

## COMP 204 – Assignment #5

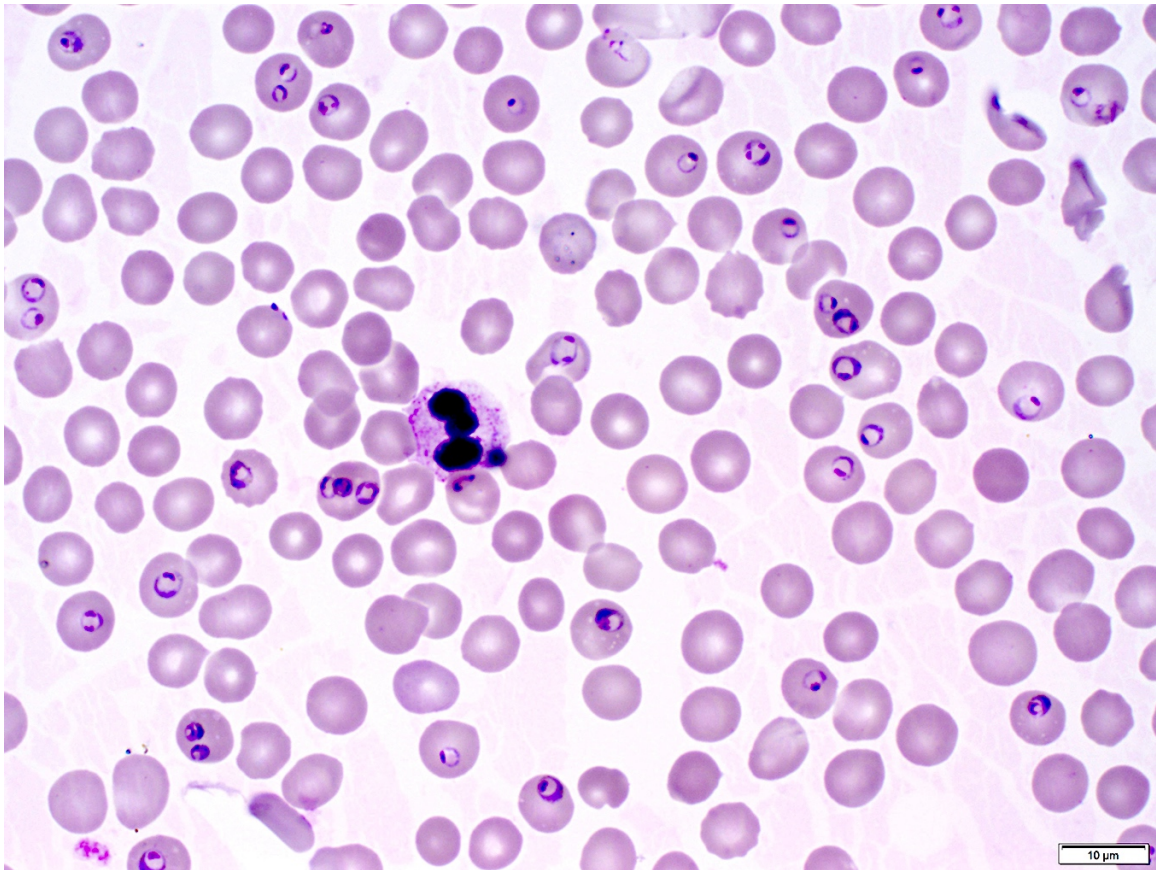
**Due date: Tuesday, December 3, 23:59**

Download `cell_counting.py` and `malaria-1.jpg`.

What to submit:

- Your modified `cell_counting.py` file.
- The images produced for each question, generated by your code.

In this assignment, you will continue the work started in class to develop a program that accurately identifies red blood cells in a microscopy image, and then counts the fraction of those cells that are infected by *Plasmodium Falciparum* (the causative agent of malaria). We will analyze the image below. Each red blood cell is a pink, roughly circular region, often with a lighter center. Some cells are infected with Plasmodium, which shows as a dark-purple ring due to Giemsa staining. The image also contains some additional stuff, like this very dark blob in the center – I don't know what it is...



