Creation of Spatial Structure by Activator/Inhibitor Cellular Automaton

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Introduction

Cellular automata (CAs) can be used to replicate many of the patterns and behaviors of many systems found in everyday life. One common use for CAs is the simulation microscopic cellular and particle interactions. One of the most visible kinds of patterns found is life is ones created by the arrangement of skin and hair cells. Many animals such as zebras, fish, snakes – even humans – have distinct, visible patterns made by the specific arrangement of skin and hair cells. Interestingly, these patterns are completely independent of overall cell and animal size. Each separate cell has no way to know the color or pattern of another cell, but distinct patterns are still able to arise across the animal.

This phenomenon is achieved by short-range activation and long-range inhibition of cells and their states (colors). Through the use of an activator/inhibitor cellular automaton (AICA), one can replicate and alter these patterns. An activator/inhibitor network is created by its state update rule:

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

Figure 1: State Transition Rule for AICA model

Each of the variables (*h, R_1, R_2, J_1,* and J_2) have distinct effects of the overall pattern produced by the model. Through the manipulation of these variables, this experiment will explore, investigate, and measure the creation of spatial structures by an activator/inhibitor cellular automaton.[1]

Theory and Methodology

To measure the spatial structure of an AICA model, one must first develop terms to accurately quantify the overall structure. The first of these terms is *spacial correlation*. Spatial correlation measures "the extent to which the states of cells at various distance are correlated to each other.[1]" This variable can be calculated by the following formula:

$$\rho_l = \left| \frac{2}{N^2 C_l} \sum_{\substack{\langle \mathbf{ij} \rangle \\ r_{\mathbf{ij}} = l}} s_\mathbf{i} s_\mathbf{j} - \left(\frac{1}{N^2} \sum_{\mathbf{i}} s_\mathbf{i} \right)^2 \right|.$$

Figure 2: Formula for calculating spacial correlation at distance *l*

The second quantitative term that will assist in examining the structures of AICA models is *mutual information.* Mutual information is a "way to measure the correlation between cells states.[1]" The equation for mutual information is given as:

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

Figure 3: Equation for Mutual Information of cells at distance *l*

In this variable, it is clear that mutual information is closely related to the overall *entropy*, *H*(S), of the system as well as the *joint entropy*, H_l, between cells as at distance *l.* The formula to calculate overall entropy utilizes the probabilities of each state within the model. As such, the formula to calculate entropy as well as the probabilities of each state is as follows:

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

Figure 4: Probability equations for each possible cell state (+1 or -1)

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

Figure 5: Equation for average entropy of the cellular space S.

Joint entropy is computed for each possible distance *l* (0 to 14). The joint entropy equation also uses the probabilities of each pairing of states. There are three possible pairs of states (two positives, two negatives, and one positive/one negative) The equations for joint entropy and the probabilities of the matching of each state is as follows is:

$$P_l\{+1,+1\} = \frac{2}{N^2 C_l} \sum_{\substack{\langle \mathbf{ij} \rangle \\ r_{\mathbf{ij}} = l}} \beta(s_{\mathrm{i}})\beta(s_{\mathrm{j}}) \ .$$

$$P_l\{-1,-1\} = \frac{2}{N^2 C_l} \sum_{\substack{\langle \mathbf{ij} \rangle \\ r_{\mathbf{ij}} = l}} \beta(-s_{\mathrm{i}})\beta(-s_{\mathrm{j}}) \ .$$

$$P_l\{+1,-1\} = P_l\{-1,+1\} = 1 - P_l\{+1,+1\} - P_l\{-1,-1\} \ .$$

Figure 6: Probabilities for states of two separate cells

$$H_l = -\left(P_l(+1,+1)\lg P_l(+1,+1) + P_l(-1,-1)\lg P_l(-1,-1) + P_l(+1,-1)\lg P_l(+1,-1)\right).$$

Figure 7: Equation for joint entropy for each distance *l*.

