Self-Organizing Primitives for Automated Shape Composition
Linge Bai, Manolya Eyiyurekli, David E. Breen
Department of Computer Science, College of Engineering

Introduction
• Motivated by the ability of living cells to form specific shapes and structures, we present a new approach to shape modeling based on self-organizing primitives whose behaviors are derived by genetic programming.
• The key concept of our approach is that local interactions between the primitives direct them to come together into a macroscopic shape. Given a prescribed shape as a goal, what is the local interaction rules that direct this primitives to form an aggregation similar to the target shape?
• The interactions of the primitives, called Morphogenic Primitives (MP), are based on chemotaxis-driven aggregation behaviors exhibited by actual living cells. Here, cells emit a chemical into their environment. Each cell responds to the stimulus by moving in the direction of the gradient of the cumulative chemical field detected at the surface. MPs do not completely mimic the behavior of real cells. Their chemical fields are explicitly defined as mathematical functions and are not necessarily physically accurate.
• Genetic Programming (GP), an evolutionary computing process, is employed to discover the local interaction rules between the primitives.

Morphogenic Primitives (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.
• Actions are based on local information.
• MPs respond to information with prescribed behaviors. Each individual is compiled into a population of individuals, which are going to evolve in the evolutionary process, represents a number of candidate solutions to the problem. Therefore, a population of individuals, which are going to evolve in the evolutionary process, represents a number of candidate solutions to the problem.

We start with a population of expressions, which is initially randomly generated. Each individual is compiled into a chemotaxis-based cell aggregation simulation, as the chemical field that surrounds the individual cells.
• 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-defined shape, and a scalar fitness value is calculated that quantifies how well the input shape matches the desired 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.

Cell Aggregation Simulation
• Each MP simulation process begins by randomly placing a number of MPs (500 for our examples) in the computational environment. A morphogenic primitive is represented by a small disk existing in a toroidal 2D environment.
• We assume that MPs travel at a constant velocity through a viscous fluid environment, therefore an MP's velocity is directly proportional to the chemical field gradient (VC). When an MP moves in the direction of the chemical gradient, its velocity is calculated as Velocity = k*VC, (3)
• Where k (for our example) is a constant that determines the magnitude of a cell’s response to the gradient. At each simulation time step (dt) the displacement of the MP is
\[ \Delta x = \text{Velocity} \times \Delta t \] (2)