**1) (10 points) Better edge detection** [Expected length: 4-6 lines of code]

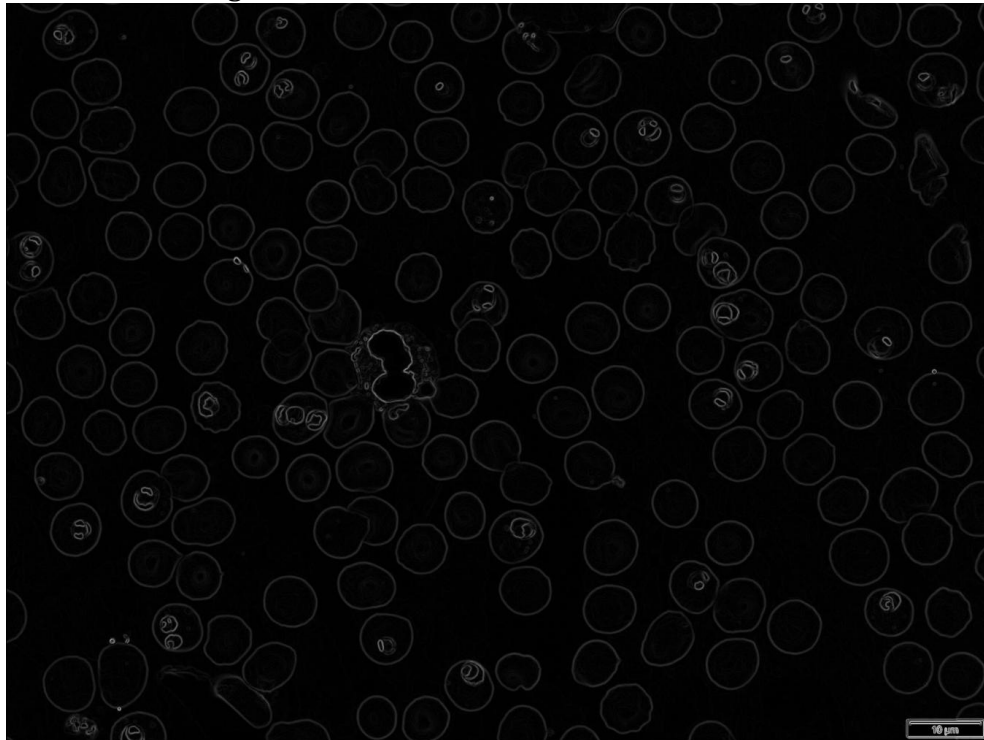
The edge detection algorithm seen in class is not the most accurate. A more commonly used edge detector is the Sobel algorithm, which is part of the `skimage.filters` module. See

<https://scikit-image.org/docs/dev/api/skimimage.filters.html>

Apply the Sobel algorithm to image `malaria-1.jpg`. Write your code in the dedicated portion of the `cell_counting.py`. Your code should save the resulting image in a file called `"Q1_Sobel.jpg"`. Submit it on MyCourses.

Notes:

