**Automated Cellular Automata Rule Extractor For Images of Extremophiles.** R. Cai[1], K. E. Schubert[1], E. Gomez[2] and P. Boston[3], [1]Baylor University, [2]California State University, San Bernardino, [3]NASA Ames Research Center.

**Introduction:** Biological patterns are common, but some are particularly striking and appear as if drawn. In some resource constrained environments, biological systems form patterns which may serve to optimize their return on the effort to acquire the needed resources [1]. This is particularly noticeable in caves, where communities of microbes form distinctive and recognizable patterned mats or thin films on surfaces, which are called biovermiculations for their worm-like or hieroglyphics-like appearance. These patterns persist over time, partly because cave environments are not perturbed by surface weather, and some only rarely by events like flooding or animal activities, and some microbial activities result in ongoing mineralization of patterns. Thus, such patterns can provide evidence of life even when the microbial activities may have long ceased.

**Model Genereration:** Models are usually generated and tuned by experts to mimic the patterns observed in nature. To extend these tools in a practical fashion to the search for life on Mars or other astrobiology targets, requires an inversion of this approach. Namely, images from rovers or other exploration craft must be used to automatically generate models to analyze the potential that life either still is or at one time was present. Using imaging to pre-screen test sites can provide a huge advantage, given the limited number of available chemical or physical tests that a rover can do. Each image can be treated as a cellular automaton (CA) state, then the inverse problem must be solved to determine the rules that generated it. This is an extremely difficult problem, since, in general, it is not actually possible. This issue could be addressed by using time series data [2], but that is often not available. We only restrict the type of CA to the "potential well" models of [1] then use a swarm algorithm to determine the rules with only one state/picture.

**Particle Swarm:** A particle swarm is an optimization algorithm in which a large number of guesses (dubed particles) are tried and modified. The particles have a location (the guess) and a velocity (how to modify the guess), which are modified by the behavior of the swarm adapting to the environment (what you are optimizing). The entire algorithm is described in [3], but is summarized for our case by

1. Initialize particles with random rules.
2. Simulate rules and compare to target (fitness).
3. Calculate a velocity for each particle based on the comparison, and both the swarm's and that particle's best guesses so far.
4. Update the position of each particle, using it's current position and velocity.
5. Go back to step 2 and iterate until criteria is met.

**Results:** Simulated patterns were generated so the true ruleset could be used to test the accuracy of the method. After 20 iterations of the swarm, we consistently obtained good rule sets that had parameters within 2-5% of the original rule set as long as there are sufficient data in the region, i.e. if you have a high density pattern you will get rules governing how the unknown organism behaves in high density situations but not necessarily how it would behave in low density situations. Figure 1 shows a target pattern from the rule [0.2,0.25,0.3,0.35,0.5,0.55,0.6,0.65]. Note that the pattern has mostly red (maximum biomass per cell) or blue (no biomass in cell). Density is calculated by averaging all nearby cells up to a set range and grouped by dead centers (middle cell is blue) and live centers (middle cell is not blue). The target density plot in Figure 2 shows that we have more data on the denser part of the graph (higher probabilities on the right) so these are the rules we best obtain. After 20 iterations, the best resulting pattern in Figure 3, is remarkably similar. The estimated rule, [0.24,0.416, 0.429,0.433,0.467,0.546,0.595,0.629], is a good fit for the four larger numbers (high density) consistent with our prediction based on density plots.

Figure 1. Target Pattern

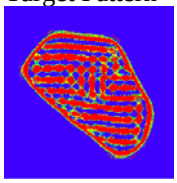


Figure 3. Result Pattern

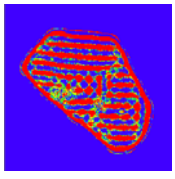
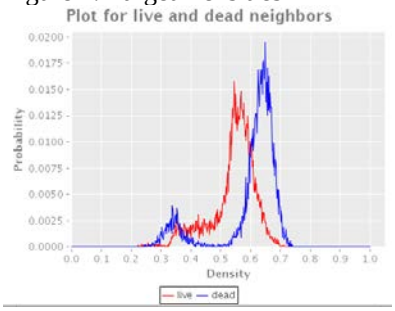


Figure 2. Target Densities




**References:** [1] P. Boston, et al (2015) AbSciCon, abstract #7720. [2] F. Richards, et al (1990) Physica D: Nonlinear Phenomena, vol. 45, no. 1-3, pp. 189–202. [3] G. Venter et al, (2002) AIAA Journal, pp. 1583–9.