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CS 420

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## Project 2: Creation of Spatial Structure by Activator/Inhibitor Cellular Automaton

### Introduction

The purpose of this assignment was to introduce to the students how cellular automata could be activated and inhibited based on a variety of factors. In particular, the parameters that were changed over the course of the project were R1, R2, H, J1, and J2. R1 referred to the maximum distance at which nearby cellular automata would affect each other, and R2 referred to the maximum distance at which far away cellular automata would affect each other. H referred to the bias factor. J1 held the value that determined the activation system threshold, and J2 held the value that determined the threshold of the inhibition system. As these parameters were changed, the object was to allow the cellular matrix to run its course as the cellular automata interacted until it reached a deadlock. Then, using this final product, the correlation, entropy, joint entropy, and mutual information could be discerned. Also, due to the fact that this project made an attempt to complete experiment 1 and 2 in addition to experiment 3, there was ample opportunity to play around with the J1 and J2 values.

### Methodology

The heart of this lab revolved around a 30x30 2d array whose elements were randomly set to either a 1 or a -1. Using this array, the first step in the project was to allow the array to progress along its path based upon several parameters. In particular, the parameters that were changed over the course of the project were R1, R2, H, J1, and J2. R1 referred to the maximum

distance at which nearby cellular automata would affect each other, and R2 referred to the maximum distance at which far away cellular automata would affect each other. H referred to the bias factor. J1 held the value that determined the activation system threshold, and J2 held the value that determined the threshold of the inhibition system. As these parameters were changed, the object was to allow the cellular matrix to run its course as the cellular automata interacted until it reached a deadlock.

The process behind the progression of the array had to do a few simple calculations. Each automata, represented as a cell within the array, would look around at the other cells around it, as well as on the other edge, as the array represented a torus. Then, based upon the distance between it and the cells around it, found by this formula:

$$r_{ij} = |i_1 - j_1| + |i_2 - j_2|$$

Each cell was able to determine whether or not it would change its state, using this formula:

$$s_i(t+1) = \text{sign} \left[ h + J_1 \sum_{r_1 < R_1} s_j(t) + J_2 \sum_{R_1 \leq r_1 < R_2} s_j(t) \right]$$

In this equation, s with the j subscript represents the sum of the cell values around the s subscript i cell. The first summation represents all of the cells within radius R1 of the Si cell, and the next one represents the sum of the cells between R1 and R2. Everything beyond R2 was disregarded. If the right side of that equation was greater than 0, then the cell would have been set to 1. Otherwise it would have been set to -1. This would happen to each cell, randomly, as it progressed through the entire array. Once the array had been traversed through, the program would either repeat the process if changes had been made, or it would determine that there could be no further changes made, as there would have been none in the preceding process.

Once that was done with, the program would have been left with the final array product, which is needed to compute the rest of the project. The first thing that would have been found following the final array is the correlation. The correlation can be found using this equation:

$$\rho_l = \left| \frac{2}{N^2 C_l} \sum_{\substack{i,j \\ |i-j|=l}} s_i s_j - \left( \frac{1}{N^2} \sum_i s_i \right)^2 \right|$$

This equation finds the sum of all correlations with the distance set to l, where l ranges from 0 to 14.

Once that was completed, the program would move on to calculate the entropy of the array. This is a multistep process, though none of them are all too complicated. The first step here would be to calculate the sum of converted cell values. Converted cell values can be represented by this equation:

$$\beta(s) = (1 + s) / 2$$

Where s simply represents the 1 or -1 value of a cell. This value would be summed over the course of the entire array, as represented by this equation:

$$\Pr\{+1\} = \frac{1}{N^2} \sum_i \beta(s_i)$$

Which gives the probability of state 1. Conversely, the probability of state -1 is given with this equation:

$$\Pr\{-1\} = 1 - \Pr\{+1\}$$

These two values are needed to calculate the overall entropy, represented as H(s)

$$H(S) = -(\Pr\{+1\} \lg \Pr\{+1\} + \Pr\{-1\} \lg \Pr\{-1\})$$

This value is required to calculate the mutual information, but first the joint entropy needs to be calculated. This is done in a similar way to how the correlation was calculated, but there is also a lot of commonality with the original overall entropy calculation. However, before the program can deduce the joint entropy, it needed to first find a few different values using these equations:

$$P_{\ell}\{+1,+1\} = \frac{2}{N^2 C_{\ell}} \sum_{\substack{\langle i,j \rangle \\ r=\ell}} \beta(s_i) \beta(s_j)$$

$$P_{\ell}\{-1,-1\} = \frac{2}{N^2 C_{\ell}} \sum_{\substack{\langle i,j \rangle \\ r=\ell}} \beta(-s_i) \beta(-s_j)$$

$$P_{\ell}\{+1,-1\} = P_{\ell}\{-1,+1\} = 1 - P_{\ell}\{+1,+1\} - P_{\ell}\{-1,-1\}$$