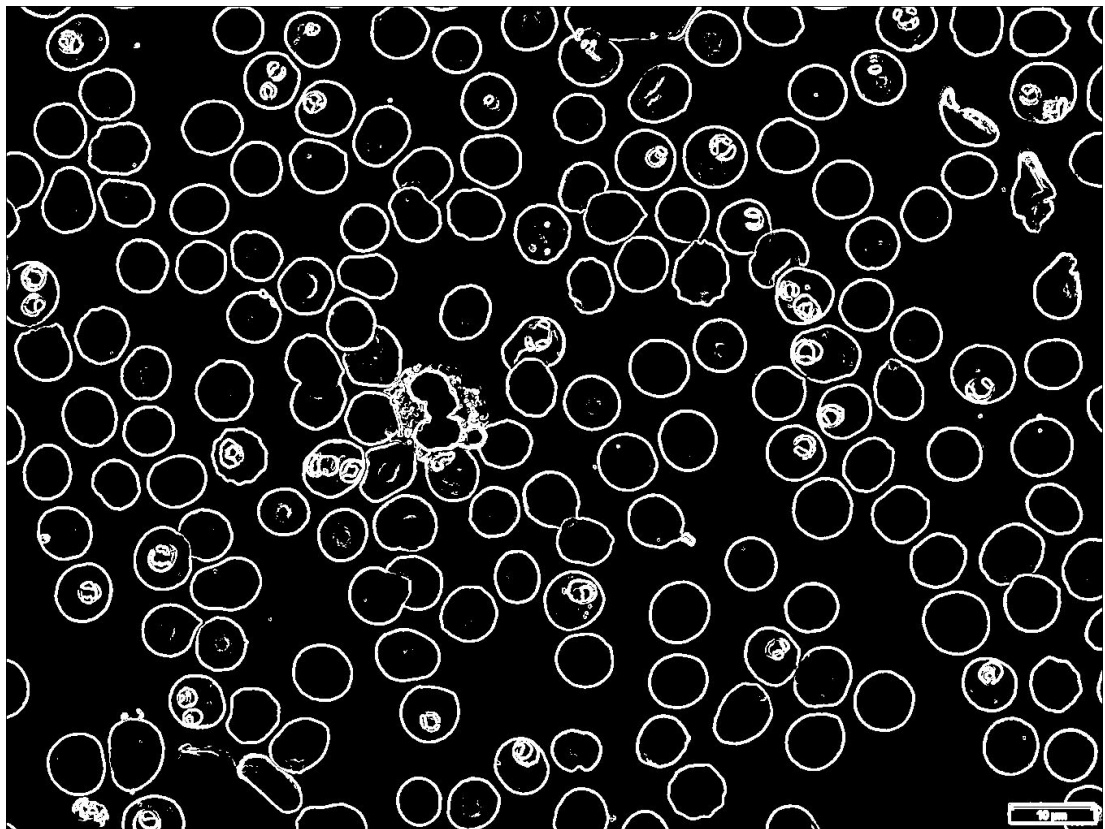
- The Sobel algorithm can only be applied to grayscale images, so you will first need to convert the original color image to a grayscale image as described in class.
- Reminder: Grayscale images have pixel values between 0 and 1, not between 0 and 255.
- Your image should look like this:



**2) (10 points) Detecting strong edges** [Expected length: 4-20 lines]

The Sobel algorithm measures the “edginess” of a pixel with a number between 0 and 1. In order to turn these real-valued images into black-and-white images (white = edges, black = non-edge), we need to threshold the image, i.e. to produce a new image where the pixel value at location  $(r,c)$  is set to 0 if  $\text{edginess}(r,c) < T$ , and to 1 if  $\text{edginess}(r,c) \geq T$ , where  $T$  is a user-defined threshold.

