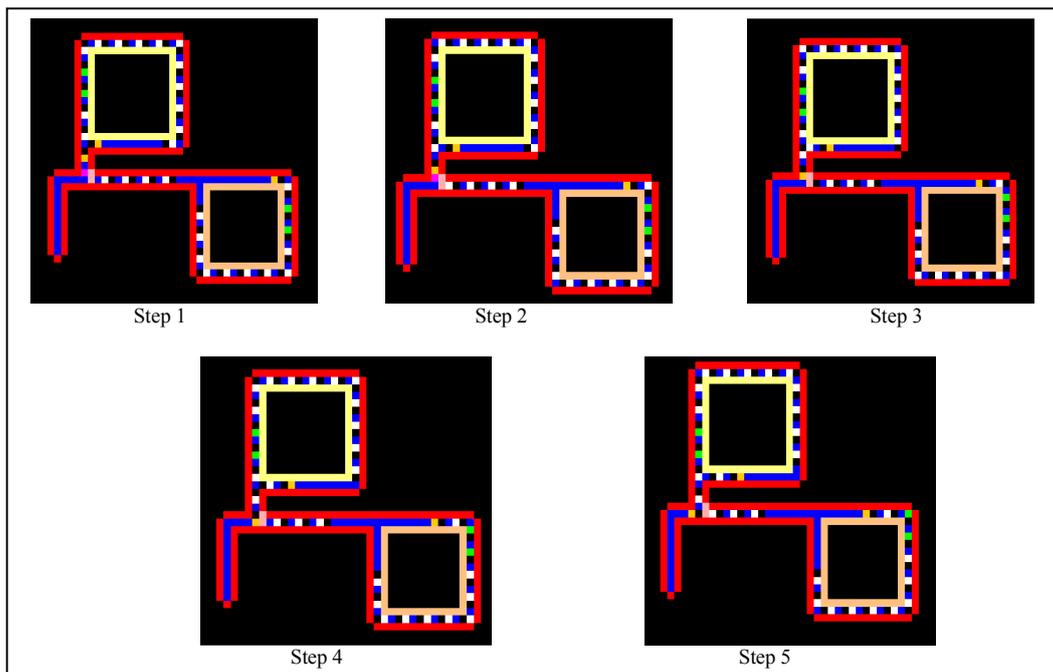


Fig. 4. Transfer of genetic material from an 'attacker' loop (top) into the arm of another loop from an actual F-sexyloop CA run. The sex junction is already made and the signal blocker and detection sheath 'A' were created by the sex gene coming from the attacked loop (bottom). At steps 1 and 2, the signal coming from the attacker arrives at the junction while the signal of the attacked loop is being erased by the blocker. At step 3, the sex gene deletes the border so the transfer can begin (steps 4 and 5).

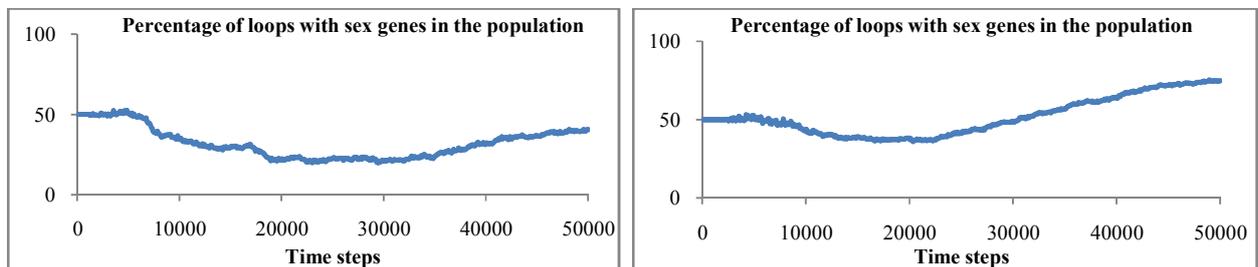


Fig. 5. Mean Values for Percentage of loops that have a sex gene in their genome. The graphs show the mean values of ten runs where two loops (one with a sex gene, one without) were placed randomly in the environment. The graph on the left shows the results using an environment of size 500 x 500 and the one on the right shows the results using an environment of size 1000 x 1000.

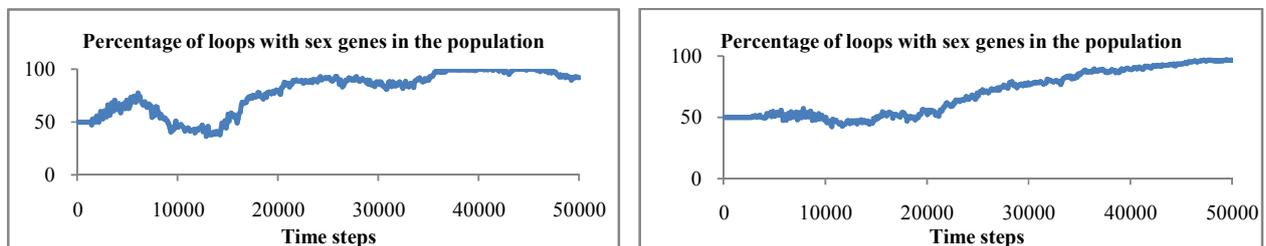


Fig. 6. Percentage of loops that have a sex gene in their genome from two sample evolutionary runs. The graphs show the values for one run only where two loops (one with a sex gene, one without) were placed randomly in the environment. The graph on the left shows the results using an environment of size 500 x 500 and the one on the right shows the results using an environment of size 1000 x 1000.

