CS 470/548: Assignment 03

Programming Assignments (80%)

Your goal is to detect the bounding boxes for cells in the BCCD dataset.

CS 470: Find white blood cells only.

CS 548: Find white blood cells AND red blood cells (in separate functions).

WARNING: You will have to install one more package: the nightly version of tensorflow-datasets:

pip install tfds-nightly

A03.py

In this module, you must write a function, **find_WBC(image)**, that:

- Takes a color image
- Finds the white blood cells (which tend to have **blue blobs in the center** and to be **fairly large**)
- Computes the bounding box (ymin, xmin, ymax, xmax) for each white blood cell found
- Returns a list of detected bounding boxes

CS 548: In the same module, include a function, **find_RBC(image),** that find the red blood cells and returns the bounding boxes. There are a few advantages, difficulties heir to this:

- The red blood cells tend to be about the same size (although not always).
- The red blood cells tend to have a seemingly hollow center (although not always).
- The red blood cells hedge towards a darker red.
- **Most critically, the dataset does NOT SEEM TO HAVE all red blood cells in an image marked.** Unlike the white blood cell detection, I am really looking for a reasonable approach (with less focus on the metrics), considering you may detect cells that the dataset has not marked.

The way you approach the problem(s) above is largely up to you. It is assumed that this will be done via some manner of color segmentation.

I am NOT assuming that you are going to use machine learning / deep learning (since we have not really covered this in depth). HOWEVER, if you do, you are ONLY allowed to train on the training dataset, NOT the testing dataset!

Unlike some of the other assignments, **you are permitted to use OpenCV, Numpy, Tensorflow, Scikit-Learn, and scipy functionality**, including:

- numpy
    - where
    - expand_dims
    - sum
    - sqrt
    - argmin
    - flatten
    - reshape
- skimage.segmentation
    - slic
- cv2
    - mean
    - kmeans
    - connectedComponents
    - floodFill
    - cvtColor
    - Any of the edge detection approaches
    - Any of the Hough approaches
    - Any of the morphological approaches

General_A03.py

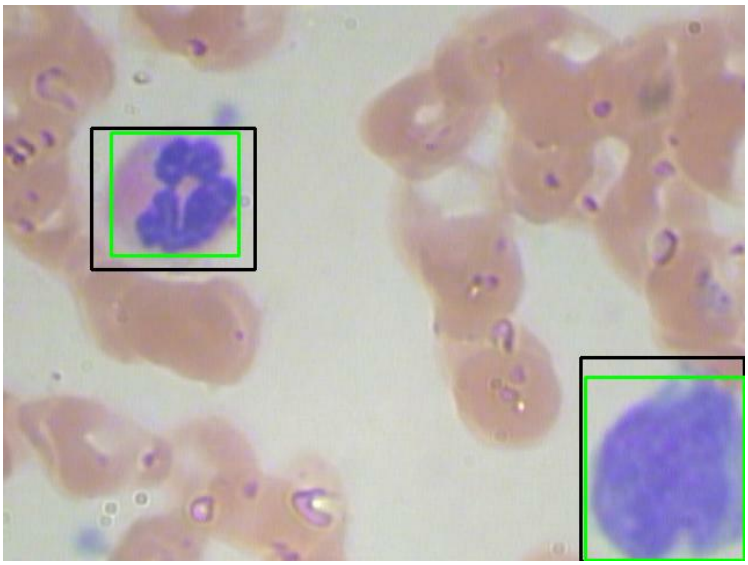
This is the core functionality of both training programs.

Train_A03.py

The main program (together with dataset loading and evaluation code) has been provided: **Train_A03.py**.

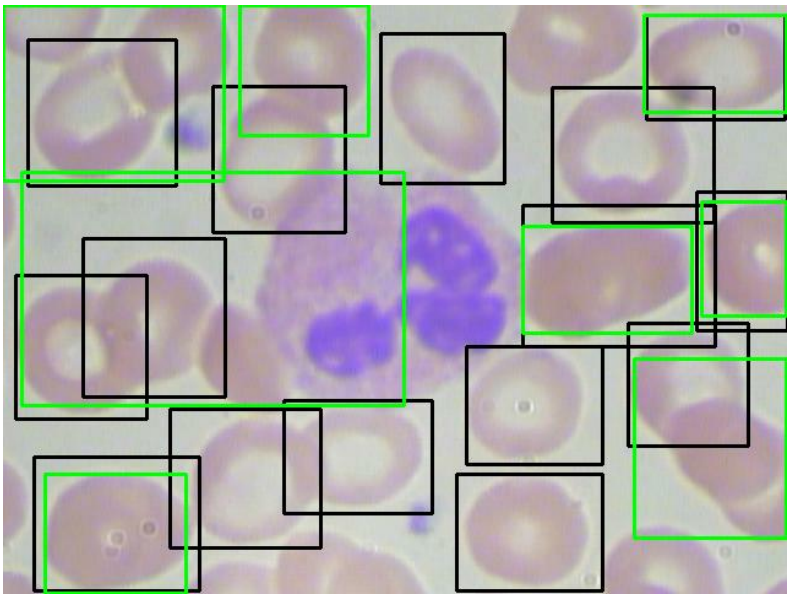
This program:

- Loads the BCCD dataset into training and testing tf.datasets.
- Creates an "assign03/output_wbc" directory
    - If it already exists, the program will ask you if you want to overwrite it
- Calls your prediction approach on the training and testing images, computing the accuracy of the count as well as the IOU (Intersection-Over-Union) of the predicted bounding boxes.
    - It also saves the output images with ground truth (black) and predicted (green) boxes.
- Prints the metrics as well as saves them to a file, assign03/output_wbc/RESULTS_WBC.txt.



