Vanderbilt – Live cell

Description

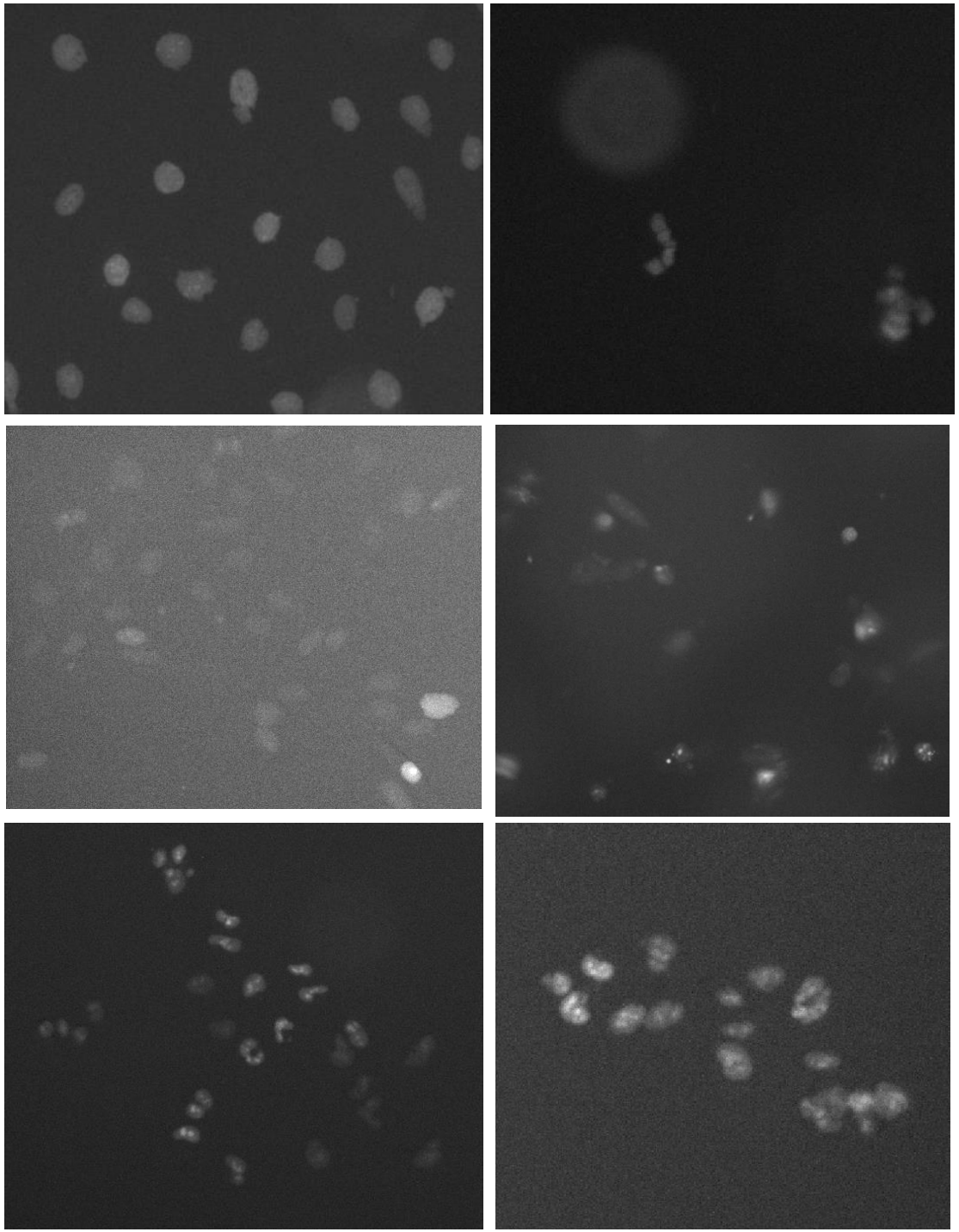
erbilt_live_cell

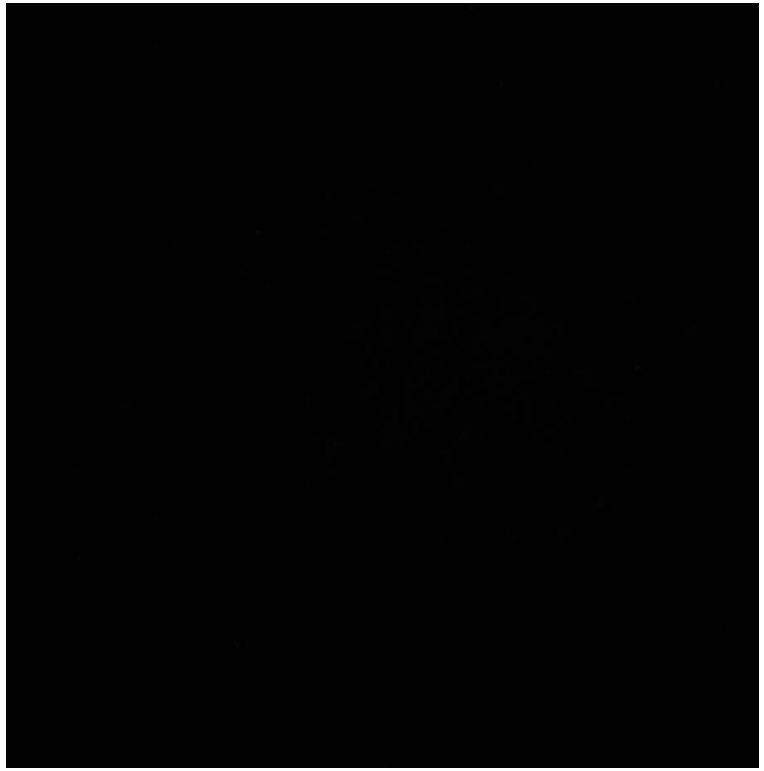
