Title: Yash's Awesome Project: GreenScreen

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What is the problem?

Currently, the problem is classifying Arabidopsis plants in a phenotype screen after mutagenizing a background to look for return to wild type (WT) function.

How is it addressed currently & what are the limitations?

Currently, in each flat, there is one pot for a WT control, one for the background control, and the remaining are the mutagenized F2 plants. By comparison to each of the controls, the mutants are manually classified by looking at parameters such as anthocyanin levels (visually), petiole length, and relative leaf width & height compared to petiole length. The main limitation is time and accuracy. It takes ~15 minutes per flat and there are concerns over consistently characterizing plants in the grey area.

What is your approach to addressing it & why is it likely to be successful?

I hope to use Python's SciKit-Learn package for machine learning to try to integrate a facial recognition software such that I can simply take a picture and have the program screen it for me. It's likely to be successful because there already exists a facial recognition software for plants called DeepStomata except it focuses on stomatal measurements rather than the phenotypes.

If successful, why does it matter?

If successful, it will cut time of screening 10x since all the process would require would be to take a picture. If unsuccessful, I would still have gained the experience of understanding how facial recognition software works and would be able to apply to other situations.