

Eye Development Model A Python Simulation





Using Similarities Between Species To Form The Hypothesis

Given the many scientific benefits with studying Drosophila (fruit flies,) the underlying biological processes in these creatures are well understood. The same is true when discussing the mechanisms for eye development. However, our understanding with most other species regarding the eye development process is limited. What the scientific community does know is that many of the same genes between different species are expressed within the fruit fly eye and popular belief is that the mechanisms are similar. Our group attempts to provide an exploration into this matter on the basis of this conjecture.



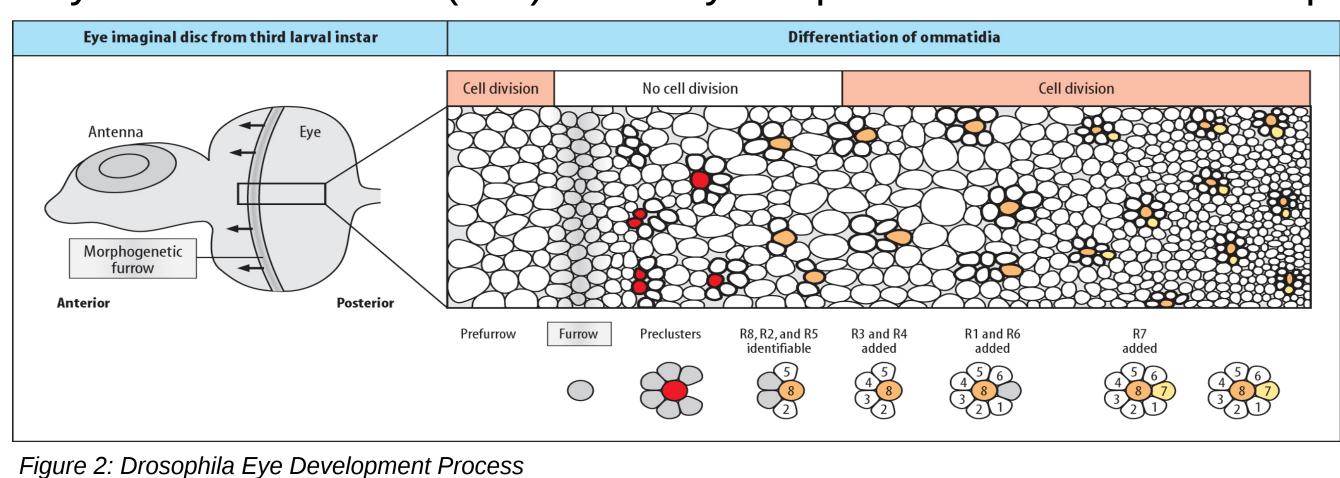
Figure 1: Close up of Drosophila eyes

Hypothesis: By observing variants of the Drosophila eye development process, we can learn about the eye development of other species through simulated results.

Using this hypothesis, our team attempts to simulate the development of eyes by projecting known growth models onto variable biological constraints. The first step is developing a simulation which accurately represents the fruit fly model.

Researching The Eye Development Process

Extensive research was done regarding both the drosophila eye development process and the possible design choices we could make based on some major goals provided by the UC Neurobiology dept. Current existing Drosophila eye simulations, while useful in their own right, either focus on displaying only one ommatidium (unit) of the eye or provide a macro level display of the process. Our simulation



needs to show the development of all ommatidium into a fully developed eye. Therefore, it is important that our simulation is not only accurate, but provides the right amount of information to explore the hypothesis.

Establishing Project Goals, Requirements, And Tools

The primary goal throughout the development of this project was to create a simulation which is easily extensible. By creating a framework that can be easily tailored and edited, we can allow for many different users to customize and add their own varaible constraints and test different theories postcompletion of a successfully simulated fruit fly eye. Due to this major goal our team has set, we have

defined specific requirements which will help us achieve this.

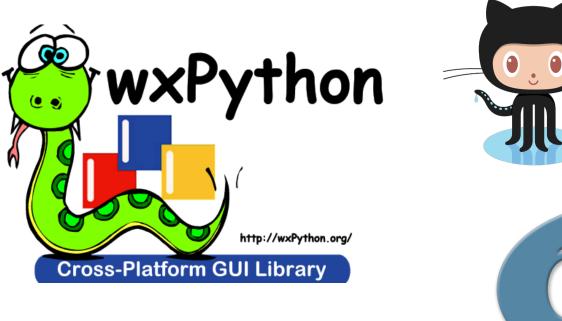


Figure 3: Tools used for development



Requirements:

- Python 3.x (chosen for ease of language)
- Windows, Mac, and Linux friendly
- Restrictions on GPU utilization
- Easily customizable GUI
- Support for 3D modeling

Displaying Achievements And Results

To address the requirements regarding the GUI, our team has developed a dynamic GUI generation system that displays new input options as new constraints are added to the code. This modular setup allows users to easily add new constraints without manually changing the GUI. Our particle-based simulation technique allows for collisions between cells. This solution more accurately represents cell behavior than techniques that use rigid body physics. Also, due to its efficiency, our solution allows a simulation pass to complete in O(n) time.

