AICA Spatial Structures

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CS420

February 17th, 2019

Introduction:

In this project we coded the creation of spatial structures with AICA. This simulation program was written in Python and tested with parameters J1, J2, R1, R2, and h to create images and calculate spatial correlation, entropy, totalistic entropy, and mutual information. There were three different types of experiments conducted: One where J1 (activation) is set to zero and disabled, another where J2 (inhibition) is set to zero and disabled, and another where both J1 and J2 are enabled. Over the course of the experiments the interaction ranges (R1 is the small range, R2 is the large range) and bias (h) were manipulated to find patterns in behavior. With each experimental set a measure of correlation, joint entropy, entropy, and mutual information was calculated and stored. A total of 54 sub-experiments between the three types. In addition, a .csv file was created to store the data at each distance and created graphs/charts for each experiment.

Theory and Methods:

The AICA accepts arguments for J1, J2, R1, R2, h, whether the user would like to create a chart, and a unique ID number. After randomly creating a 30x30 grid of -1's and 1's (denoting white or black color) it is then sent to a state update function where each cell is updated. This allows the AICA to converge and leads to the AICA stabilizing after a few iterations. This update sets the stage for the calculation of distance, joint entropy, entropy, mutual information, and spatial correlation.

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

Figure 1: State Update Rule Formula

The state update rule represents what cell *i* should be at time step *t+1* and is based off of the state of itself and its neighbors at time step *t*. The elements of the calculation are as follows: *h* represents the bias, the second term is the effect of all nearby cells and the third term is all far away cells. Nearby cells are determined by a simple check; if the distance (denoted in Figure 1 as r_{ij}) between two cells is less than R1, then it is considered near and multiplied by J1. Far away cells are determined by checking whether the distance between two cells is greater than or equal to R1, but less than R2. This is multiplied by J2. The multiplication by J1 and J2 respectively allow for local interactions to distinguish between states at long and short range (J1 is an activator and diffuses slowly, J2 is an inhibitor that diffuses rapidly). All cells are updated

asynchronously, and the updating process continues until no cell has changed from one step to the next.

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

Figure 2: Distance Calculation

The distance calculation is simple: Take the absolute value of the row and column values of a given two cells in the grid. If this value is greater than 15, the value of 30 to account for the wrapping of cell indices.

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

Figure 3: Joint Entropy calculation

Joint entropy, as shown in Figure 3 above, is calculated by summing over distances l and finding the probability of a black or a white cell. These are found using the formulas below:

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

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

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

Figure 4

The probability of two positive cells is equivalent to the summation of grid indexes i and j over each cell in the grid. In this case, $\beta(s) = (1+s) / 2$. This is multiplied by the two and the product of the number of cells in the grid and 4*distance. This is the same for two negatives, but each cell's value is negated. For one positive and one negative it is simply the probabilities of the above positive and negatives subtracted from one. After fetching the three terms needed for the final entropy calculation, the inverse sum of each multiplied by their logs gives the final value for each distance l.

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

Figure 5: Entropy Calculation

Entropy will also compute the probability of a state 1 or -1. To acquire the probability at a state 1: The sum of all $\beta(s_i)$ is taken for each cell in the grid and is multiplied by one over the number of cells in the grid. The probability of a state -1 is equivalent to the probability of a state 1 subtracted from 1.

$$I_l = 2H(S) - H_l$$

Figure 6: Mutual Information Calculation

The mutual information calculation between cells at a distance l is related to the joint entropy at that distance related to the conditional entropy. It uses state probabilities to use as another measure of cell state correlation.

$$\rho_\ell = \left| \frac{2}{N^2 C_\ell} \sum_{\substack{(ij) \\ r_{ij} = \ell}} s_i s_j - \left(\frac{1}{N^2} \sum_i s_i \right)^2 \right|$$

Figure 7: Spatial Correlation Calculation

To calculate spatial correlation, each cell i and j is iterated over and summed if the distance of the outermost distance loop (0-14) is equal to the distance between the two distinct cells (term one in Figure 7). This is multiplied by the quotient of two and the product of the size of the grid and 4*(distance). To note, N is equal to 30 in the above calculation, and N^2 is equivalent to the total number of cells in the grid. The second term in Figure 7 represents the accumulated sum of all cells i multiplied by the inverse of the number of cells in the grid. This calculation will result in the absolute spatial correlation at the distance.