Different drug-treated cell lines (histone2B-RFP)

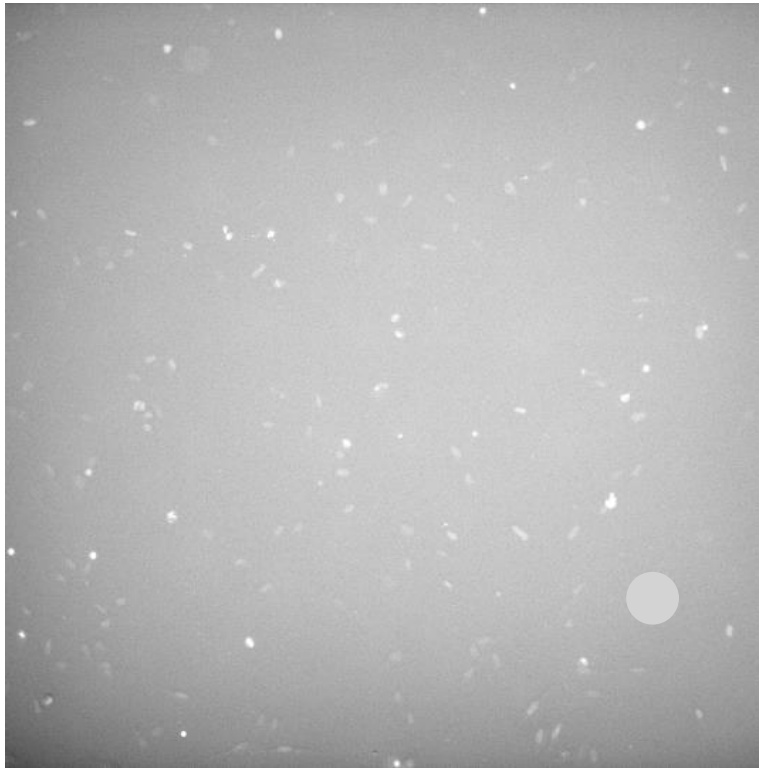
Challenges:

