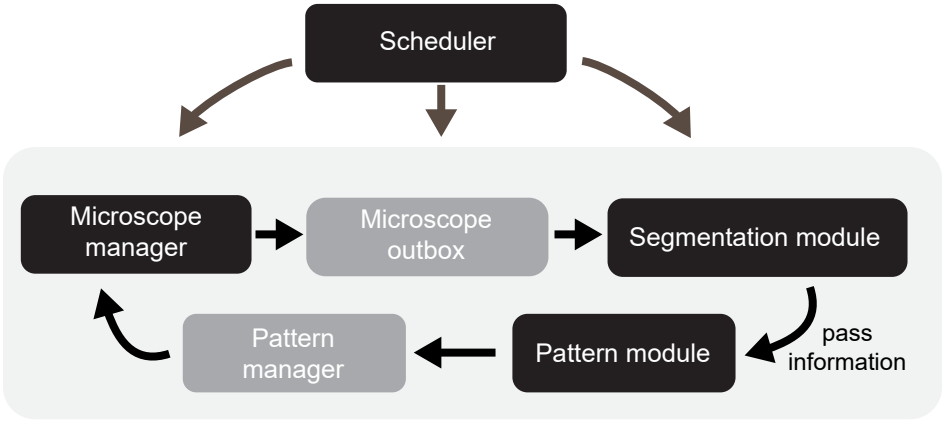
A **PyCLM**: closed-loop microscopy for image-guided stimulation



B **Running a PyCLM experiment**

Define XYZ position (multipoints.xml)

```
<Point1>
 <strName value="feedback.1"/>
 <dXPosition value="4533"/>
 <dYPosition value="2742"/>
 <dZPosition value="5416"/>
 <dPFSOffset value="1004"/>
</Point1>
```

Define a schedule (scheduler.toml)

```
[timing]

steps = 200
interval_seconds = 30
setup_time_seconds = 3
time_between_positions = 3
```

Define experiments (feedback.toml)

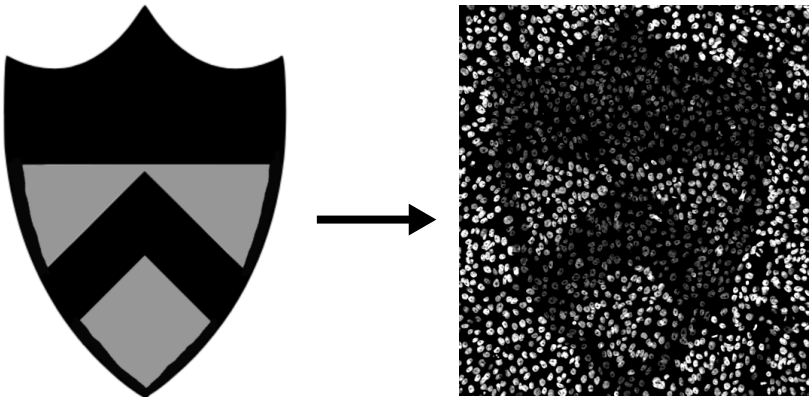
```
[imaging]
every_t = 1
exposure = 200

[stimulation]
every_t = 1
exposure = 500

[segmentation]
method = "cellpose"
method = "cpsam"

[pattern]
method = "centered_image"
tif_path = "logo.tif"
```

C **Example application: controlling single-cell intensity**



grayscale set point

single-cell feedback