WBC Type Prediction
and
Quantitative prediction of WBC, RBC, and Platelets using Object Detection

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1. What is the problem?

One of the most crucial and frequently performed procedures in medicine is counting blood cells. An individual's blood cell count is used to make a health assessment. Currently, samples are checked and examined manually using glass slides and a microscope to determine blood counts which is a slow and laborious process. Furthermore, not all labs can afford using expensive counting equipment. The suggested real-time implementation can automate the process and deliver results instantly, so that healthcare professionals can focus on other important tasks.

2. Why is it interesting?

The count of White Blood Cells (WBC), Red Blood Cells (RBC) and Platelets in our blood indicates our blood health and any underlying diseases. Therefore, to have faster ways to analyze a person's WBC, RBC and Platelet counts will help healthcare professionals make better prognosis resulting in early estimations of a person's aliments making potential lifesaving decisions.

There are 4 different types of WBC which have distinct functions and their respective quantity will tell us various information about a person's blood health. As each type of WBC (Eosinophil, Lymphocyte, Monocyte, Neutrophil) is responsible for a different responsibility and if their quantities are lower the body's immunological response will be hampered.

An average blood test's turnaround time ranges from a few hours to a few days which is a wide range for potential life-threatening reports. Therefore, a faster and more economical method to find the counts of WBCs, RBCs, and platelets can potentially help doctors and the healthcare community.

3. What is the approach we propose to tackle the problem?

The Blood Cell dataset available on Kaggle and Github contains two sub-datasets, one which contains images of WBCs and its associated types; and the other which contains images of blood cells (containing RBCs, WBCs, and Platelets) and its associated annotations in xml format (annotations explain the bounding boxes of the blood cell and its type).

The first part would be to use the first sub-dataset to train a CNN to classify the WBC type. We would use some pre-defined CNN architecture (e.g., ResNet, AlexNet) according to our use-case. Next, we would also attempt to define our own CNN architecture and see how it behaves for this dataset. Classification metrics such as Accuracy, Precision, Recall etc. can be used to evaluate the model's performance.

The second part would be to use the second sub-dataset to predict the blood cell type. Since this dataset is small, we would perform some image augmentation (e.g., image rotation, flipping etc.) to increase the number of images and train CNN better. We would use the corresponding annotations to understand the boundaries of a particular cell type. We would use a pre-defined object detection model (e.g., YOLO) to detect and classify the blood cell type and attempt to build our own model as well. There are various metrics to define the accuracy of an object detection model e.g., Intersection over Union (IoU).

4. Why is this a good approach compared with other competing methods?

Our approach is to use an existing model architecture and create our own architecture and compare our model against the benchmarked existing model to evaluate its performance. We also plan to extend the scope of our project to perform object detection to identify the types of blood cells and its associated bounding boxes.

5. What are the key components of our approach and results? What are the limitations?

The BCCD dataset, which is dense and heavily overlapping, is dominated by RBCs. One of the limitations which we are speculating is that the dataset used for quantitative prediction of blood cells has only 410 different images of blood samples which is relatively small. To tackle this issue, we will be implementing image augmentation. Another potential limitation we foresee is model generalization; the images available in this dataset are of a particular format/resolution. This implies that to test these models on unseen images, we might have to transform the images to a similar format as the images available to us today.