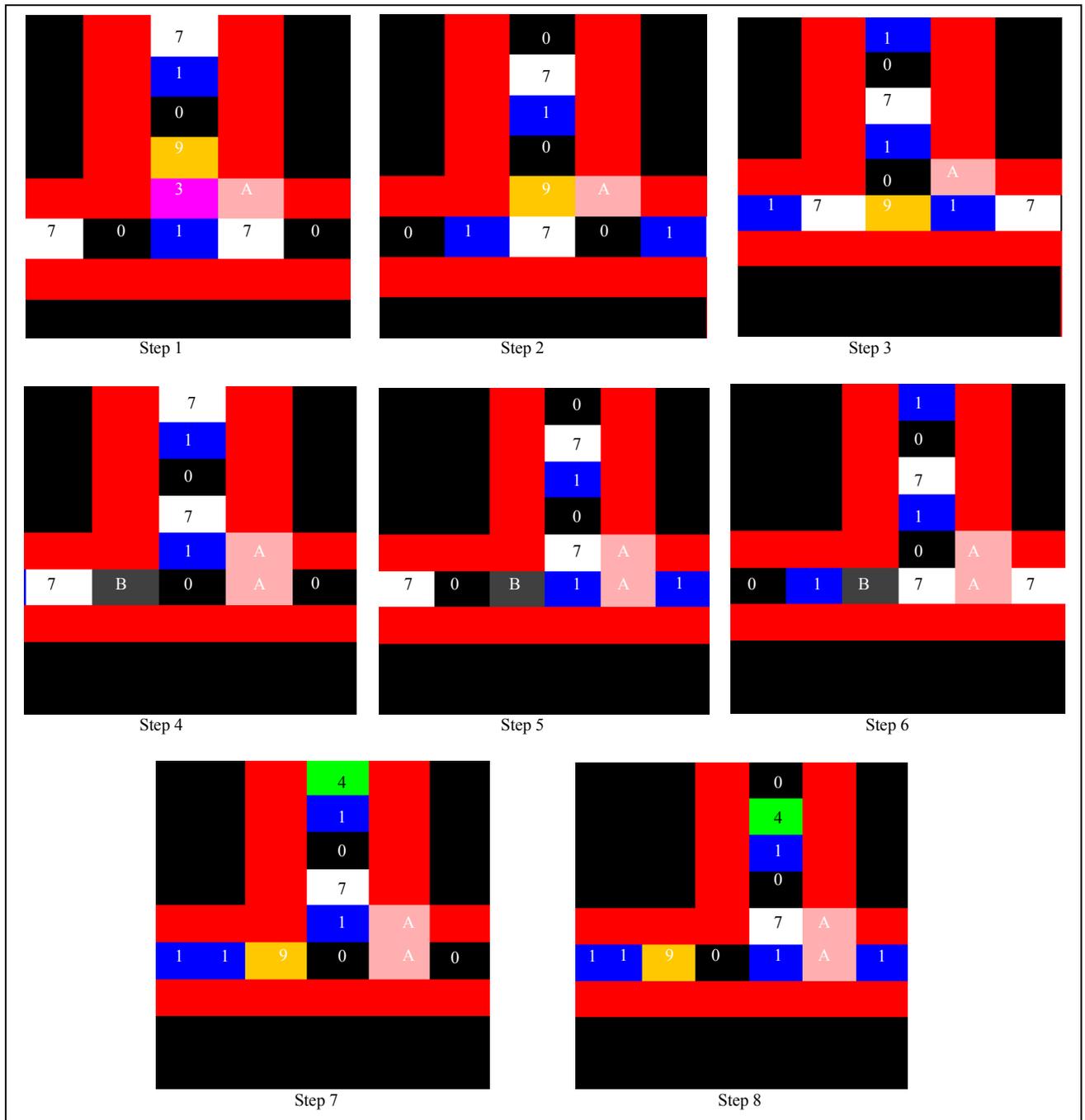


Fig. 7. Error correction during transfer of genetic material from an attacker loop (top) into the arm of another loop. The sex junction is already made and the detection sheath 'A' was created. At step 1, the signal coming from the attacker arrives at the junction while the signal of the attacked loop is moving. At step 2, the sex gene deletes the bonder so the transfer can begin. But both signals have to merge, creating an inconsistent signal (step 3). So an error corrector 'B' is created by the sex gene '9' (step 4). This corrector will then stay at a fixed position and correct the signal (step 5) until a '7' comes in (step 6). When the '7' merges to the 'B', the latter becomes a '9' so the signal is valid again and the sex gene is still in the genome (steps 7, 8). This process adds a gap (extra '1' in the signal).