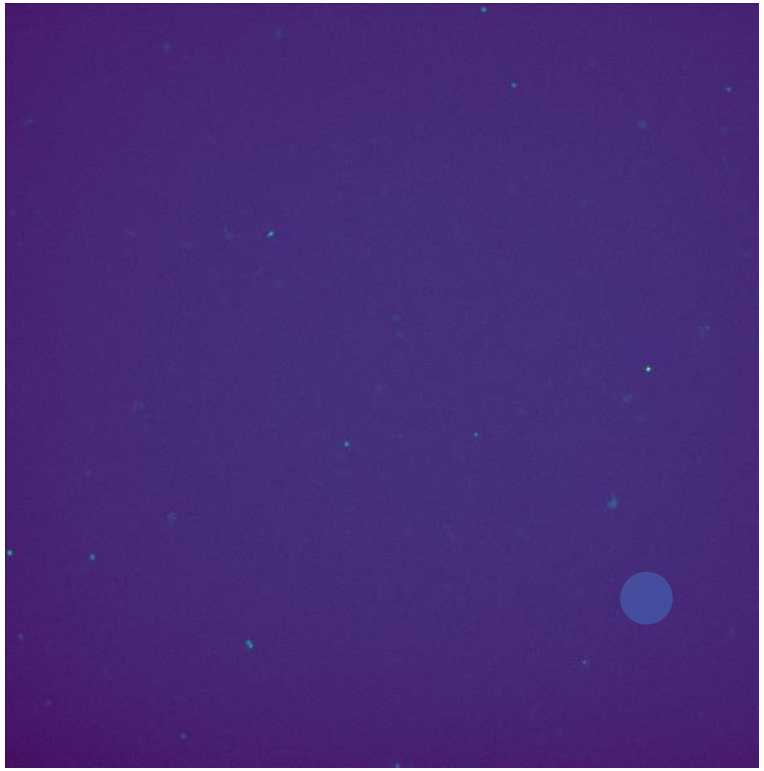
- Low signal-to-noise
- Uneven illumination
- Out-of-focus intensity (dead cells)
- Highly variable nuclear shapes and intensities