Then, using these three entropy values, the joint entropy can be calculated with this equation:

$$H_{\ell} = -(P_{\ell}\{+1,+1\} \lg P_{\ell}\{+1,+1\} + P_{\ell}\{-1,-1\} \lg P_{\ell}\{-1,-1\} + P_{\ell}\{+1,-1\} \lg P_{\ell}\{+1,-1\})$$

It should be noted that these equations are run through for each length  $l$ , where  $l$  ranges from 0 to 14

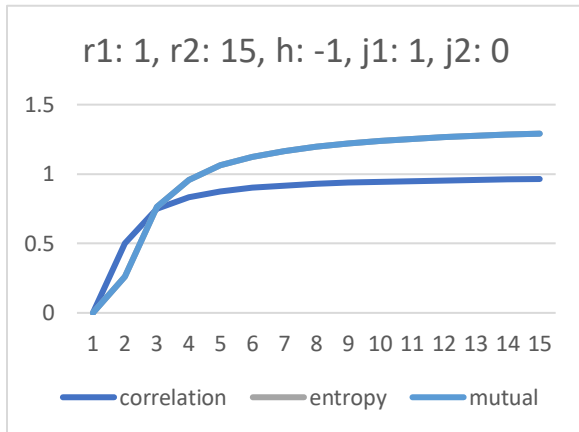
Lastly, the mutual information was calculated, and this is an even simpler calculation:

$$I_{\ell} = 2H(S) - H_{\ell}$$

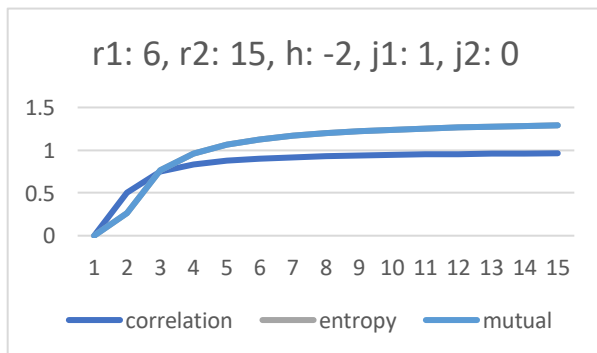
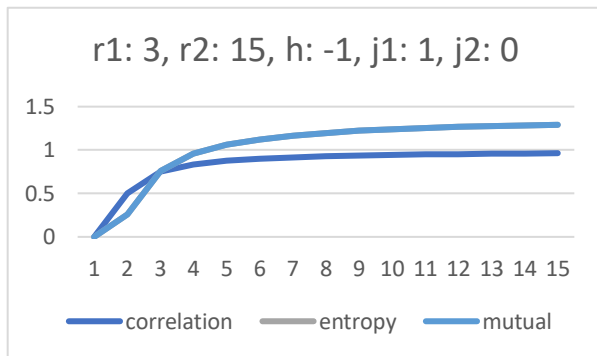
Though, like the joint entropy and correlation, it has to run through for each value  $l$ , ranging from 0 to 14.

## Results

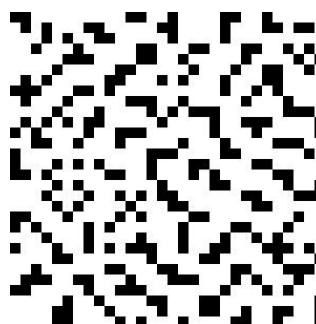
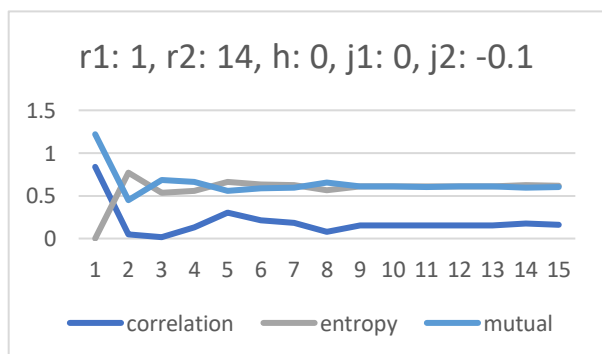
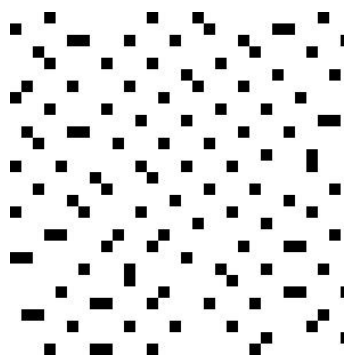
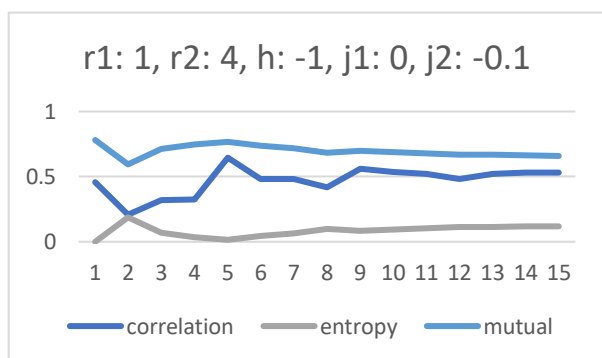
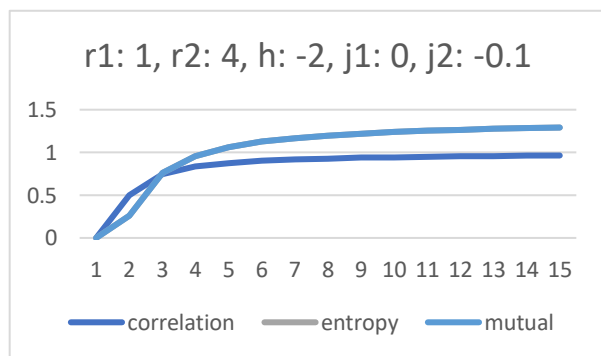
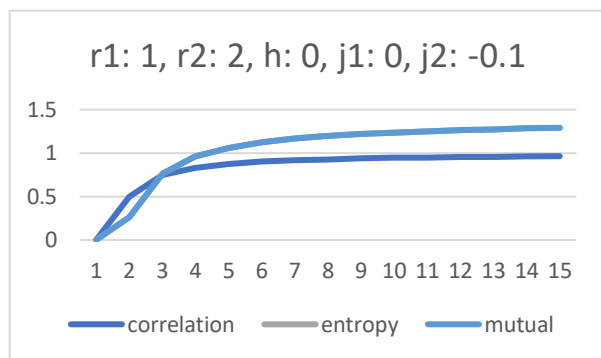
### Experiment 1