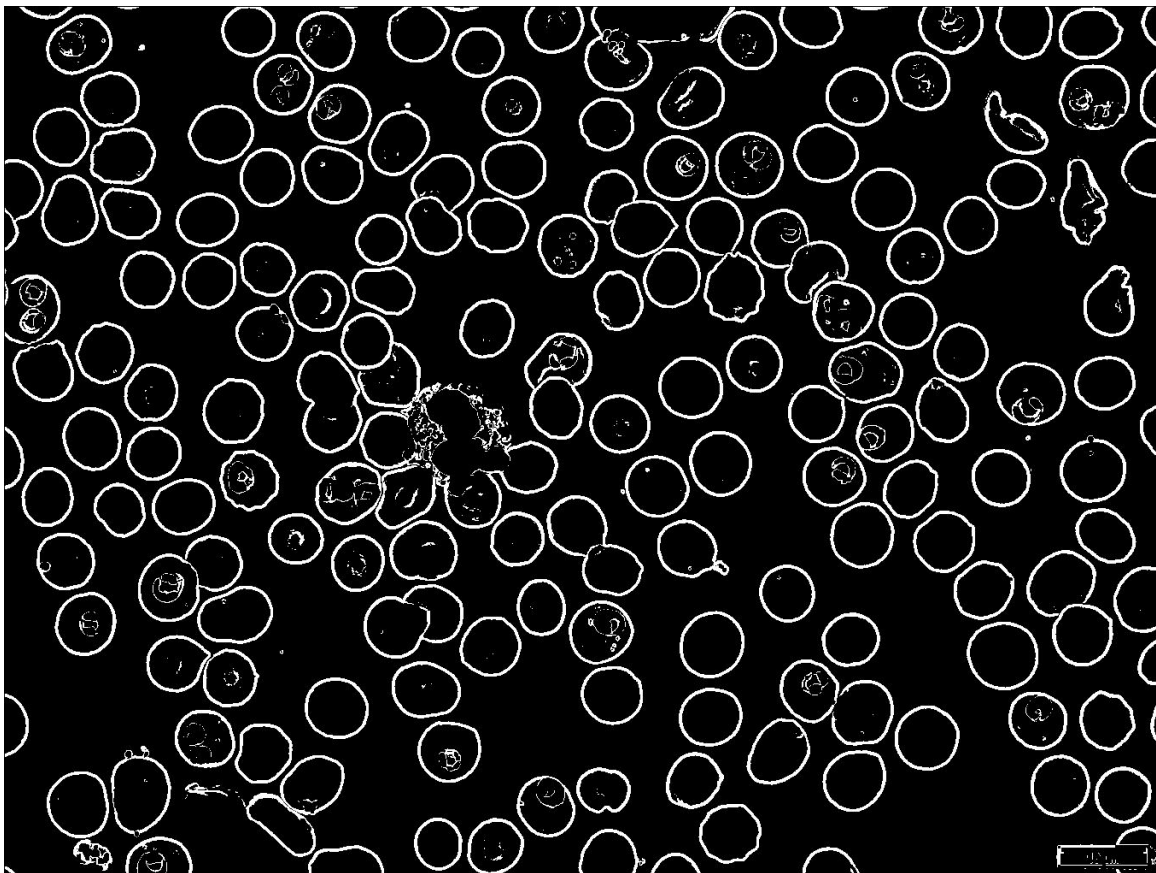
Write the code to threshold the Sobel edginess image, using  $T=0.05$ . Save the images in files called “Q2\_Sobel\_T\_0.05.jpg”. Your images should look like this:



3) **(10 Points) Cleaning up Plasmodium.** Expected length: [8-20 lines of code]

The thresholded images obtained in question 2 include edges corresponding to cell perimeters, as well as edges corresponding to the periphery of the darker plasmodium cells, inserted within red blood cells. In order to best delineate each red blood cell, we need to first remove the edge pixels caused by the Plasmodium cells. Pixels corresponding to Plasmodium cells tend to have graytone values less than 0.5. Starting from the Q2\_Sobel\_T\_0.05.jpg black-and-white image, produce a modified back-and-white image where any white pixel at position (r,c) is replaced by a black pixel if the value of pixel (r,c) or of any of the 8 surrounding pixels in the original graytone malaria-1 image is below 0.5. Save modified edge image as "Q3\_Sobel\_T0.05\_clean.jpg".

This should give you the image below. The edge pixels caused by Plasmodium are not completely gone, but this will be sufficient anyway.