Goal: detect viable nuclei



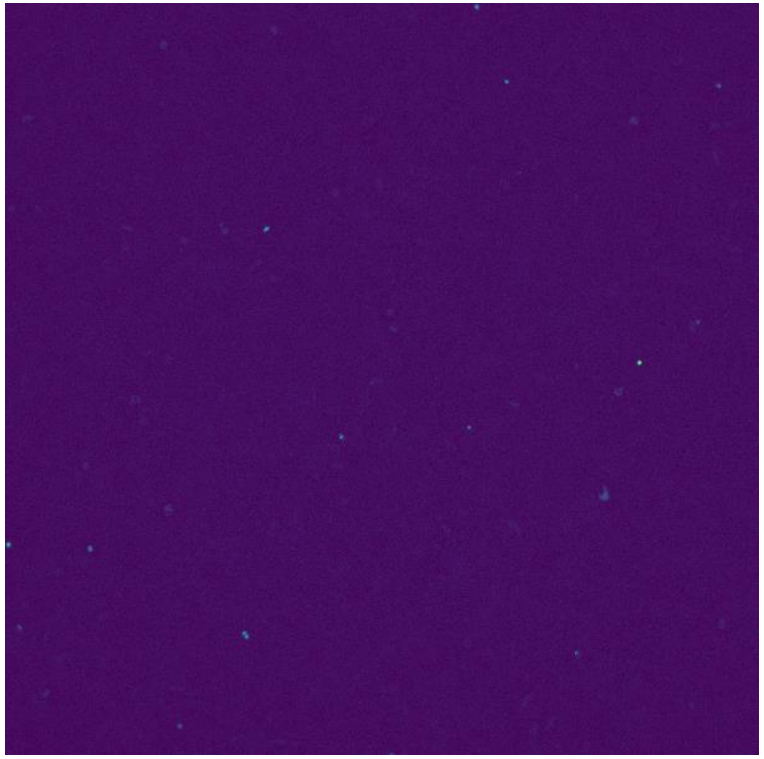
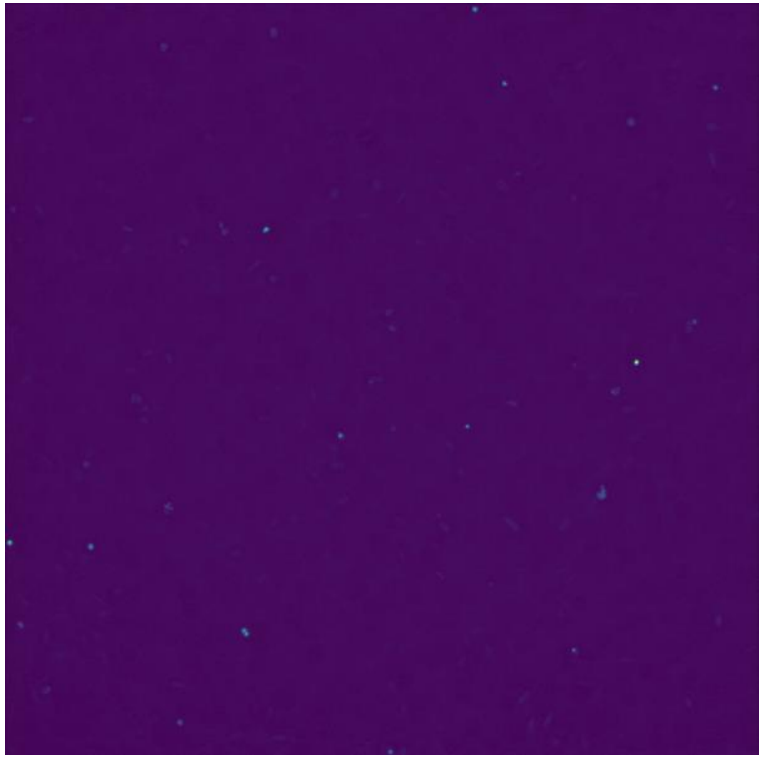
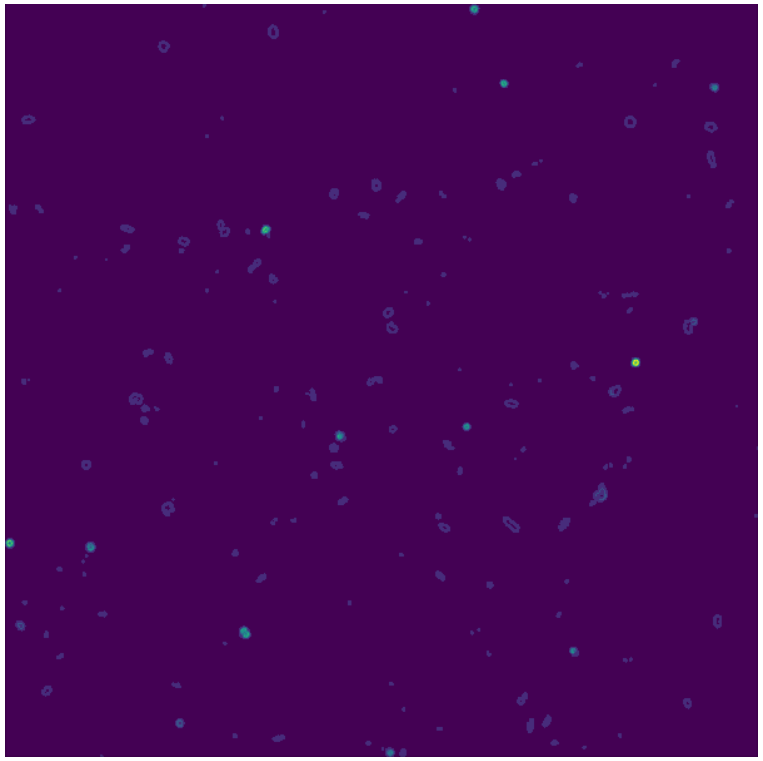