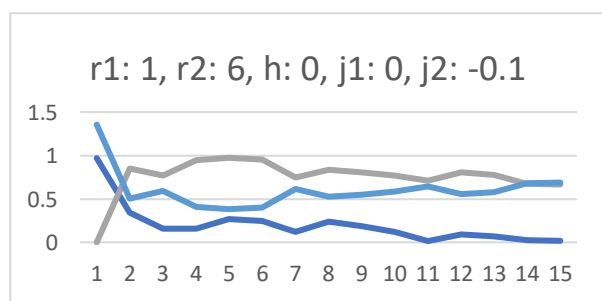
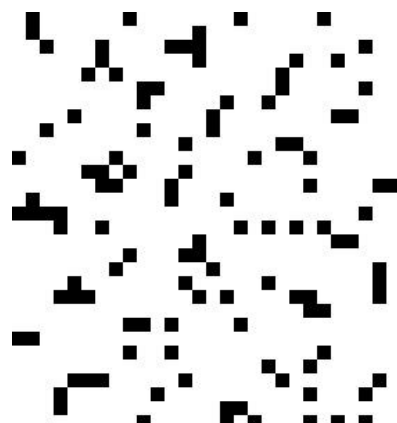
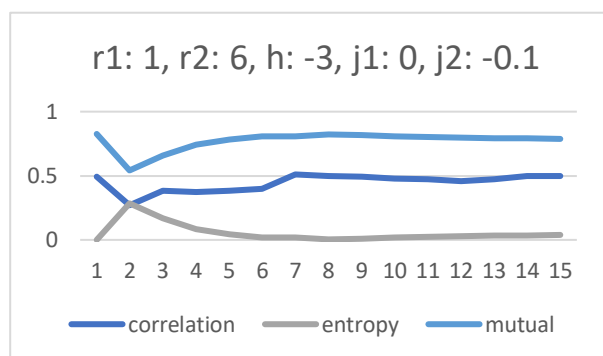
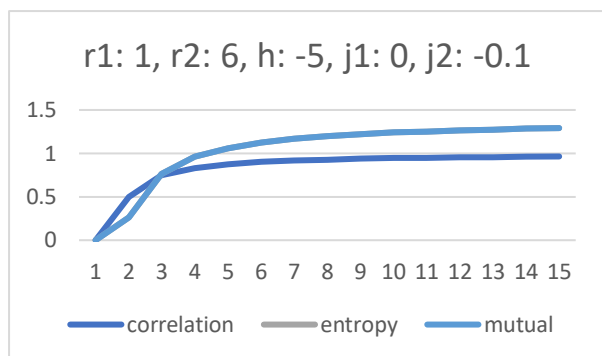


