

## Introduction

In microscopic study of cell morphology, a tissue sample taken out from human body is prepared for viewing under microscope and then staining techniques are applied. However, using this process different components of tissue can be dye with different stains. It is very difficult task to diagnose a disease after manually analyzing these biopsy slides. And hence it becomes a labor intensive and complicated work for pathologists. But due to recent advancement in digital pathology, the automatic recognition of pathology patterns in microscopic image has the potential to give valuable assistance to the pathologist.

For most of the modern day pathology tasks, automatic nuclei detection and segmentation is a challenging task. The detection and segmentation of nuclei in cytological images can be done by well-separated nuclei and the absence of complicated tissue structures. Due to the presence of overlapping nuclei and other tissue structures in the biopsy slides an effective and efficient nuclei segmentation should be done.

In this project we have done a analysis on how different segmentation techniques can be applied in this domain and have tried to make it more effective and efficient

## Scope of the Project

The task of segmenting cell nuclei in microscope images is a classical image analysis problem. An accurate nuclei segmentation may contribute to development of successful system which automate the analysis of microscope images for pathology detection.

The objective of our work is nuclear segmentation. We are using a cell sample dataset available at murphy labs for our work . In this dataset we are provided with fifty images of cell sample and the fifty images have been hand segmented also for comparing the result of the segmentation with the standard image that has been manually segmented.

Accurate results of cell nuclei segmentation are often adapted to a variety of applications such as the detection of cancerous cell nuclei and the observation of overlapping cellular events occurring during wound healing process in the human body.

## Methodology

We have analysed and implemented various segmentation methods. The basic ones are Thresholding, Adaptive Thresholding and Otsu Binarization. We have also implemented edge detection techniques based segmentation. We have also implemented some advanced techniques such as Kmeans clustering based segmentation and Watershed method.

Thresholding is the simplest method of image segmentation. In this method, we choose a threshold value to create binary image. The intensities above the threshold are maximised and the ones below are minimised. For example, anything that is greater than 127 in the grayscale, can be set to 1 in the binary image and anything that is less than or equal to 127 in the grayscale image can be set to 0 in the binary image. In adaptive threshold unlike fixed threshold, the threshold value at each pixel location depends on the neighbouring pixel intensities.

Otsu Binarization is a really advanced Thresholding technique. It follows the mechanism of Gaussian Mixture Models(GMM). In Otsu's method we exhaustively search for the threshold that minimizes the intra-class variance(the variance within the class), defined as a weighted sum of variances of the two classes.

For Edge Detection Based segmentation there are a lot of methods for edge detection. Faster ones being Sobel, Canny and Laplacian. We have implemented these methods to detect the edge of the object of interest and then applied Thresholding for Binarization. Most of these algorithms use first or second derivative gradient measure and apply convolution.

Kmeans clustering based segmentation aims to partition n observations into k clusters in which each observation belongs to the cluster with the nearest mean, serving as a prototype of the cluster. This results in a partitioning of the data space. Kmeans can be used to binarize the image by taking k=2 and clustering the pixels into 2 clusters according to their intensities.