Original image

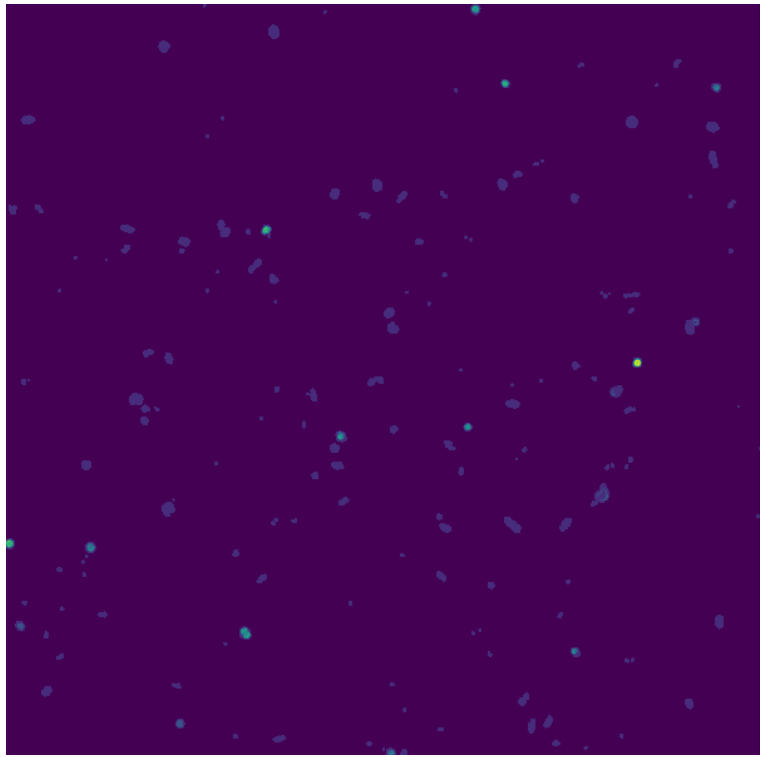
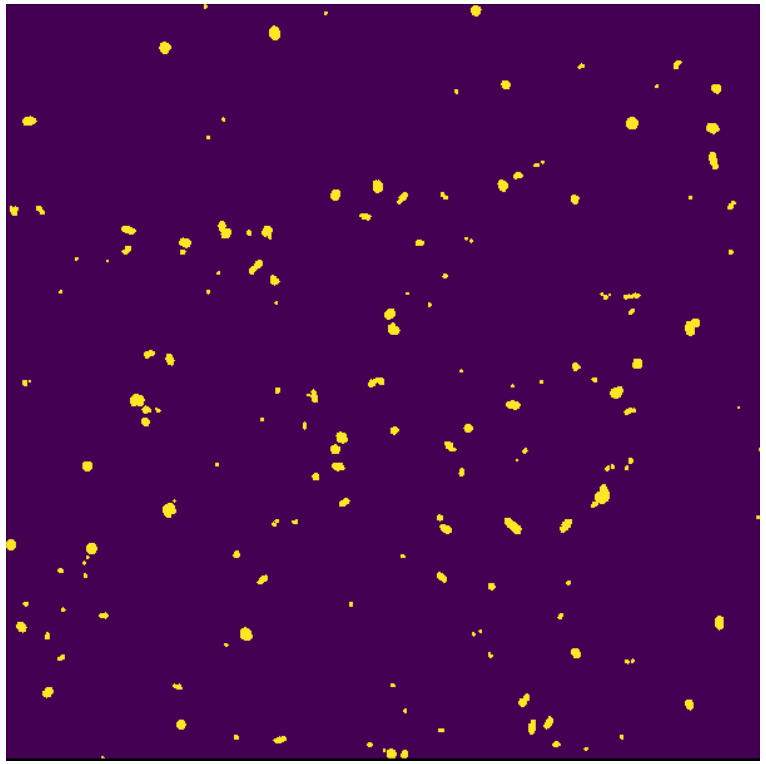
