A deep learning pipeline for segmentation of *Proteus mirabilis* colony patterns

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**Acknowledgements**
This work was supported by an NSF CAREER Award (1847536), Blavatnik Fund for Innovations in Health (T.D.), and National Science Foundation Graduate Research Fellowship (A.D.).

**References**
2. Schaffer & Pearson, Microbial Spectr 2015, 3.5.10.

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**Background**

- *Proteus mirabilis*, a bacterium commonly found in water and soil, can cause infections of the lungs, wounds, and urinary tract. In the USA, it accounts for ~44% of catheter-associated UTIs.
- A critical part of its virulence is its “swarming motility,” a highly coordinated movement propelled by flagella.
- *P. mirabilis* swarming is typically studied through colony development assays in which the bacterium forms a characteristic macroscopic bullseye pattern.

**Problem:** There is no computational state-of-the-art method for efficient, comprehensive, and scalable analysis of macroscopic *P. mirabilis* colonies.

**Overview of Project**

1. Dataset & Preprocessing
2a. Colony Segmentation
2b. Ring Boundary Segmentation
3. Measure Colony Features

**Model Performance**

<table>
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<tr>
<th>Model</th>
<th>Label Fusion Method</th>
<th>Accuracy</th>
<th>Precision</th>
<th>Recall</th>
<th>Dice</th>
<th>IoU</th>
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