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Abstract

Segregating White blood cell from microscopic urine samples using Image processing techniques

Image processing for Automatic urinanalysis

# **Primary methodology adopted**

Hough Circle transformation with canny edge detection algorithm along with median filtering, was found to be the best performing algorithm for the given dataset. WBCs, are grainy in structure and to detect this noise, various high pass filters were implemented using OpenCV. The study found that the inbuilt Sobel filter, automatically applied with the HoughCircles() method worked best for our application. Median filtering proved best to distinguish WBC from the sharp-edged dust particles that were enhanced by Sobel filter. Parameters for this function were tuned with the help of literature based on a similar application. Minimum and Maximum radius (parameters) for WBC was approximated from work by Jennifer et. al. Hyperparameters were further fine-tuned due to the difference in dpi/resolution used by the authors and our dataset. Fine-tuning was performed using a trackbar implementation.

After applying the above methodology to all images, the study found that the algorithm was performing poorly, particularly on image 0047, a possible explanation for this was because of the image lacking proper focus. The variance of the Laplacian operator was found for all images to test this hypothesis. The variance of the last image (0047) was indeed found to be very high compared to other images. The algorithm was modified to bypass the median filtering based on a certain threshold value to reduce the effect of blur in the last image.

**Evaluation**

The number of WBCs were manually counted based on the given description to evaluate the performance of the model. The model performed accurately on properly focused images (least variance of laplacian) and with well-spaced cells. It underestimates when WBCs are present in clusters and very close to each other.

|  |  |  |
| --- | --- | --- |
| **Image Name** | **Manual count** | **Model count** |
| 0003 | 10 | 10 |
| 0005 | 9 | 14 |
| 0007 | 8 | 10 |
| 0011 | 11 | 9 |
| 0012 | 38 | 25 |
| 0047 | 42 | 38 |

# **Alternate methodologies and their shortcomings**

Template Matching

Multiple templates of WBCs were obtained, but owing to the homogeneity of the image, the thresholding value for proper segmentation was set at .985. Such a high threshold prevented the templates from matching with other WBC that might be similar. Hence only the WBCs whose template was taken, along with a few very similar ones were identified by this algorithm. Scalability was a major concern in this approach.

## HSV segmentation

The HSV values for the mask was found using dynamic track bar implementation. However, these values were not universal and not even close for the images in the dataset. Moreover, the mask produced an inverted result on the image, i.e. classifying the background as positive and cells as negative. A separate mask was to be found for every image, while that is possible to automate, it takes a lot of computational resources and increases the complexity of the algorithm.

## Contours mapping

Adaptive filtering was used with mean approximation. It was further eroded before finding contours. The number of edges for contours was set greater than 10 to detect circles. The algorithm found various complicated irregular shapes along with the correct cells. Multiple overlapping circles were found too. This approach can be scaled if a more complicated algorithm based on convexity and moments are used to define circles along with a number of edges. The major shortcoming for such an approach in the innumerable number of hyperparameters to tune with no guarantee of generalizability.

# **References**

* Jennifer C. *et al. ‘Microscopic Image Analysis and Counting of Red Blood Cells and White Blood Cells in a Urine Sample’*
* S. Pavithra .et al.*‘ White Blood Cell Analysis Using Watershed and Circular Hough Transform Technique.’*
* [Watcharin Tangsuksant](https://www.researchgate.net/profile/Watcharin_Tangsuksant) et al. *‘Development algorithm to count blood cells in urine sediment using ANN and Hough Transform*