Computer Simulation of *Drosophila*'s Early Segmentation in Virtual Drosophila Project

Shugo Hamahashi [1] Hiroaki Kitano [2]
shugo@mt.cs.keio.ac.jp kitano@csl.sony.co.jp
[1] Department of Computer Science, Keio University
3-14-1 Hiyoshi, Kohoku-ku, Yokohama 223, Japan
[2] Sony Computer Science Laboratory
3-14-13, Higashi-Gotanda, Shinagawa, Tokyo 141, Japan

Abstract

Embryogenesis is one of the most important and mysterious process of animal's development. The embryogenesis is quite complex and hard to be understood because it has too many elements, such as cells or nuclei, which interact with each other. We replicated the system of Drosophila's early segmentation by using computer. Computer simulation enables us to understand a whole system of animal's development. The work reported here is an attempt to observe the mechanism of segmentation during the early development of Drosophila in detail by using computer simulation, which is a part of Virtual Drosophila project.

1 Introduction

The segmentation during the early development is very significant process in animals. To understand the mechanism of segmentation during the development would significantly contribute to developmental biology and molecular biology, because the process of segmentation is well preserved in many animals. *Drosophila* enables us to create the model quite in detail because numbers of experiments are carried out and a lot of data is available [2, 3, 4]. The Virtual Drosophila[1] is an project to create detailed model of *Drosophila*. The concept behind the Virtual Drosophila signifies "understanding by synthesis". At the first step of this project, we concentrated on the segmentation during the early embryogenesis of *Drosophila*, in which some of the genes interact with each other; bicoid, nanos, hunchback, Krüppel, knirps, giant, tailless, torso, huckebein and even-skipped are the genes actually interacted in this simulation.

2 Modeling

At the first stage of the Virtual Drosophila project, we have focused on the anterior-posterior body axis and body segment determination. We modeled the whole system of the embryo with consideration of the shape of the embryo and the behavior of each elements, such as diffusion, transcription and translation. We approximate the shape of *Drosophila*'s early embryo as a cylinder, shown in Figure 1. In the cylindrical container, we have to take account of the dynamics along only anterior-posterior axis. The equation of the diffusion of the each ingredient in *Drosophila*'s embryo is as follows:

$$\frac{\partial U_i}{\partial t} = D\frac{\partial^2 U_i}{\partial x^2} + g \cdot U_i + f(\mathbf{U}) \qquad (1)$$

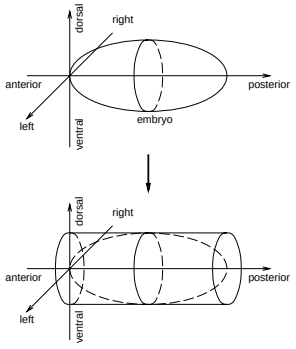

Fig. 1: Modeling the Embryo

In the equation 1, U_i is concentration of protein i, x is position along anterior-posterior axis, t is time step, D is diffusion parameter, g is deletion parameter (the value of g is always set at -0.2 in this paper), f is transcriptional function, and **U** is concentration vector. The transcription and the translation are also designed to actually work during the simulation steps.

3 Simulation Overview

The period this simulator can reproduce is from first to 14th nuclei division cycle untile *even-skipped* is formed in the seven stripes. At the beginning of the simulation, a certain amount of mRNA of maternal effect genes is localized into a certain place. Next each mRNA is translated into a certain kind of protein and each protein freely diffuse all over the embryo.

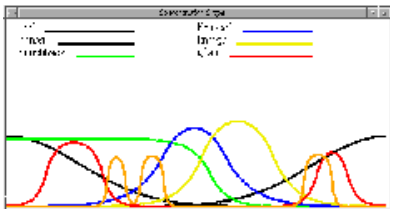

Fig. 2: Concentration Graph

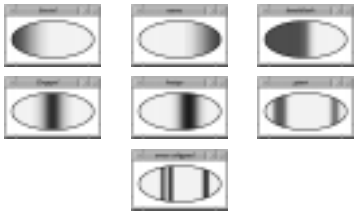

Fig. 3: Concentration Map

This simulator enables us to observe the mutant-analysis like experiments and the temporal dynamics during the simulation steps. Figure 2 and 3 show the screen capture of the simulator.

4 Summary and Conclusions

This paper reports that the expression patterns of major genes during *Drosophila*'s early embryogenesis can be successfully reproduced by well designed computer simulation. The advancement of this system is that this system enables creation of various mutant. We have also reported that there is very critical parameter sensitivity in the series of an embryo developing by observing the temporal dynamics during the development.

The Virtual Drosophila project aims at the detailed modeling of *Drosophila*, which is extremely well-investigated model animal. Using these methods, the Virtual Drosophila system can replicate most of the mutation analysis actually carried out by molecular biologists. The model enables us to reproduce and observe biological phenomena such as transcription of various genes.

References

[1] Kitano Hiroaki, et al., "The Virtual Biology Laboratories: A New Approach of Computational Biology," *Proc. of Fourth European Conference on Artificial Life*, 274-283, 1997.

[2] John Reinitz and David H. Sharp, "Mechanism of *eve* stripe formation," *Mechanisms of Development*, 49:133-158, 1995.

[3] Peter A. Lawrence, "The Making of a Fly," *Blackwell Science*, 1992.

[4] Scott F. Gilbert, "Developmental Biology," *Sinauer Assoc*, 1994.