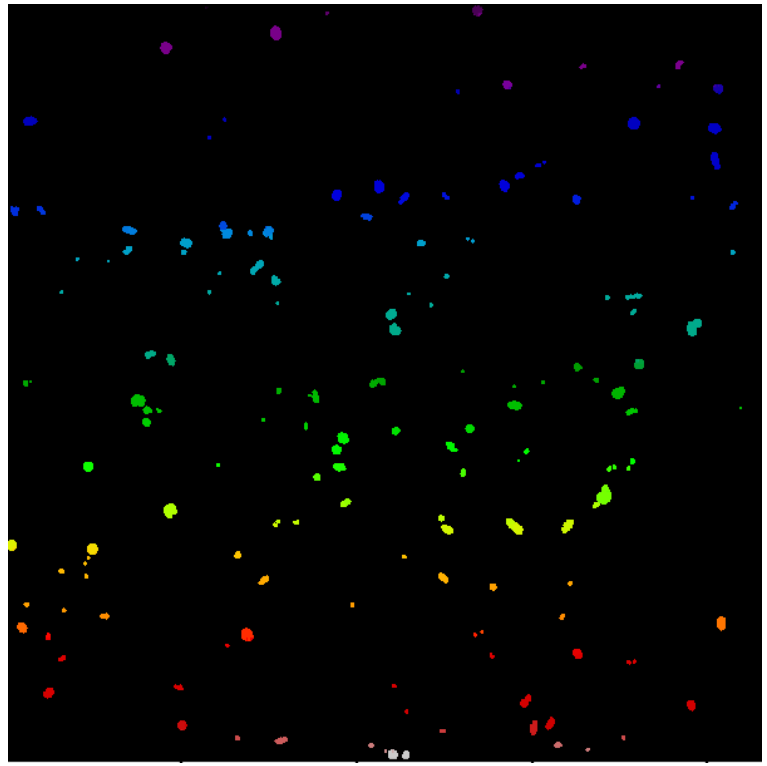
- Left: Open it without processing
- Mid: Increase contrast
- Right: Matplotlib show()