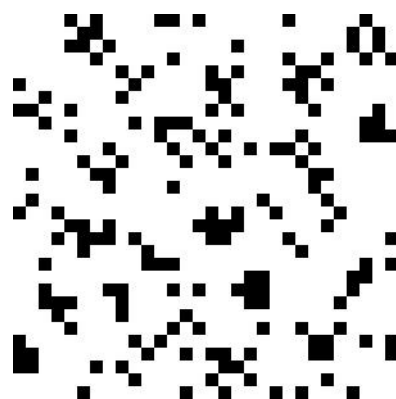
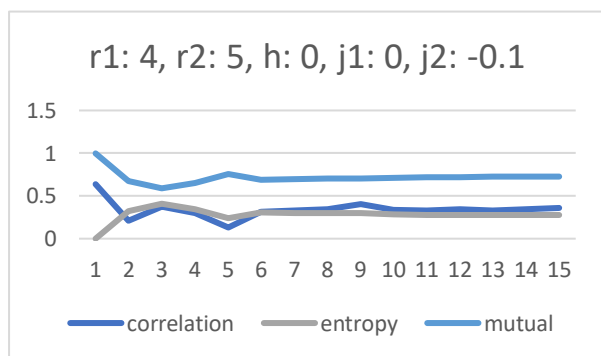
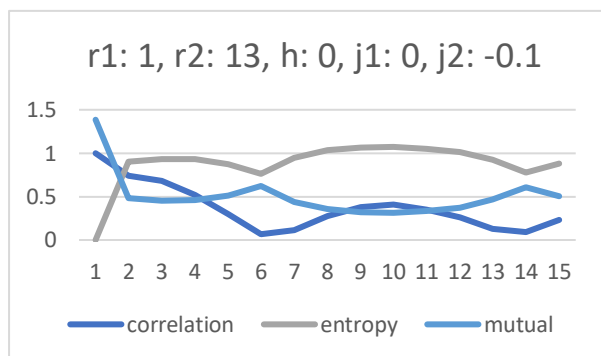
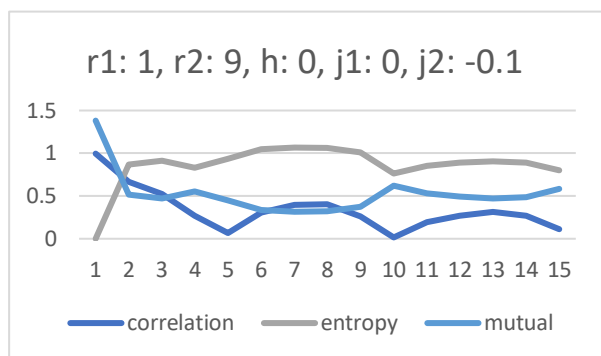
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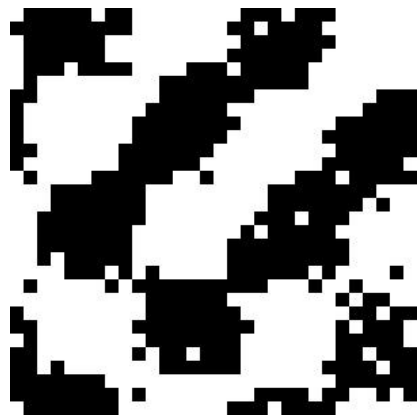
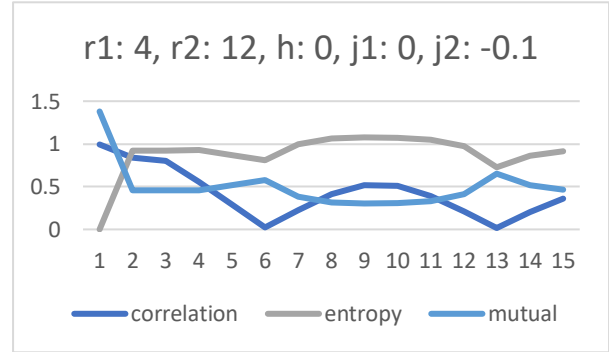
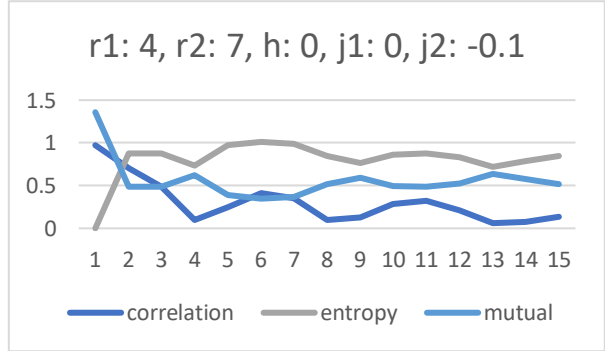