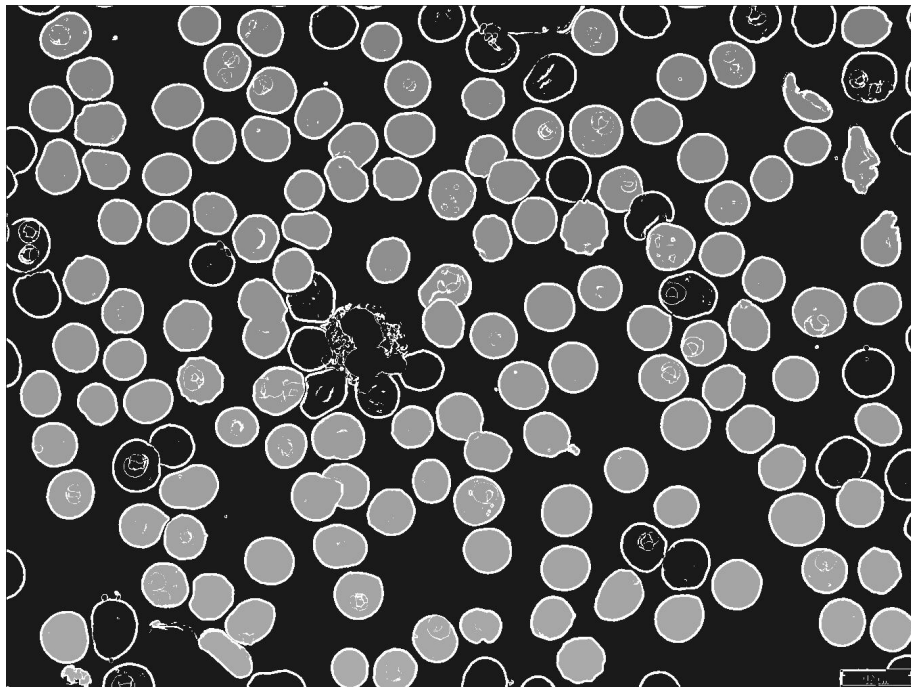
**4) (20 Points) Labeling cells.** [Expected length: 12-25 lines]

Write the `fill_cells` function. The function should take as argument an edge image (e.g. the image obtained in Q3), with black background and white edges. The function creates a new image that is a copy of the edge image provided as argument, but with each closed region filled with a different grayscale value (see result below). This is achieved by repeatedly calling the `seedfill` function (provided to you), using as seed pixel various pixels determined by your code, as described below.

Start by making a copy of the edge image, which is the one you will then modify and ultimately return. Then call the `seedfill` from pixel (0,0), with `fill_color=0.1`. This will mark the background of the image with a dark gray. Then, as seen in class, look for pixels that remain black. Whenever you find one, initiate a `seedfill` from that location, this time choosing `fill_color` as  $0.5 + 0.001 * n\_regions\_found\_so\_far$  (where `n_regions_found_so_far` is the number of closed regions identified to date by your search). So the first closed region will be colored 0.5, the second 0.501, the third 0.502, etc. Once your function is done looking at the entire image, return the resulting image. Save this image as “Q4\_Sobel\_T\_0.05\_clean\_filled.jpg”. When executed on the image obtained in Question 3, your function should return the image shown below.

**Notes:**

- On my computer, my code takes about 1 minute to run; it's normal that it is a bit slow, because the `seedfill` function is not fast and the image is large.
- The Sobel edge detection algorithm never calls edges in the first and last rows and columns of the image. This is why cells that are at the periphery of the image are not identified. Do not worry about this.



5) **(30 Points) Classifying cells.** [ Expected length: 25-50 lines of code]

Each detected closed region is now labeled with a different graytone: 0.5, 0.501, 0.502, ..., 0.623. For each region detected, we now need to determine if (i) is a red blood cell, and (ii) if the cell is infected or not. We will say that a region with grayscale value  $g$  is a valid cell if its size is between 1000 and 5000 pixels (this eliminates tiny closed regions that are not actual cells). We will say that a cell is infected if at least 2% of the pixels it contains (those labeled with grayscale value  $g$ ) have pixel grayscale value below 0.5 in the *original* grayscale image.