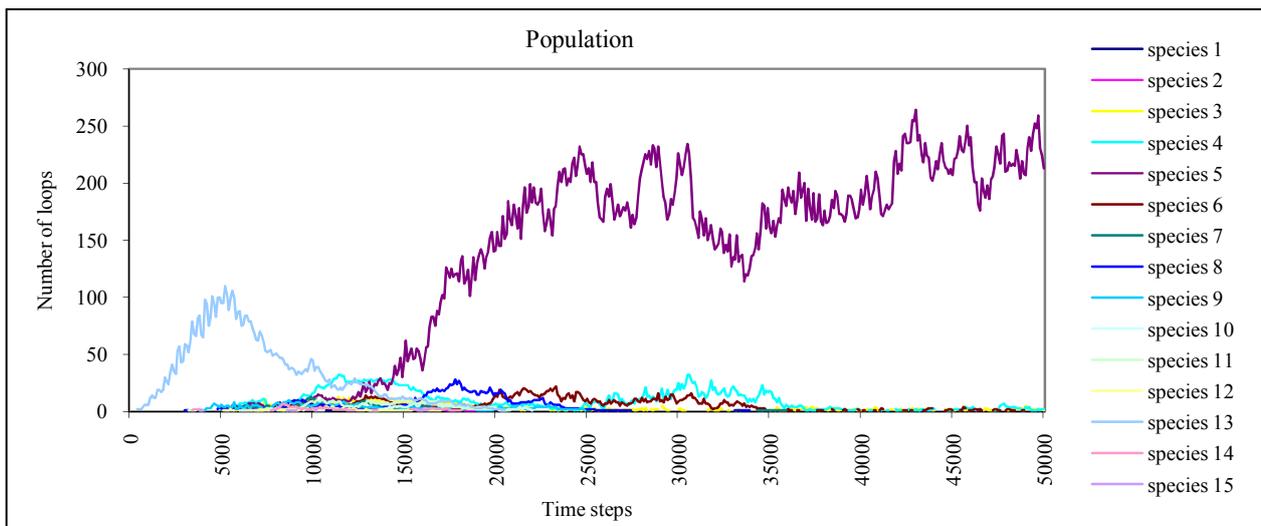


Fig. 8. Population of a typical run where two loops (one with sex gene, one without) were placed randomly in an environment of size 500*500. (same run as shown in Fig. 6, left)

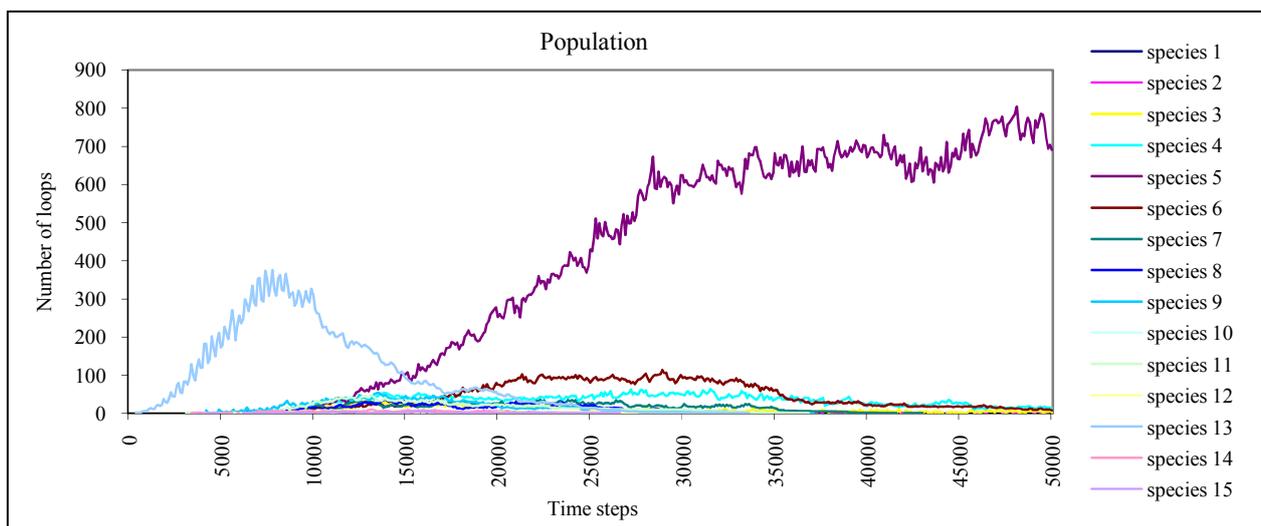


Fig. 9. Population of a typical run where two loops (one with a sex gene, one without) were placed randomly in an environment of size 1000*1000. (same run as shown in Fig. 6, right)

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