After utilizing the state transition formula to update each cell in the grid an image is generated, and the grid is used with the said formulas to get the data at each distance l. After the data is gathered and inserted into a .csv file. If the user would like to create a graph containing the joint entropy, spatial correlation, and mutual information at each distance; then a plot is generated.

Results and Discussion:

A. Experiment 1:

In this experiment, activation is set to 1 and inhibition is disabled (J1=1, J2=0). In this experimental set the system only depends on R1 and h, since the disabling of inhibition will nullify R2. With more R1 in the system activation makes a much greater impact. This essentially means a new cell state was determined by activation.

Table 1

Experiment ID	R1	R2	h
35	1	15	-1
36	3	15	-1
37	6	15	-2

The greater impact of R1 and activation caused more convergence to single states and a much greater impact made by near neighbors. This caused many graphs to become "splotchy", such as Figure 8 below:
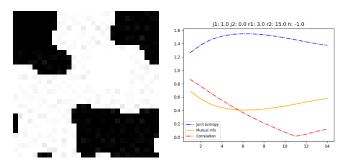

Figure 8: Experiment 36: R1=3, R2=15, h=-1.

Notice the un-interesting behavior and lack of symmetry in the graph.

A possible explanation for the behavior above could be that cells are only concerned with the state of neighbors within R1, since inhibition and R2 are disabled. Overall, in this experiment set there were not many interesting patterns. It is also worth noting that in this experiment set, as seen in the graph in Figure 8, joint entropy and mutual information were mirrored. This would be expected, since entropy is a random variable that acts as a measure of uncertainty, whereas mutual information actually uses this value to help determine a measure of correlation in a system.

B. Experiment 2:

In this experiment, activation was disabled, and inhibition was enabled (J1=0, J2 = -0.1). Since activation is disabled, R1 ceases to make an impact on the state transition: the new

state is determined by inhibition along with R2 and affected by bias. Near neighbors will not make an impact in this experiment.

Table 2

Experiment ID	R1	R2	h
38	1	2	0
39	1	4	-2
40	1	4	-1
41	1	4	0
42	1	6	-5
43	1	6	-3
44	1	6	0
45	1	9	0
46	1	13	0
47	4	5	0
48	4	7	-5
49	4	7	-3
50	4	7	0
51	4	12	0
52	9	12	-6
53	9	12	-3
54	9	12	0

Due to the lack of activation in the system and a greater impact from far cells and R2; these systems tended, in some cases, to be such more ordered than Experiment set 1 or 3. Bias still had a significant effect on the states of the cells in the grid.
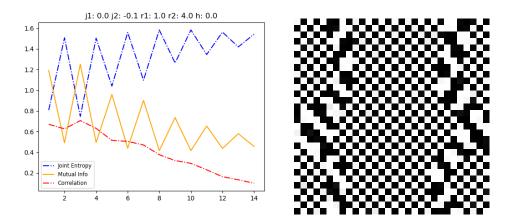

Figure 9: Experiment 41: Notice how ordered this system is and how the right and left sides are mirror images of each other, split down the middle. Also notice that Joint Entropy and Mutual Information are mirrors of each other.

With activation disabled and inhibition/R2 determining the cell states, it seems to lead to a fair amount of behavior of the sort displayed in the image in Figure 9. Split down the middle, the cell is a mirror image of the other opposite side. Additionally, as seem in the graph in Figure

9 the joint entropy's and mutual information calculations are also mirrors of each other. The grid stabilizes itself by striving to change to the state of the cell on the opposite side of the grid.

It is also worth noting that bias also plays its part in this experiment in the same way as sets 1 and 3, as seen in Figures 9 and 10 below, where each has a R2 value of 6:
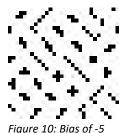

Figure 10: Bias of -5

Figure 11: Bias of 0

C. Experiment 3:

In this experiment, both activation and inhibition are enabled (J1 = 1, J2 = -0.1). I ran 35 simulations at this experiment set. In this set with both J1 and J2 enabled it was important to heavily test the affects of a small R1, a larger R1, different measures of bias, and closeness/farness of R1/R2.

