

Homework 7: Biologically Inspired Computation

Due: Monday, November 19

Reading Questions

Submit computer-formatted, spell-checked, proofread answers to the following questions.

1. Briefly describe in your own words (in a paragraph or so) the “Distributed Change Detection” system proposed by Forrest, Hofmeyr, and Somayaji. What aspect of the immune system is it inspired by?
2. Explain (in your own words, a paragraph or so) why “negative detectors” in this system are more efficient than “positive detectors” would be.

Exercises: Evolving Cellular Automata with GAs

For these exercises you will experiment with a genetic algorithm that evolves cellular automata to perform the majority classification task. The code (in a gzipped tarball) can be downloaded from the class web site. See the attached Guide for information about this code.

For each exercise below, define S to be the number of runs (out of 10) that produce at least one CA with a fitness of 0.9 or greater in some generation, T is the average (over runs reaching 0.9) first generation in a run at which a fitness of 0.9 or greater is reached.

For each exercise, change only the parameter mentioned and leave all others at their default values.

If possible, write scripts (in bash, perl, or whatever scripting language you prefer) to extract the required statistics listed below from the output files.

Note: Using this code with the default parameters, one run takes about 1 minute on my (rather old) Linux machine. I am asking you to do about 70 runs total, so you will need to start early. **DO NOT WAIT UNTIL THE LAST MINUTE!**

1. Do a set of 10 runs with the default parameters. Determine what S is. Call this number $S_{default}$. Determine what the T is over the 10 runs. Call this number $T_{default}$.
2. Compare $S_{default}$ and $T_{default}$ with the S and T observed when using both a larger and smaller population (you choose the sizes). If there are differences between the defaults and the new values, speculate on what causes them. (Note: you need to do 10 runs of each population size.)

3. Compare $S_{default}$ and $T_{default}$ with the S and T observed when using no crossover. If there are differences, speculate on what causes them.
4. Compare $S_{default}$ and $T_{default}$ with the S and T observed when using uniform crossover (as described in class). You will need to implement the uniform crossover routine, as is described in the attached Guide to Code. If there are differences, speculate on what causes them.
5. Compare $S_{default}$ and $T_{default}$ with the S and T observed when using a higher mutation rate and when using a lower mutation rate. (You choose the rates.) If there are differences, speculate on what causes them.
6. **Optional (advanced):** Compare $S_{default}$ and $T_{default}$ with the S and T observed when using coevolution. You will need to implement coevolution, as is described in the attached Guide to Code. If there are differences, speculate on what causes them. (If you are interested in doing this optional step, see me.)

Turn in a computer-formatted, spell-checked writeup describing the results of the exercises described above. Include your speculations on the causes of any differences in S that you observe. Summarize your results at the end of your writeup. **You don't need to turn in any code!**