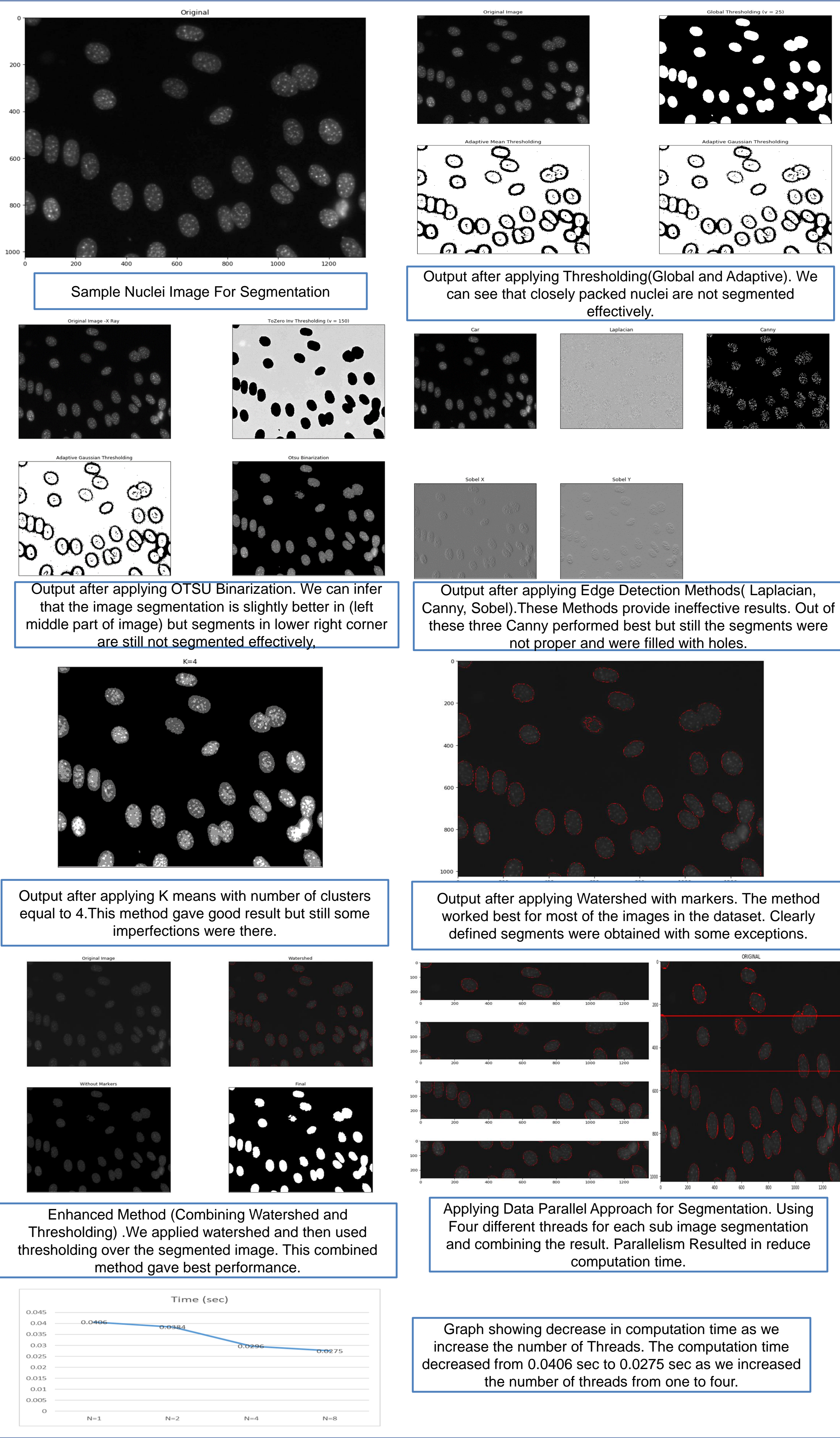
Watershed is a transformation defined on a grayscale image. The name refers metaphorically to a geological watershed, or drainage divide, which separates adjacent drainage basins. The watershed transformation treats the image it operates upon like a topographic map, with the brightness of each point representing its height, and finds the lines that run along the tops of ridges.

The basic idea consisted of placing a water source in each regional minimum in the relief, to flood the entire relief from sources, and build barriers when different water sources meet. The resulting set of barriers constitutes a watershed by flooding.

Image Segmentation is computationally intensive task and just like most computing tasks, there is great advantage to splitting up workload into multiple workers and partitioning the task into different, multiple tasks for these multiple actors.

So after this we tried to implement data parallelism for these segmentation methods and analysed how parallelism affects the results of segmentation in terms of effectiveness and efficiency.

## Results



## Conclusions

The implemented techniques were able to segment the nuclei in the image. Some of the techniques like edge detection and thresholding were less effective in segmenting the images when compared to K means and Watershed Algorithm. The Watershed algorithm provided the most effective result among these methods. However the enhanced method using Watershed Algorithm followed by use of Thresholding provided the best result for segmentation and densely packed nuclei were also separated effectively.

The data parallelism approach was also implemented to increase the efficiency and decrease computation time. The multithreading concept was used to implement parallelism with each thread working on a part of the image. The overall efficiency was improved and computation time decreased drastically.

## Contact

|                         |           |  |
|-------------------------|-----------|--|
| Shashank Pathak         | 15BCE1287 | <a href="mailto:shashank.pathak2015@vit.ac.in">shashank.pathak2015@vit.ac.in</a>               |
| Ayush Sharma            | 15BCE1335 | <a href="mailto:ayush.sharma2015@vit.ac.in">ayush.sharma2015@vit.ac.in</a>                     |
| Shashank Shekhar Shukla | 15BCE1012 | <a href="mailto:shashankshekhar.shukla2015@vit.ac.in">shashankshekhar.shukla2015@vit.ac.in</a> |
| Aayush Pandey           | 15BCE1058 | <a href="mailto:aayush.pandey2015@vit.ac.in">aayush.pandey2015@vit.ac.in</a>                   |
| Kunal S. Kasodekar      | 15BCE1045 | <a href="mailto:kasodekarkunal.sunil2015@vit.ac.in">kasodekarkunal.sunil2015@vit.ac.in</a>     |

## References

- Chen X, Zhou X, Wong STC. Automated segmentation, classification, and tracking of cancer cell nuclei in time-lapse microscopy. IEEE Trans Biomed Eng. 2006;53:762–766. doi: 10.1109/TBME.2006.870201.
- Tscherepanov M, Zollner F, Kummert F. Classification of segmented regions in brightfield microscope images. Proceedings of the IEEE International Conference on Pattern Recognition. 2006;3:972–975
- Ropers S-O, Bell AA, Wurfinger T, Bocking A, Meyer-Ebrecht D. Automatic scene comparison and matching in multimodal cytopathological microscopic images. Proceedings of the IEEE International Conference on Image Processing. 2005;1:1145–1148
- L.Dorini et al, "White blood cell segmentation using morphological operators and scale-space analysis", IEEE conference on Computer Graphics and Image Segmentation,2007.