Table 3

Experiment ID	R1	R2	h
0	1	2	0
1	1	5	-4
2	1	5	-2
3	1	5	0
4	1	5	2
5	1	5	4
6	1	9	-6
7	1	9	-3
8	1	9	0
9	1	9	3
10	1	9	6
11	1	14	-6
12	1	14	-3
13	1	14	0
14	1	14	3
15	1	14	6
16	3	5	-1
17	3	5	0
18	3	5	1
19	3	9	-6
20	3	9	-3
21	3	9	0

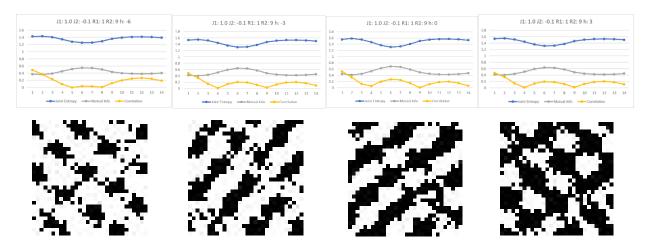| 22	3	9	3
23	3	9	6
24	3	14	-6
25	3	14	-3
26	3	14	0
27	3	14	3
28	3	14	6
29	7	9	0
30	7	9	1
31	7	14	-3
32	7	14	0
33	7	14	3
34	12	14	0

Figure 12: Experiments 6-9: J1 = 1, J2 = -0.1, R1 = 1, R2 = 9, h = -6, -3, 0, 3

Notice the black cells diverging out from a nucleus like block when bias is increased. It seems to be diverging slowly, as the graphs from one experiment to the next do not change radically.

In the above Figure 12 graphs and corresponding images for the final states of experiments 6 through 9, the effect of bias can be seen in the patterns. This can be expected, since a negative bias will cause a higher concentration of white cells, and a positive bias will lead to a higher concentration of black cells. This is due to the influence of the state update rule. Since J1 is higher than J2 here, cells will be affected much more by closer cells than cells that are further away and is why the cells look as though they are clustering together around a nucleus. It is also illustrated in the graphs of the final parameters, as they do not differ significantly. It is also worth noting that a low R1 and a higher R2 will also lead to a closer cell relation to its neighbors, also contributing to the clustering.
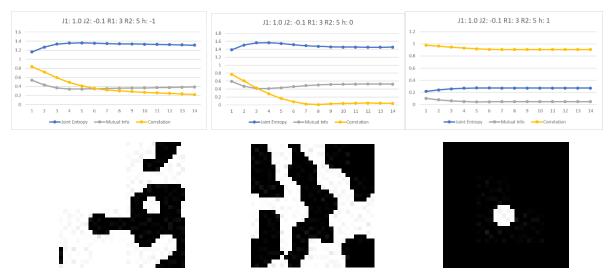
Figure 13: Experiments 16-18: J1 = 1, J2 = -0.1, R1 = 3, R2 = 5, h = -1,0,1

Notice the cells converging to a single state with a small change in the bias.

When R1 and R2 are closer like in the situation in Figure 13, then the spatial correlation will be greater. As such, the experiments above show that with small changes to bias there are significant effects. The cells will try much harder to be the same state as their neighbor and leads to the grid converging to an all-black state (also illustrated in the graph with correlation converging to 1 and joint entropy/mutual information converging to 0) when the bias is larger than 0 and an all-white state when the bias is negative. With the 0 bias, R1-J1 and R2-J2 determine the state transitions and the updates are entirely rely upon these relations.

Overall, in Experiment 3 the farther R1 and R2 were apart such as in Figure 13, the lesser the magnitude the bias had on the final states of the AICA's. When R1 and R2 were closer together such as in Figure 13 the radii had a much more profound impact. This can particularly be seen using the bias at 0 in Figure 13 (sub-experiment 17) compared to a mere single change in the positive and negative directions in sub-experiments 16 and 18.

Conclusions:

Throughout each experiment, the parameter that was most consistent in influencing a cell's transition state was bias. As shown in the experiments above, it never ceased to make an impact on the results. In Experiment 1 and Experiment 2, the findings were fairly predictable in nature. In Experiment 1 inhibition is disabled so the system cell updates depend only on R1 and h (since activation is 1 in this Experiment set). This led to more radical impact with only system activation, with many more experiment runs converging to a single state and cells concerned primarily about the state of near neighbors. In Experiment 2 where the state transition is dependent on inhibition and R2, the lack of activation leads to a far greater impact from far cells. In some cases, this even caused cells to strive to update to the state of the opposite cell on the grid. This led to the grid being a mirror image of itself, split down the middle. As for Experiment 3 where both inhibition and activation were enabled: bias and the difference between R1 and R2

were the deciding factors of the state update. The impact of bias turned out to be much more profound with a smaller R1/R2 difference, and much less amplified with a greater difference. With a smaller R1/R2 difference, states were also much more likely to converge to a single state more rapidly than would an experiment with a greater difference in values.