The program included in this submission, *p2.cpp*, handles all of the work with calculating these quantitative variables. Furthermore, it simulates an activation/inhibition cellular automaton network for exploration and measurement. Each of its main functions operate as follows:

- **initGrid** – initializes a 30x30 CA with cells of a random state -1 or +1
- **updateGrid** – utilizes the state transition rule to update CA cells
- **getDist** – Calculates the distance between cells by the L_1 metric
- **getEntropy** – Calculates the average entropy of the system
- **getJointE** – Calculates the joint entropy for each distance *l* (0 to 14)
- **getCorrelation** – Calculates the correlation of cells for each distance *l*
- **getMI** – Calculates the mutual information of cells for each distance *l*

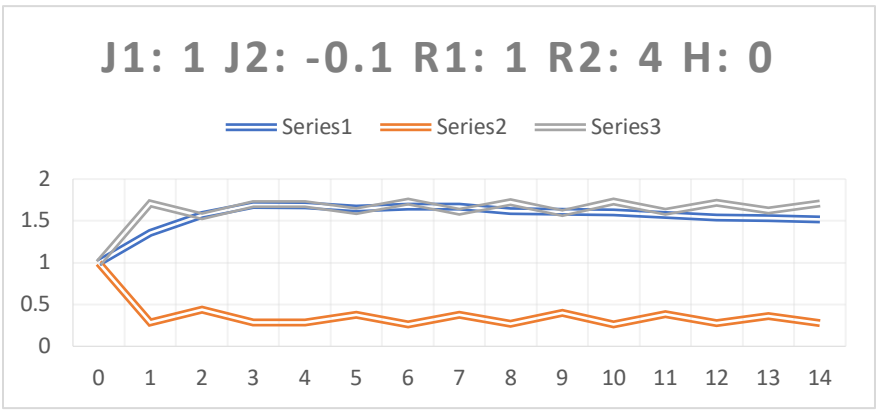
The program first initializes a 30x30 2D CA and randomly sets the states of each cell using a designated density. After initialization, the program proceeds to update the grid repeatedly until the CA has converged to a stable AICA state. After stabilization the program then calculates each of the previously mentioned quantitative variables.

The methodology of this experiment is focused on investigating the effect each of the parameters (*h, R_1, R_2, J_1,* and J_2) have on the quantitative measures and qualitative behavior of the AICA network model. To accomplish this, three overarching experiments will be conducted – each with their own restrictions and guidelines. The experiments are as follows:

Experiment 3: Enable both inhibition and activation by setting $J_1 = 1$ and $J_2 = -0.1$. This will allow the AICA network to normally operate within respects to its entire state update rule (**Figure 1**).

Results and Findings

Legend: Series 1: Correlation **Series 2:** Joint Entropy **Series 3:** Mutual Information



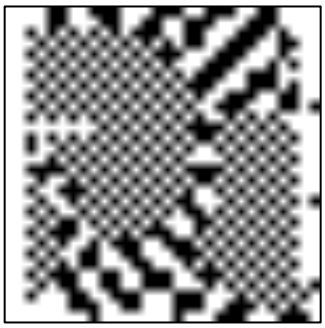
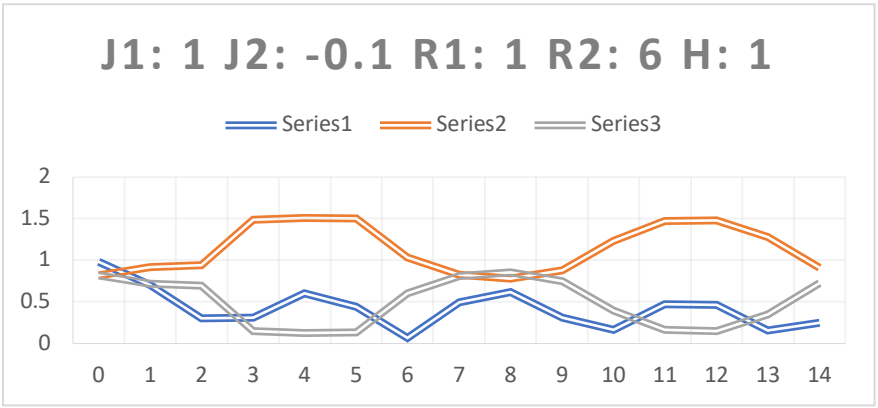