CS 548: Train_A03_Grad.py

The program **Train_A03_Grad.py** does the same thing as the undergraduate version, except it works for the red blood cells and saves results to the "assign03/output_rbc" folder and the "RESULTS_RBC.txt" file.



Results (20%)

After running the training programs, copy your result txt file(s) to the MAIN directory of your repository.

BONUS POINTS

For the entire assignment, bonus points will be awarded to the submission that has the following with respect to the **white blood cell detection**:

- (+%5) Best **testing** accuracy in class (provided it is over 90%)
- (+%5) Best **testing** IOU in class (provided it is over 0.4)

Example Results

The example results were generated using the following approach:

- **(Step 1) Get superpixel groups (to honor color and edge boundaries).**
    - Let's assume the image with superpixel indices is given by *segments*.
    - Make sure to set *start_label* parameter to zero!
    - The number of groups found can then be extracted using:
        - cnt = len(np.unique(segments))
- **(Step 2) Compute mean color per superpixel**
    - Create a numpy array to hold the mean color per superpixel:
        - group_means = np.zeros((cnt, 3), dtype="float32")
    - Loop through each superpixel index (i.e., for specific_group in range(cnt)):
        - Create mask images using np.where:
            - mask_image = np.where(segments == specific_group, 255, 0).astype("uint8")
        - Add the channel dimension back in to the mask using np.expand_dims()
        - Use cv2.mean (with mask) to compute mean value per group
            - Note that cv2.mean() returns a 4-channel value, so you will want to slice the result:
                - group_means[specific_group] = cv2.mean(image, mask=mask_image)[0:3]
- **(Step 3) Use K-means on GROUP mean colors to group them into 4 color groups.**
    - Let's assume cv2.kmeans() returned the following:
        - *ret* = not used
        - *bestLabels* = list of which superpixel mean colors map to which kmeans group
            - E.g., if superpixel group 3's mean color fits into kmeans group 1, then:
                - bestLabels[3] → 1
        - centers = kmeans group center values
            - E.g., if kmeans group 1 has a color of (2,56,120), then:
                - centers[1] → (2, 56, 120)
- **(Step 4) Find the k-means group with mean closest to:**
    - **White blood cells → blue (255,0,0) (REMEMBER: BGR for OpenCV)**
    - **Red blood cells → dull red (125,142,175)**

    - E.g., find the color in *centers* closest to target color
    - Can use Euclidean distance color segmentation
- **(Step 5) Set that k-means group to white and the rest to black.**
    - I.e., we only want to keep the group closest to target color
    - E.g., if group 1 was the closest to target color, then this step should give you:
        - centers[0] → (0,0,0)
        - centers[1] → (255,255,255)
        - centers[2] → (0,0,0)
        - centers[3] → (0,0,0)

- **(Step 6) Determine the new colors for each superpixel group**
    - Convert *centers* to unsigned 8-bit
    - Get the new superpixel group colors:
        - colors_per_clump = centers[bestLabels.flatten()]
- **(Step 7) Recolor the superpixels with their new group colors (which are now just white and black)**
    - You can use numpy broadcasting and indicing to create a new image *cell_mask*:
        - cell_mask = colors_per_clump[segments]
    - **Convert cell_mask to grayscale!**
- **(Step 8) Use cv2.connectedComponents to get disjoint blobs from cell_mask.**
    - Slide 14 of region slide deck
    - Remember this function returns:
        - retval = number of connection components / blobs found
        - labels = image with labels marked
- **(Step 9) For each blob group (except 0, which is the background):**
    - Get the COORDINATES of the pixels that belong to that group using np.where:
        - coords = np.where(labels == i)
    - As long as coordinates are found, get the min and max x and y coordinates to get the bounding box (ymin, xmin, ymax, xmax).
    - Add bounding box to list of bounding boxes.

You absolutely do NOT have to use this exact approach. You may opt for a subset of this idea (e.g., just use k-means or superpixels), or you may use a completely different approach.

I will recommend though that you take a good look at np.where, which can be very useful: https://numpy.org/doc/stable/reference/generated/numpy.where.html

Submission

You must include the following in your repo:

- A03.py
- Result txt file(s)

Grading

Your OVERALL assignment grade is weighted as follows:

- 80% - Programming assignments
- 20% - Results