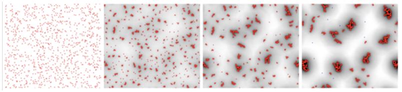
A Genetic Programming Framework for the Simulation and Design of Self-assembling, Chemotaxis-driven Cell Aggregates

David E. Breen and Linge Bai
Department of Computer Science, Drexel University

Introduction

- Motivated by the ability of living cells to form specific shapes and structures, we have developed spatial self-organization algorithms based on chemotaxis-driven cell aggregation behavior.
- The algorithms utilize a cell aggregation simulation system that accurately models individual cells, chemical diffusion, cell motility along chemical field gradients, and cell attachment.



- The self-organizing primitives, called Morphogenetic Primitives (MP), do not completely mimic the behavior of real cells. Their individual chemical fields are explicitly defined as mathematical functions.
- Genetic Programming (GP), an evolutionary computing process, is employed to discover the functions needed to produce a specific shape.
- We intend to combine the accurate cell simulation system with the GP framework to produce an approach to designing self-assembling, chemotaxis-driven aggregates of living cells.

Morphogenetic Primitive (MP)

A macroscopic, user-defined shape emerges from the combined actions of the individual primitives. The design principles of the primitives are:

- MPs are autonomous agents with no central controller.
- Actions are based on local information. Chemical fields are finite and MPs do not know their global location.
- All MPs respond to stimuli with the same behaviors.
- MPs have no representation of the final, macroscopic shape.
- Shape emerges from the aggregation of local interactions.

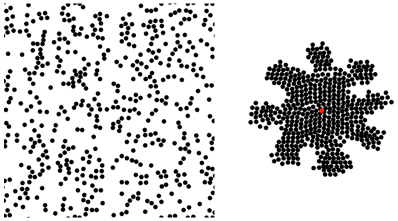


Figure 1. A set of randomly placed MPs (left) aggregate to form a "gear" (right).

Cell Aggregation Simulation

- Each MP simulation process begins by randomly placing a number of MPs (500 for our examples) in the computational environment. A morphogenetic primitive is represented by a small disk existing in a toroidal 2D environment.
- We assume that MPs travel at a terminal velocity through a viscous fluid environment, therefore an MP's velocity is directly proportional to the chemical field gradient (∇C). When an MP moves in the direction of the chemical gradient, its velocity is calculated as

$$\text{Velocity} = \lambda * \nabla C, \qquad (1)$$

- Where λ (1 for our example) is a constant that determines the magnitude of a cell's response to the gradient. At each simulation time step (Δt) the displacement of the MP is

$$\Delta x = \text{Velocity} * \Delta t . \qquad (2)$$

Genetic Programming Framework Overview

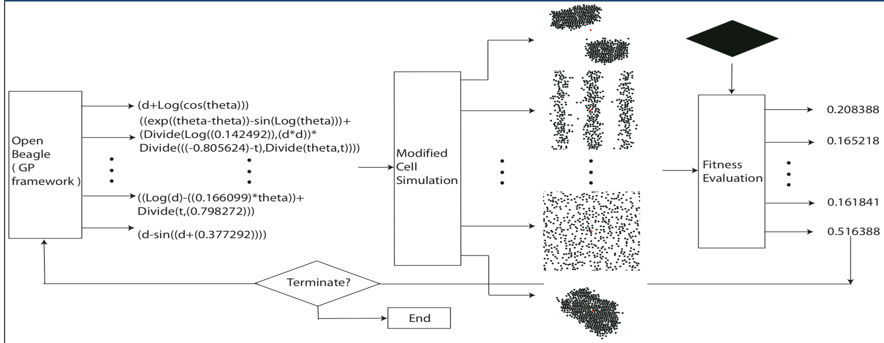
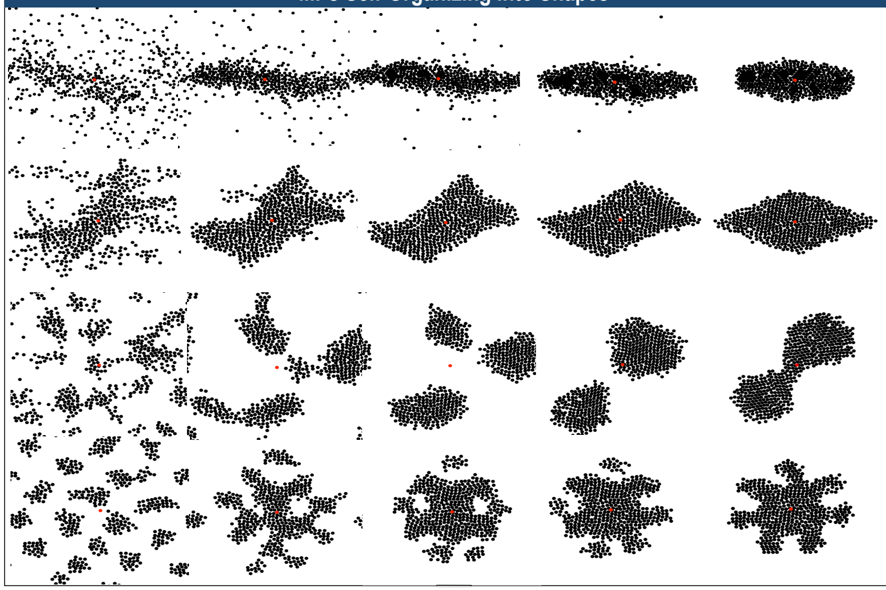


