Automated Detection of Mating Phenotype in *Saccharomyces Cerevisiae*

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Background and Problem

Biologists often study higher order organism functions by using *Model Organisms*, those which functionally display the same functions, but in a much smaller or simpler way. *Saccharomyces cerevisiae*, commonly known as Brewer's Yeast, is one of the simplest model organisms used in biology, however, the cellular mechanisms discovered in *S. cerevisiae* are the same processes that occur in human cells every day [1]. For this reason, *S. cerevisiae* yeast is still studied and used as a common Model Organism for genetic engineering, drug testing, and even further understanding intracellular processes. For example, *S. cerevisiae* is used as a model organism for developing the emerging technology of CRISPR/Cas9, which allows advanced genome editing [2].

Because of the widespread use of *S. cerevisiae* in biological research, it is important to have tools for high-throughput data collection of this yeast. One unique aspect of the Brewer's Yeast is the clear visual distinctions throughout its life cycle [3]. This clear visual distinction has been a way for biologists to study phenotypic changes due to certain drugs and the effects of manipulating proteins involved in the mating response. However, currently, biologists have to sit at the microscope with a hand counter to identify cells in different stages, this is not conducive to high-throughput research. Secondly, counting by hand introduces extra experimenter bias that is not desired in biological research.

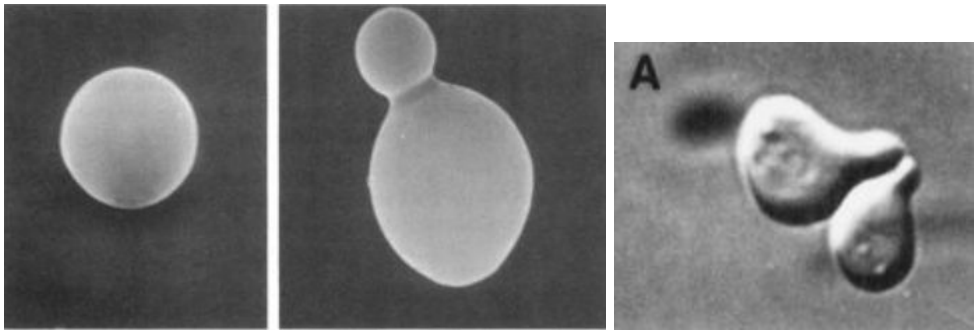

Figure 1: (left) Normal morphology of *S. cerevisiae* cell. (middle) Budding morphology of *S. cerevisiae* cell during mating [3]. (right) "Shmoo" morphology of *S. cerevisiae*, during initial stage of mating after the sensing the other cell's pheromone [4].

Proposed Solution

Our team proposes to create an easy to use software that can identify different cell morphologies from an image. The proposed workflow for a biologist would then be to take a picture under the microscope with an inexpensive microscope camera, and use that image as the input to our software. The program would then output a count of cells that are in the normal morphology, "shmooing" morphology, and budding morphology. Not only would this increase the

speed with which researchers can study *S. cerevisiae*, but it would also reduce experimenter bias in identifying cells that may only exhibit slight changes in morphology.

Steps to Solution

To create a software that can analyze images like this, we will need three pieces:

1. Easy to use user interface where the researcher can input the photo
2. An algorithm to detect the three different cell morphologies
3. Easy to use output where the researcher can copy the output numbers

These three pieces can be made separately, and with MATLAB, the user interface should be fairly easy to create. The main piece of code then will be the algorithm to detect the cell morphologies. For this algorithm, a probable first step would be to filter out noise, most likely through a weak Gaussian blur, or a Median blur. The next step could be converting the image to a binary image and detecting the edges, this would give us the location of the cell boundaries. Then for each cell, a method to determine cell morphology would probably be taking the relationship of the edge length to the area, or possibly curvature. A threshold value could be set (probably through testing) to bin the cell into the three morphology categories based on how round the cell is. The threshold value could be manually set by the researcher, which could again adapt the algorithm for their specific purpose and limit experimenter bias.

Timeline

Initial steps 9/25-10/3:

- Create Trello for project management
- Create Github
- Create Website

Meeting and setting up Project outline/Diving tasks among members 10/3-10/12:

- Lay out Edge Detection Algorithm

Coding UI and Algorithm 10/12-10/31:

- Create UI
- Code Algorithm
- Write Mid-semester Report

Testing on Pictures and Updating Website 10/31-12/12:

- Work on website
- Test with real pictures from Biocore Lab
- Adjust the algorithm and finish UI.

References

[1] D. Botstein, S. A. Chervitz, M. Cherry, “Yeast as a Model Organism,” *Science*, vol. 277, no. 5330, p. 1259-1260, Aug. 1997.

[2] T. Jakociunas, I. Bonde, M. Herrgard, S. J. Harrison, M. Kristensen, et al., “Multiplex metabolic pathway engineering using CRISPR/Cas9 in *Saccharomyces cerevisiae*,” *Metabolic Engineering*, vol. 28, p. 213-222, Mar. 2015.

[3] I. Herskowitz, “Life Cycle of the Budding Yeast *Saccharomyces cerevisiae*,” *Microbiological Reviews*, vol. 52, no. 4, p. 536-553, Dec. 1988.

[4] J. Chenevert, N. Valtz, I. Herkowitz, “Identification of Genes Required for Normal Pheromone-Induced Cell Polarization in *Saccharomyces cerevisiae*,” *Genetics*, vol. 136, no. 4, p. 1287-1296, Apr. 1994.