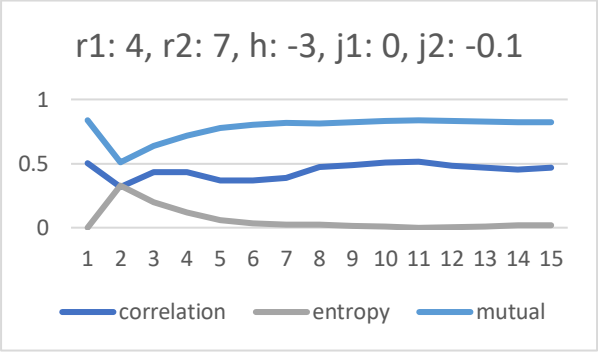
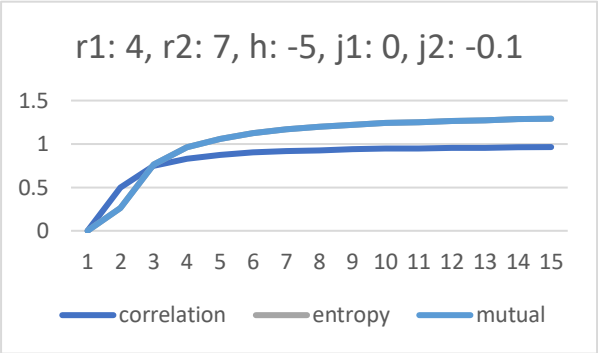
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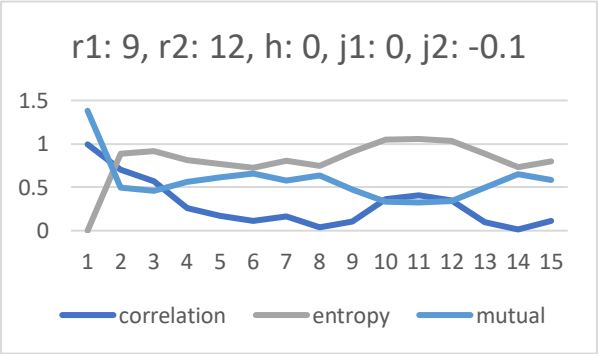
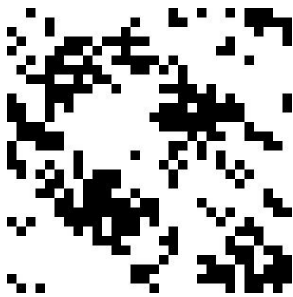
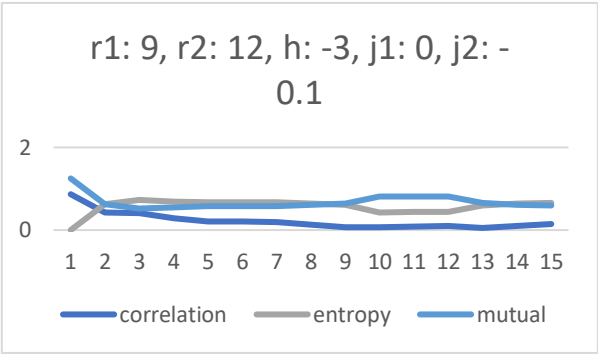
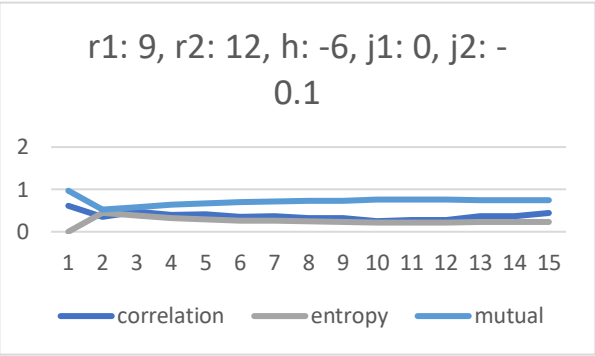