Processing - 1

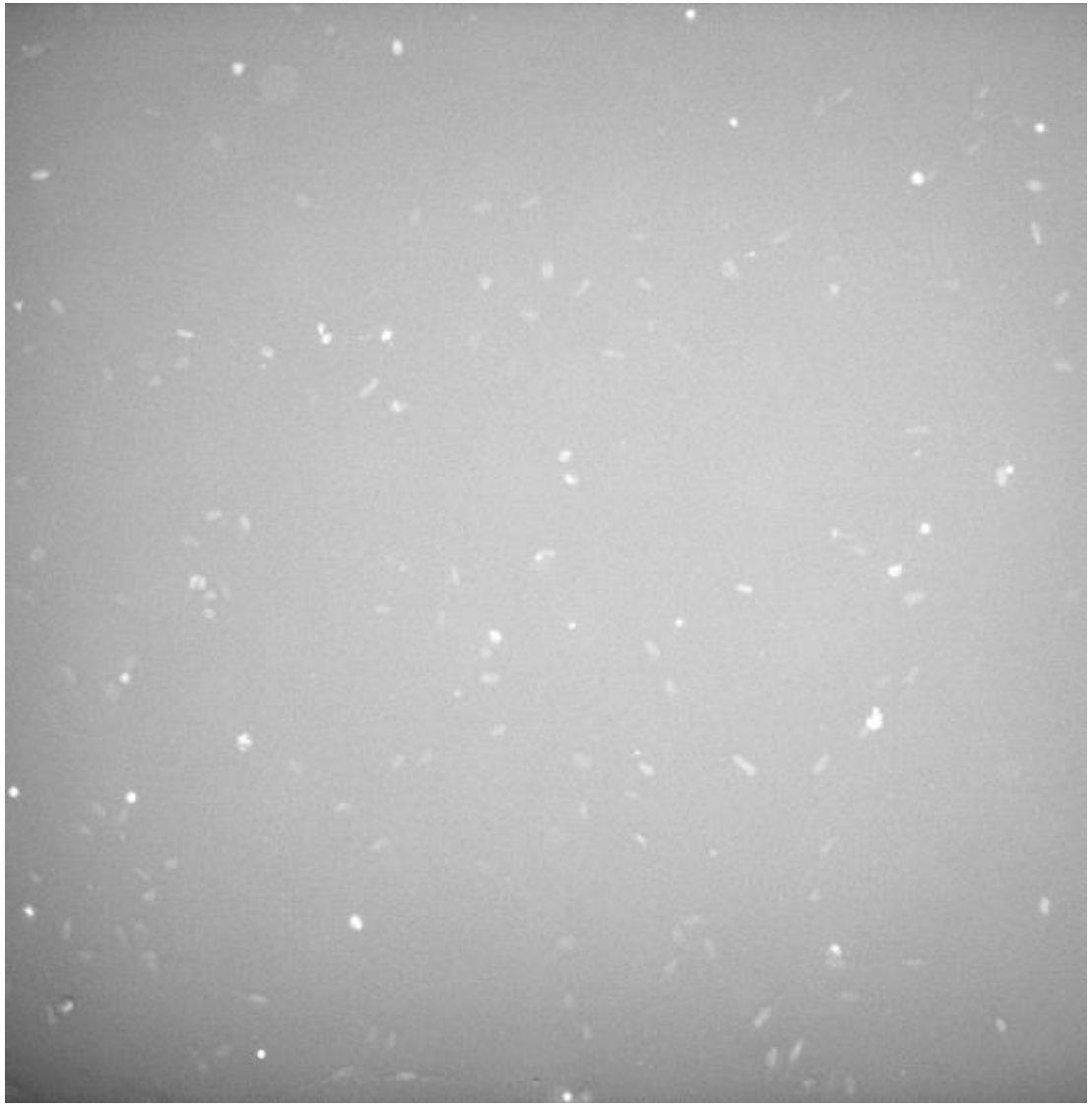
- Left: Remove big dead cell if any (lose focus) – included in starter code
- Mid: Remove noise -> bilateralFilter – better than Gaussian Blur
- Right: Get edge -> Gradient