Write the function `classify_cells`, which takes as argument:

- The original graytone image
- The labeled image obtained in Question 4
- Optional keyword arguments `min_size=1000`, `max_size=5000`, `infected_grayscale=0.5`, `min_infected_percentage=0.02`

The function should return a tuple of two Sets. The first set should contain the labels of cells that are infected, while the second set should contain the labels of cells that not infected (see below for the expected output).

There are many ways to achieve this – feel free to use the approach you feel is the best. One approach could go as follows:

- Build a Set of all grayscale values observed in the labeled image
- Initialize `infected=set()`, `not_infected=set()`
- For each grayscale value in the grayscales set:
  - Scan the image to identify pixels with that grayscale value in the labeled image, and count separately those that are dark (`<=infected_grayscale`) and light (`>infected_grayscale`) in the original image.
  - Using the counts of dark and light pixels, determine if the region with that grayscale value is a cell or not, and whether or not it is infected. Add it to the `infected` or `not_infected` sets, as appropriate.
- Return the pair of `infected` and `not_infected` sets.

Notes: Some cells actually contain pixels that are labeled white, because of left-overs from the Plasmodium edges. To make out life easier, we will not consider those pixels as being part of the cell.

With my code, the function returns:

```
{ {0.504, 0.557, 0.522, 0.516, 0.647, 0.6, 0.629, 0.588, 0.521, 0.515, 0.529, 0.548, 0.52, 0.645, 0.535, 0.575, 0.53, 0.604, 0.649, 0.503, 0.598, 0.662, 0.547, 0.56, 0.5700000000000001, 0.66, 0.628},
```

```
{0.502, 0.5, 0.577, 0.542, 0.526, 0.5609999999999999, 0.625, 0.558, 0.619, 0.593, 0.552, 0.613, 0.578, 0.642, 0.607, 0.601, 0.54, 0.665, 0.63, 0.534, 0.659, 0.624, 0.528, 0.589, 0.653, 0.612, 0.551, 0.641, 0.571, 0.635, 0.565, 0.5680000000000001, 0.533, 0.658, 0.562, 0.527, 0.556, 0.617, 0.582, 0.646, 0.55, 0.611, 0.576, 0.64, 0.544, 0.669, 0.509, 0.538, 0.599, 0.654, 0.606, 0.67, 0.545, 0.574, 0.622, 0.648, 0.539, 0.523, 0.555, 0.532, 0.616, 0.549, 0.639, 0.543, 0.633, 0.537, 0.627, 0.531, 0.592, 0.656, 0.525, 0.65, 0.554, 0.615, 0.519, 0.644, 0.632, 0.536, 0.501, 0.657, 0.655, 0.559, 0.62, 0.524, 0.585, 0.553, 0.614, 0.518, 0.579, 0.643, 0.608, 0.573, 0.637, 0.541, 0.602, 0.567, 0.631} }
```

Note that if your code labeled your cells in a different order than my code did, your solution will be different. However, it should contain the same number of infected and not\_infected cells.



**6) (20 Points) Displaying infected cells** [Expected length: 12-25 lines]

As a last step, we will produce a new color image that is a copy of the original color image, but that highlights in red cells that have been classified as infected, and in green cells that have been labeled as not infected (see result below). This would allow the scientist using our program to verify the calls that are made.

Write the `annotate_image` function, which takes as arguments:

- The original color image
- The labeled grayscale image obtained in question 4
- The Set of grayscale values corresponding to infected cells (obtained from question 5)
- The Set of grayscale values corresponding to not infected cells (obtained from question 5)

The function should return a new color image, corresponding to a copy of the original color image, modified as follows.

The annotated image should have the same pixel values as the original image, except when both (i) the grayscale of pixel  $(r,c)$  corresponds to an infected cell or not infected cell, and (ii) at least one of the eight surrounding pixels in the labeled image is white (grayscale=1). The color at those pixels should be set to red (for infected cells) or green (for non-infected cells). Save the resulting image as "Q6\_annotated.jpg". It should look like the image below.