Figure 8



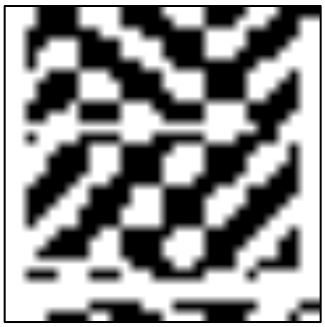


Figure 9

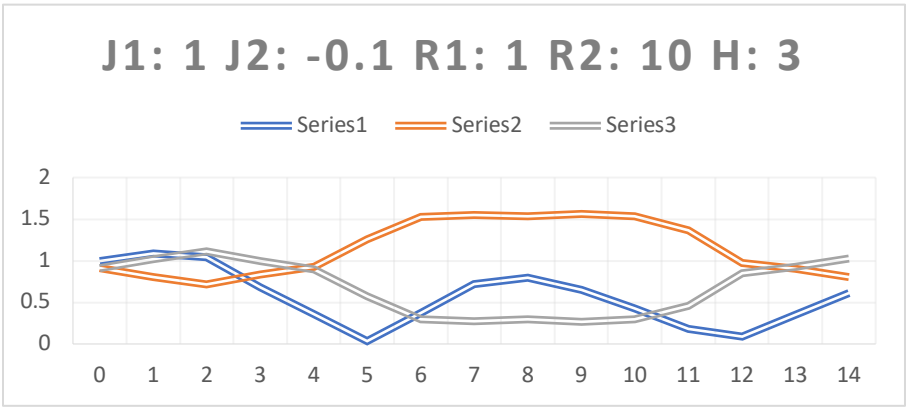


Figure 10

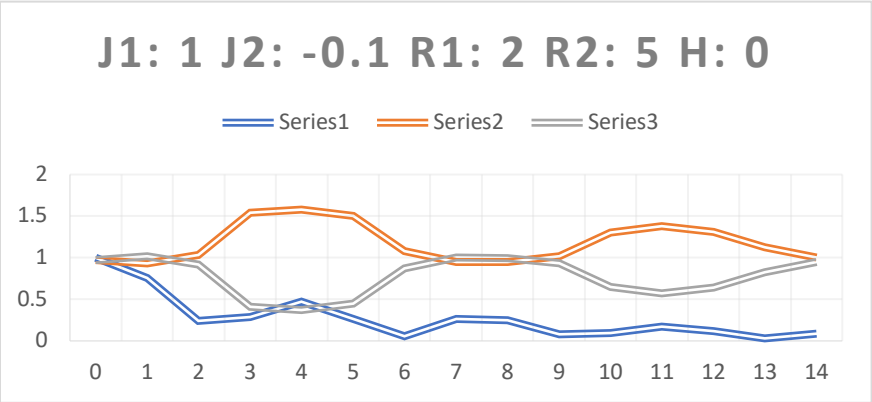


Figure 11

Conclusion

In the nominal situation – inhibition and activation both activated – there were some interesting results found. Firstly, through scaling the R_2 parameter, it was discovered that longer, more simple patterns begin to arise as R_2 approaches 14. Inversely, it was found that as R_1 increased, the patterns became more separated and bubble-like. These observations lead to the reinforcement of conclusion that R_1 dictates close-range interactions while R_2 directly influences long-range ones.

Furthermore, as R_2 began to increasingly grow in difference to R_1 the overall model tends to converge to an all-black state. To counteract this, bias was added (**Figure 10**). This strategy was used to also counteract the all-white state. This situation leads to the emergence of some very interesting patterns. However, once R_2 reached the range of [11,14], no amount of bias was able to counteract this effect.

In regard to the quantitative variables, throughout each experiment correlation seems to follow a similar trend to mutual information. They both tend to decrease early in the distances [2,5] before increasing throughout the range [6,9]. This is usually followed by a steady decrease in all variables as the distance increases. As expected, higher R_2 values resulted in a less apparent drop as the distances increased.