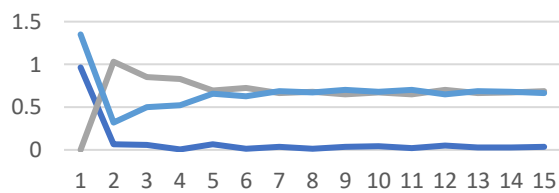




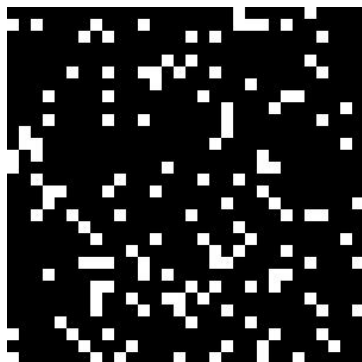
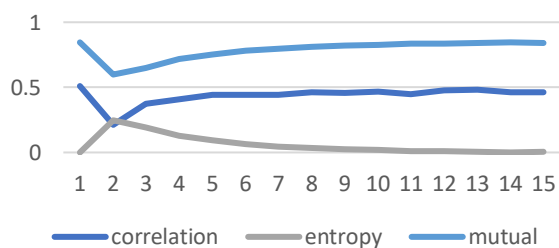
Experiment 3



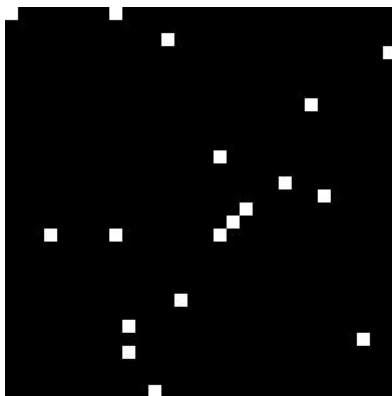
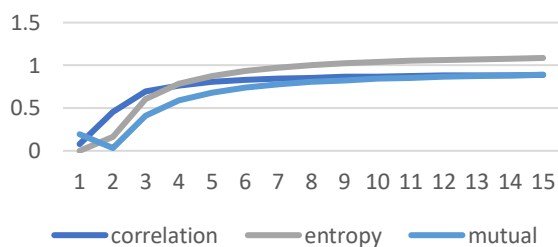
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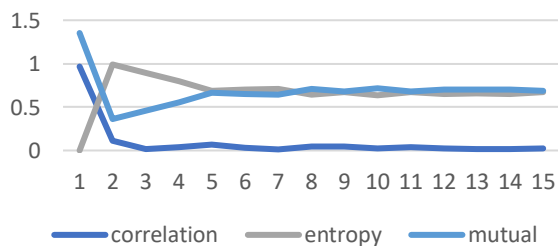
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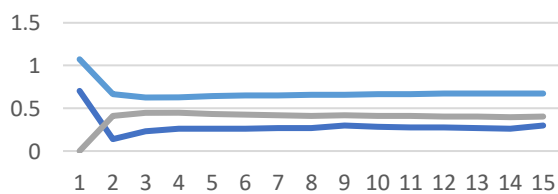
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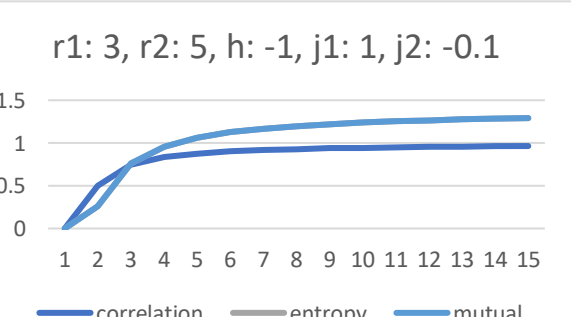
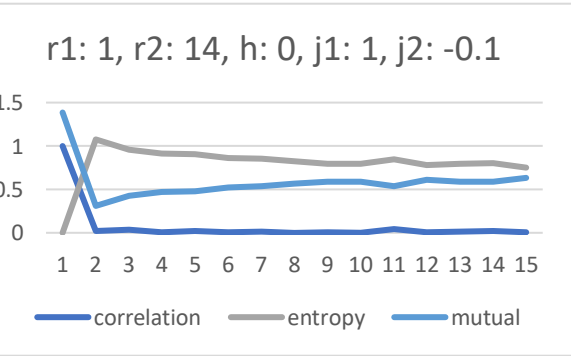
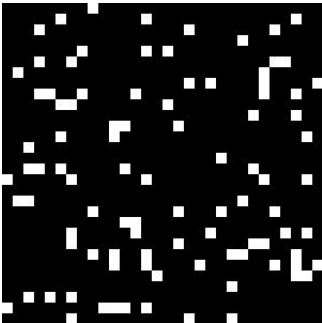
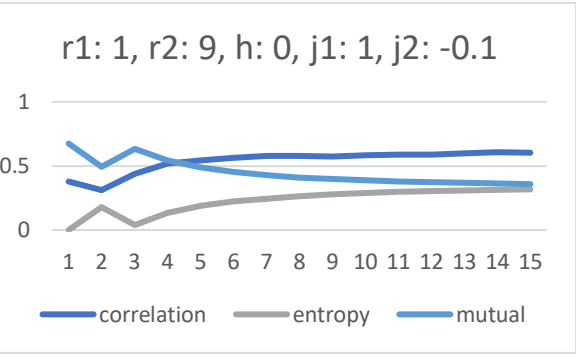
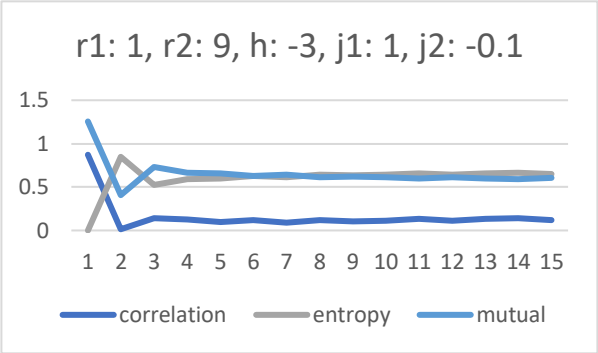


