Digital Chemotaxis

Andy Lomas
Goldsmiths, University of London
London SE14 6NW
a.lomas@gold.ac.uk

1. INTRODUCTION

Chemotaxis, the process by which cells migrate following spatial cues, is most commonly modelled with cells following simple attractive or repulsive gradients. Through their studies of the slime mould Dictyostelium discoideum (Seigert & Weijer 1992, 1995) proposed an alternative model with propagating periodic waves of chemicals where the cells actively move into the direction of wavefront propagation as well as amplify the chemical signals as the waves pass through them. They found that this system could model all the observed major structures and types of cellular motion seen during the full life cycle of Dictyostelium discoideum, including cells moving as separate individuals, joining together into tendril like aggregations, and accumulating into slug like structures composed of large number of cells that move coherently together (Weijer 2004).

The inspiration for the work presented here is a conversation the author had with Prof. Weijer while visiting the School of Life Sciences in Dundee. Rather than accurately modelling biological processes, this work focuses on abstracting the core idea to create a simulation of a field of chemicals in a medium capable of supporting periodic waves, with cellular agents immersed in the field that can amplify the chemical waves and actively move in directions based on the wavefronts of chemical propagation. The aim is to create a simplified mathematical model suitable for efficient parallel computation which can be used in an artistically led exploration of the potential range of self-organising emergent behaviour.

2. IMPLEMENTATION

The system is composed of two main components:

1. A field of chemical values.
2. Cells that occupy arbitrary positions in space.

The chemicals are represented by a bounded region of points discretely sampled on a 2D or 3D grid. To facilitate the chemicals forming periodic waves the grid is set up as a mass spring system with a restoring force at each sample point that pulls the chemical level towards an equilibrium value. There is also a process of diffusion, whereby at each time step chemicals diffuse to adjacent positions in the grid. This creates a system with dynamics sufficient to support wave propagation.

Each cell can sample the values and spatial gradients from the chemical grid at their local position. Combined with a memory of the previous sampled values this allows an estimate of the direction of wave propagation, which can be used to affect the motion of the cells. A value is also calculated for the number of cells in proximity to each grid point, which is used to affect the rate of change of chemical at that location in a manner that amplifies the chemical signal.

The system is initialized using uniform random positions for the cells, and uniform random values for the chemical levels at each point in the grid.

The author has implemented the system in a variety of frameworks, including:

- OpenFrameworks using GLSL compute shaders.
- Using the CUDA GPU parallel processing and OptiX ray-tracing libraries from NVIDIA.
- Unreal Engine's Niagara effects system.

All of these implementations take advantage of the capabilities of modern graphics processors for massively parallel processing, potentially allowing results to be computed and rendered in real-time.

As well as simply rendering the cells as point primitives or spheres, the author has explored a variety of other rendering methods, including:

- 2D planes visualizing the chemical levels.

- Using a scalar field based on cell positions to create an implicit surface so that cells in close proximity fuse together.

As well as rendering visual output, the author has explored sonification driven by attributes from the cells, such as using the velocity and acceleration values of each cell to create different frequency sounds.