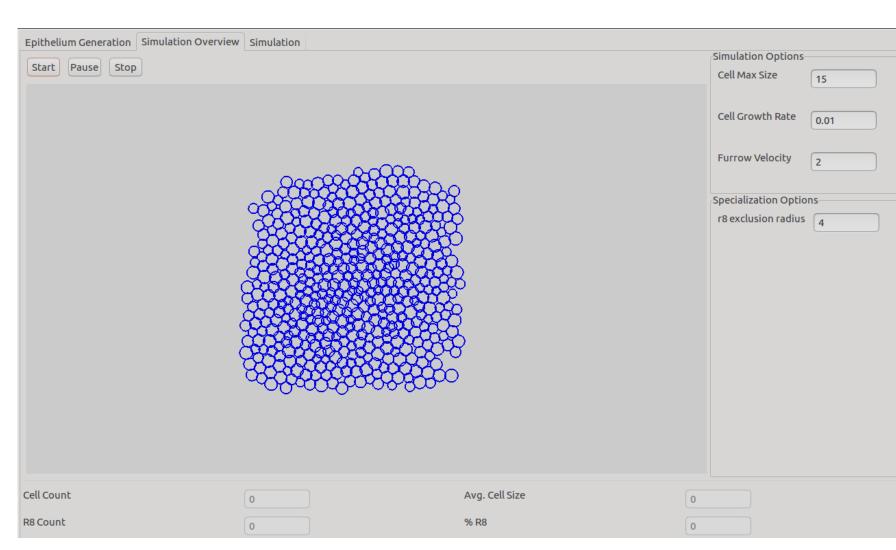
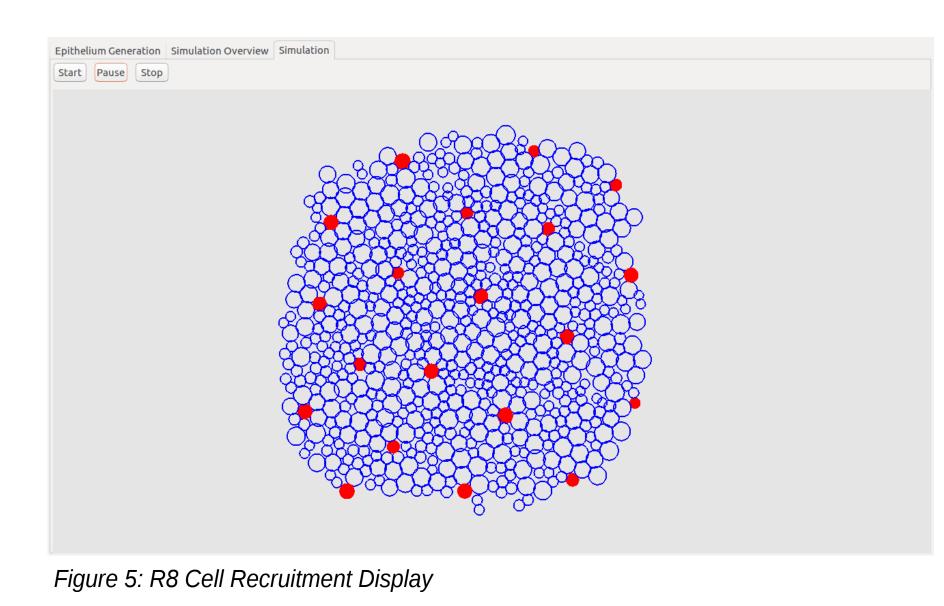


Figure 4: Epithelium Generation and GUI Display



Because of the efficient nature of our initial framework, we have successfully developed epithilia containing up to thirty-thousand cells. We have also defined the furrow **behavior** as this is an important function of the simulation. Currently, we are refining the mechanism for the **R8selection process** which is the first step in producing the eye. The foundation we have developed will allow us to easily refine the simulation as new metrics are added and currently existing variables need adjustment.