Aggregation, Morphogenesis, and Synchronicity of Xenobits

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Abstract

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1 INTRODUCTION

"Biobots" are a new area of research which has generated excitement across fields[Kriegman et al. 2020]. "Xenobots" are a particular instance of biobots, which are human-assembled aggregates of embryonic *xenopus laevis* frog cells. These xenobots present a fundamentally new landscape of engineering possibilities, blurring the line between evolved vs. designed intelligence. Xenobots have been shown to perform various tasks, including locomotion, object transport, and even kinematic self-replication [Kriegman et al. 2021].

2 MOTIVATION

Multiple clusters of chimeric cell clumps(Xenobots) in a dish self organize into a smaller number of large clumps when they interact with one another. Their interactions, observed through microscopic imaging, present observations to learn about the patterns and the mechanism that generates large scale behavior from their interactions. Be it the way they signal through calcium ion exchange, or adhere and deform in complex ways to form small numbers of large clusters, analyzing the dataset will help motivate questions around guiding self organization.

3 METHODS

Our dataset is a 45 second video (Figure 1), captured by a camera placed above a 1% agarose-covered petri dish. The dish contained 10mL of 0.75x Marc's Modified Ringers solution (MMR) and 5l gentamicin and raised at 14°C. The cells in the plate came from a *Xenopus laevis* frog, grown and staged according to [Sive et al. 2007]. The particular cells in this video were extracted during an early stage of embryo development. The video shows phenotypical behavior of these cells locomoting with cilia, exhibiting calcium flashes, and aggregating into larger clusters. We performed varied data analysis of this video in order to uncover patterns in morphogenesis, calcium-ion flashing synchronicity, and cell motion.

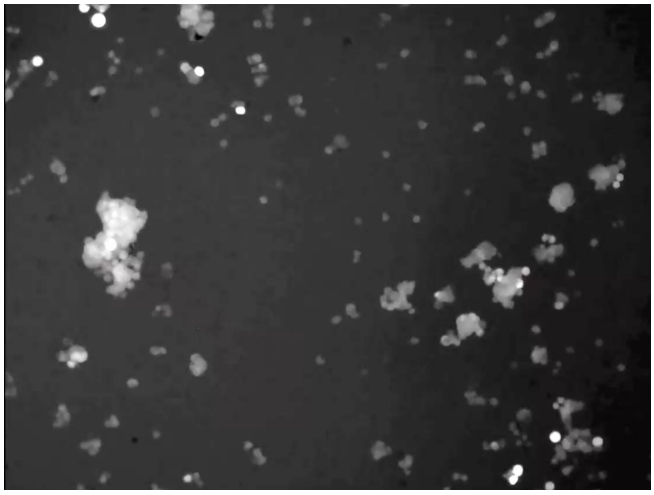

Fig. 1. A frame captured from the 45 second video dataset

3.1 Xeno-Morphogenesis

The skin cells here are in a setting that is strange. The aggregation and development behaviour outside the embryo is to be studied. We algorithmically drew outlines around each clump of cells in the video using the popular video-processing Python library OpenCV. We took the shape of the outline of a single clump - the contours and study the topological change over time.

The fractal dimension at each frame of the video is an indicator of complexity of the morphology. Other measures like smoothness/roughness of surface, and the corresponding change in these measure help quantify the xeno-aggregation. These measures are to be researched and chosen appropriately to quantify the behaviour.s

3.2 Motion

To answer the question "how random is xenobit motion?" we sought to compare the motion of xenobit clusters to a completely random model. We tracked the motion of xenobit clusters by computationally detecting them and drawing bounding boxes around each one (again with the help of OpenCV). We recorded the position of the center of each bounding box over time, which gave us a dataset consisting of many cell clusters' trajectory over the course of the video. To measure the trajectory's randomness, we measured its Shannon entropy and sought to predict the motion with a predictive model. The null hypothesis is we cannot build a model which predicts the

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motion of xenobit clumps *better* than it can predict a random walk of the same length (i.e. the xenobit motion is completely random).

3.3 Synchronicity

The calcium-ion flashes exhibited in the video appeared subjectively to be synchronized in some way. To test this, we developed a video-processing pipeline which extracted the cell flashes over time. For each bounding box's timeseries (from the Motion subsection), we computed the intensity of each pixel within the bounding box. Then, we searched for spikes in the pixel intensity timeseries data and annotated them. Finally, we took these flash timeseries and ... [TBD – need to research good methods for this or think of a method from scratch]

4 DISCUSSION

5 SUMMARY

ACKNOWLEDGMENTS

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A PLAN

Nov 11 - Data set Preparation: Calcium Flashes time series for sync analysis, Contours for fractal dimension analysis, time series of discretized directions of bounding boxes for random walk analysis

Nov 18 - Literature review of methods and models

Nov 25- Preliminary results

Dec 2 - Visualization and analysis

Dec 9 - Final Slides and report

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