3. RESULTS

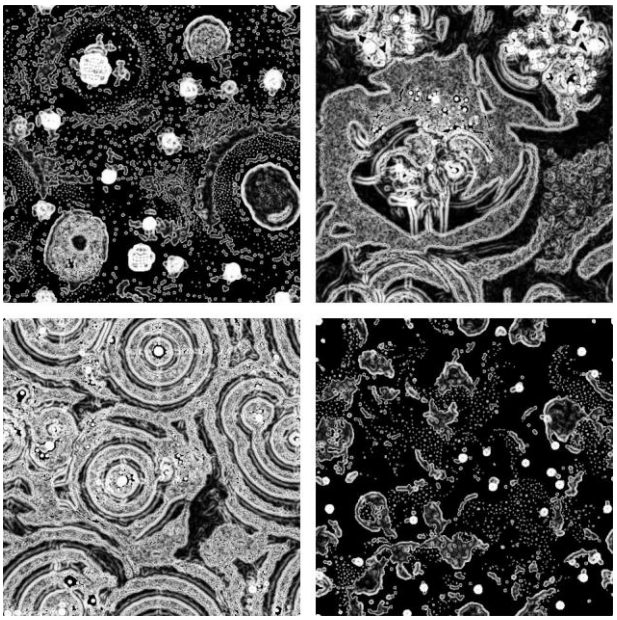

Figure 1: *Four examples of Digital Chemotaxis in 2D*

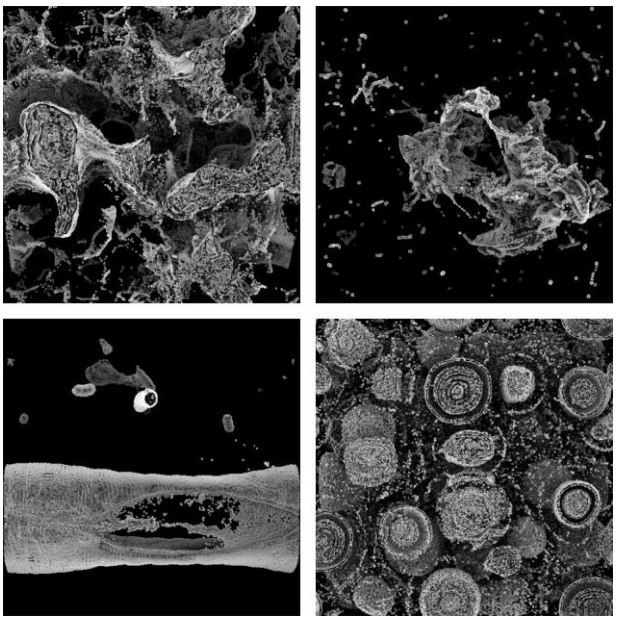

Figure 2: *Four examples of Digital Chemotaxis in 3D*

Using an RTX 4070Ti graphics processor, the author has been able achieve interactive rates of 30fps for simulation and rendering with 1 million cells and a 3D voxel grid for the chemicals with over 16 million sample points.

To explore the effects of varying parameter values, the author has coupled this system with his Species Explorer software. This allows a range of techniques for selecting parameter values, including random distributions, interactive genetic algorithms and machine learning methods (Lomas 2016).

The system has been found to generate a wide range of biologically evocative forms, both in 2D and 3D. Many emergent dynamic structures are created, including cells organizing into rotating and spiral structures, filaments of cells that accumulate and move coherently together, and sudden phase changes where the overall structure of the cells rapidly changes between different states. When testing the system with interactive controls there often appear to be tipping points, where a small change in the parameter values can cause large changes to the structure.

Even though the initialization of the system simply uses uniform random values, many of the results show the formation of large-scale complex structures. This appears to be spontaneous symmetry breaking similar to results commonly seen in systems such as reaction-diffusion.

The author is now exploring how the system could be used to create art artefacts, including using stereoscopic viewers to view cells moving in three dimensions, and generating forms to be interacted with in virtual reality.

4. REFERENCES

Lomas, A. (2016). Species Explorer: An interface for artistic exploration of multi-dimensional parameter spaces. *Electronic Visualisation and the Arts*, pp.95-102.

Siegert, F., & Weijer, C. J. (1992). Three-dimensional scroll waves organize Dictyostelium slugs. *Proceedings of the National Academy of Sciences*, *89*(14), 6433-6437.

Siegert, F., & Weijer, C. J. (1995). Spiral and concentric waves organize multicellular Dictyostelium mounds. *Current Biology*, *5*(8), 937-943.

Weijer, C. J. (2004). Dictyostelium morphogenesis. *Current opinion in genetics & development*, *14*(4), 392-398.