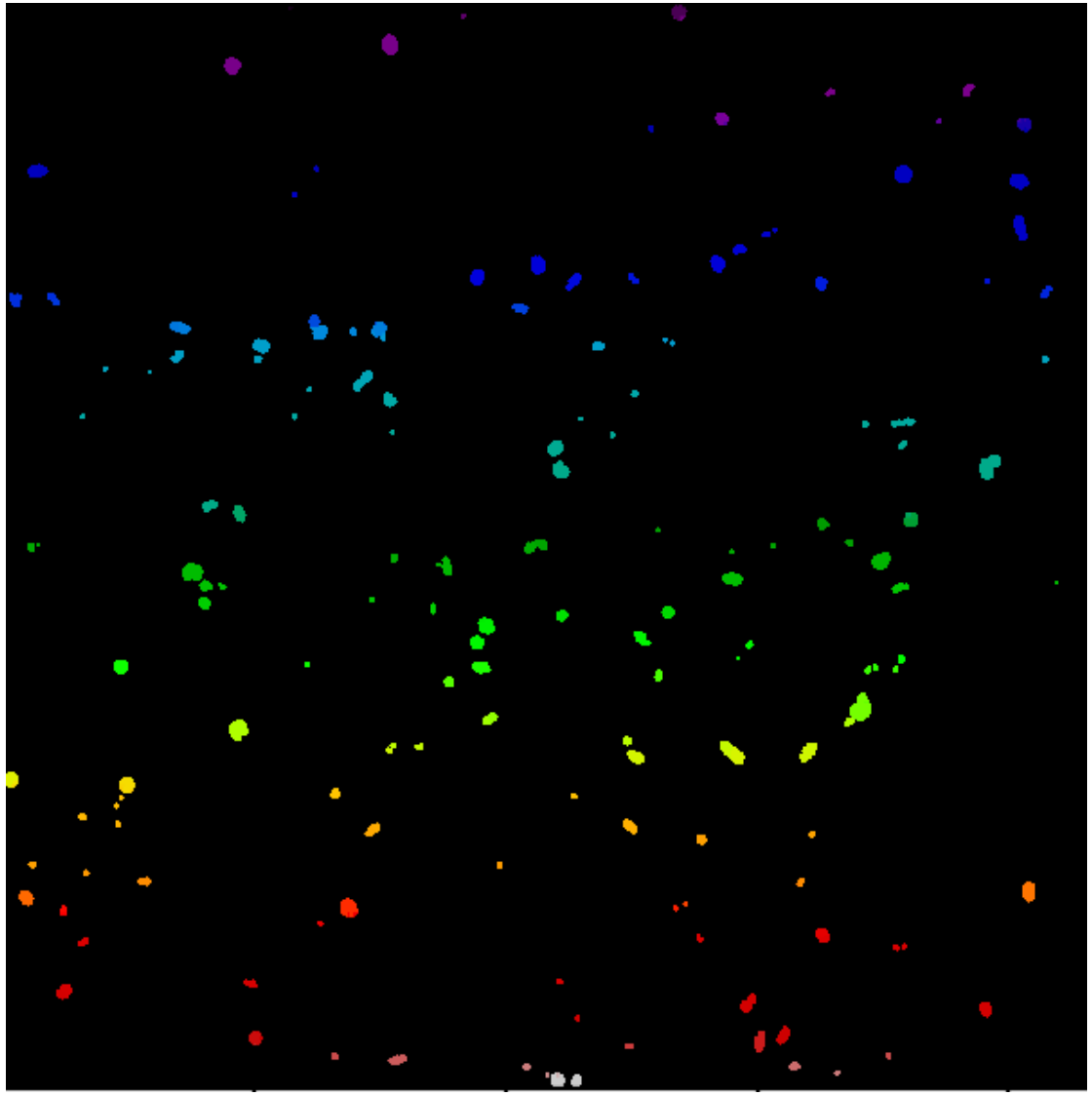
Increase the mask size

Processing - 2

- Left: Fill the holes within the edges
- Mid: Get 0-1 Mask
- Right: Get a mask with unique value for each blob/region





Compare

Review

- Pros
  - No annotation needed
  - Easy to implement
  - Not that fast, but not slow – 2s/image
  - Apply on similar project without extra training
- Cons
  - Some dead cells were not removed well so they still would count
  - Parameters need tuning
  - Accuracy – I am not sure yet, just put it here to balance the pros and cons
- To-do
  - Watershed – I tried but the result was not good enough, so I skipped it
  - Small points? – There are some small points. Sometimes when I tried to zoom in the original image, I found there was a not so clear light point there. So, I decided not to drop those small points.
  - Very interesting challenge!