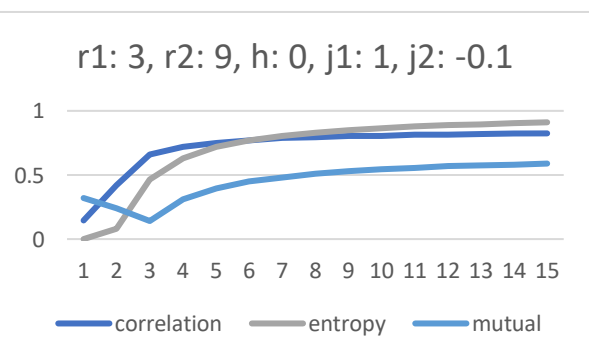
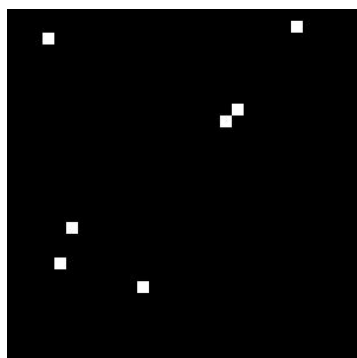
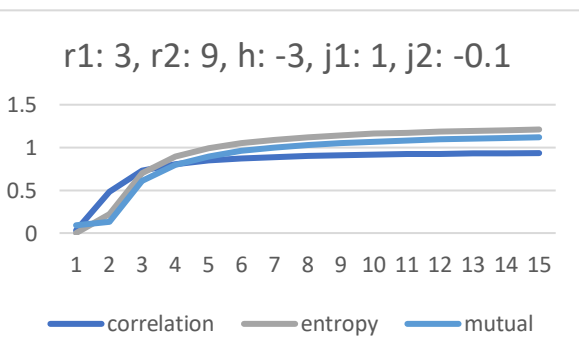
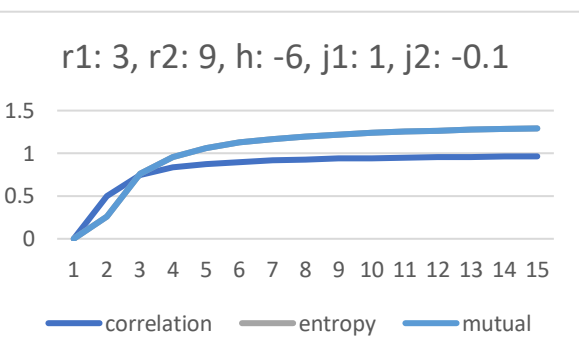
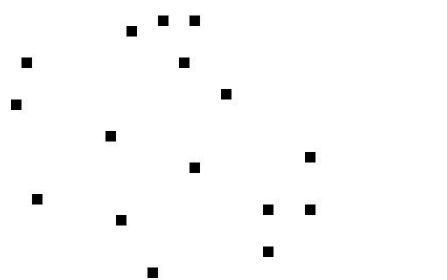
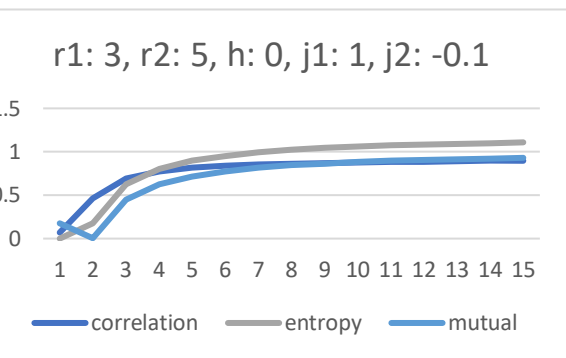
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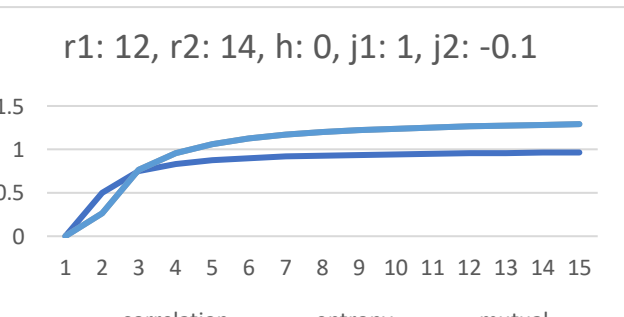
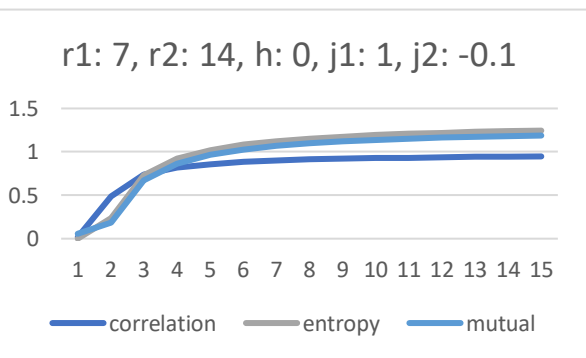
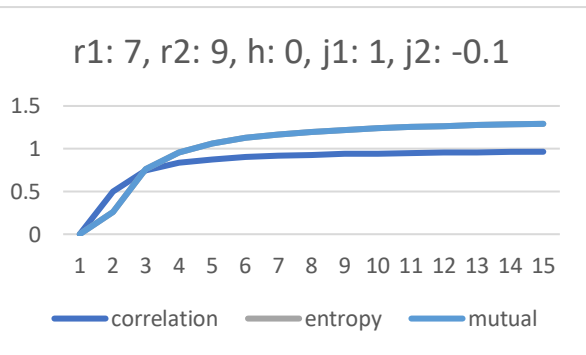
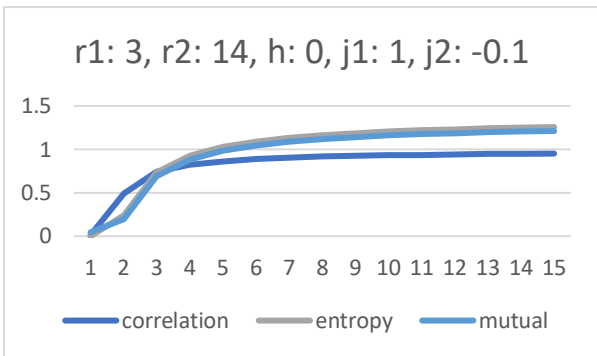
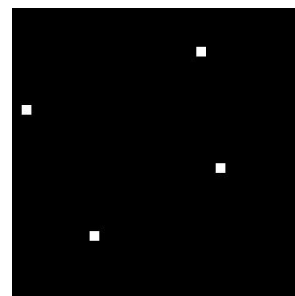
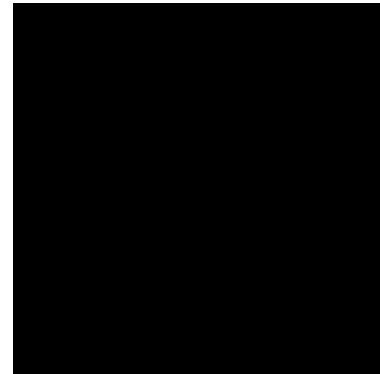
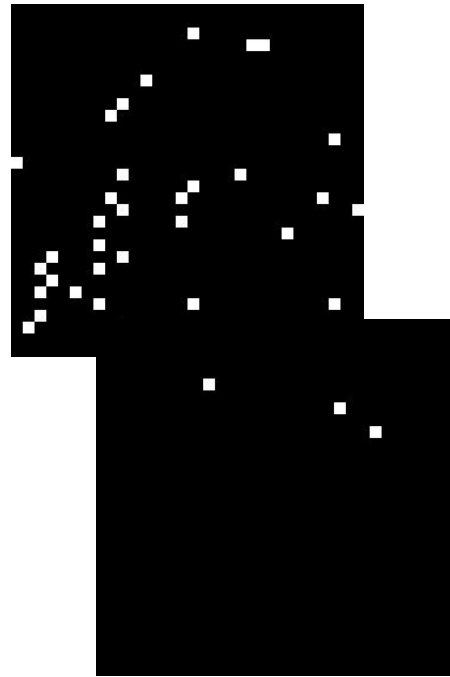