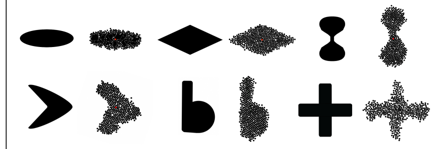
Figure 2. Overview of the genetic programming process that produces the behaviors of morphogenetic primitives

- We start with a population of mathematical functions, which is initially randomly generated. Each individual function is compiled into a chemotaxis-based cell aggregation simulation, and defines the chemical field that surrounds each cell in an aggregation simulation.
- A cell aggregation simulation is computed for each field function, usually producing some kind of aggregated structure. The resulting structure is compared to the user-desired shape, and a scalar fitness value is calculated that quantifies how well the input shape matches the target shape.
- A subset of the top candidates are then used to create the next generation of field functions. The process continues until a field function produces the desired shape or the maximum number of generations is reached.

MPs Self-Organizing into Shapes

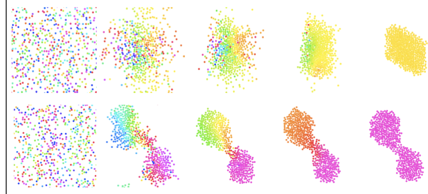


Comparisons between Goals and MP Aggregates

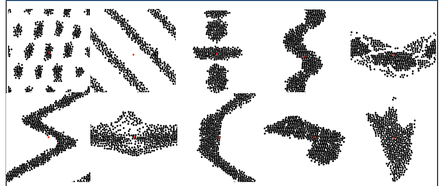


MP Self-Alignment

- Each MP has its own coordinate system and is given an initial random orientation, which is visualized with a color.
- An MP can sense the orientations of its nearest neighbors and rotates to align with their average orientation, producing an overall uniform alignment.

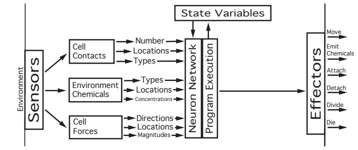


Some Unexpected Results



Extensions for Cell Aggregate Design

- Replace the internal representation of virtual cells with a programmable data flow model that accurately simulates cell behavior.



- Similar to Sims (1994), evolve the internal data flow structure and variables to produce the desired shape from the resulting aggregation behavior.
- Main challenge: To evolve the internal program of a virtual cell in a way that is consistent with living cells.

Related Publications

[1] L. Bai, M. Eyiyurekli, and D. Breen. Automated shape composition based on cell biology and distributed genetic programming. In *Proc. Genetic and Evolutionary Computation Conference*, pp. 1179-1186, July 2008.
[2] M. Eyiyurekli, P. Manley, P. Lelkes and D. Breen, "A Computational Model of Chemotaxis-based Cell Aggregation," *BioSystems,* Vol. 93, No. 3, pp. 226-239, Sept. 2008.
[3] K. Sims, "Evolving virtual creatures," *Proc. SIGGRAPH*, 1994, pp. 15–22.