r1: 1, r2: 9, h: -6, j1: 1, j2: -0.1











## Analysis

The most obvious pattern is that when the correlation, entropy, and mutual lines all trend upward towards their maximum, then the generated picture is almost guaranteed to be either almost all black or white. One thing that was curious was that there were far fewer organic looking pictures than originally expected, though there were still enough to where the result appeared satisfying.

Of all the experiments, experiment 2 tended to create the most organic looking pictures. This is likely due to the  $J1$  and  $J2$  values, which should have disabled the activation system while still keeping some semblance of an inhibition system.

While there is certain to be some relation between the appearance of the pictures and the distribution of  $R1$  and  $R2$ , it is almost impossible to tell their effect based solely on these pictures and graphs. It all seems very random.

That being said, it is interesting that in experiment 1, every single picture turned out to be white. In those cases,  $J1$  was set to 1, and  $J2$  to 0. This means that there was no inhibition in those cases, while there was still a very strong activation system.

I would hypothesize that when the activation variable is too high, it ends activating far too many cells to reach a happy equilibrium. This can be seen in experiment 3. Converse to this example is seen in experiment 1, which had almost the same  $j$  parameters save for  $j2$ , which was

set to 0 rather than -0.1. Judging from this, I would hypothesize that some sort of inhibition is required to create activated cells, as experiment 1 was completely devoid of them.

Based on the above, it should follow that a happy middle ground might exist when  $j_1$  is not set too high, and  $j_2$  is not set to 0. This is where experiment 2 makes its appearance. It has both of the characteristics hypothesized to create organic looking pictures, and as can be seen from the pictures, it does. The cells are able to die off if they are not excited, and yet it is not made too difficult for the cells to become activated. This leads to a state that is always in flux, at least more often than is seen in the other examples.

Also, while there are not enough organic pictures to say this for certain, it seems as if a smaller range of  $r_1$  and  $r_2$  creates smaller black masses and white gaps in the organic pictures.

It is difficult to say how much of an impact the bias,  $h$ , has on the formation of the pictures.

### Conclusion

All in all the project went fairly well. There were no real issues with getting the data to write to the proper locations, and the visualizations, as represented by the pictures and graphs, seemed to be fairly good representations of what the program was doing. It was very interesting to see how the different variables affected the pictures. Based on the data gathered, it seems evident that the variables most influential to the formation of organic pictures are  $j_1$  and  $j_2$ .