IMPROVED MICROSCOPIC DIGITAL IMAGE PROCESSING FOR DENGUE DETECTION USING MULTI-SUPPORT VECTOR MACHINE CLASSIFIER

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Abstract: Dengue is considered as one of the viral disease that affects the human health in various countries. The dengue virus spreading through mosquitoes is treated as a rapid spreading virus that may even lead to death of a human. Hence, it is very essential to develop a quick diagnostic system that accurately finds the dengue by counting the red blood cells (RBC), White Blood Cells (WBC) and platelets from a microscopic image acquired from a human blood. In this paper, an automated blood image processing technique is developed with Multi Support Vector Machine Classifier (MSVM) that accurately finds the RBC, WBC and platelet count from a microscopic blood sample image. The detection of these three parameter provides an effective analysis on dengue symptoms from human body. The simulation via Matlab shows that the proposed MSVM classification engine provides faster and accurate classification on blood symptoms than other existing mechanisms.

Keywords: Dengue, Multi-Support Vector Machine, Classification, Diagnosis.

1. Introduction

The study of microscopy images is also important in both the medical and computer sciences. Many microscopic examination complications, such as complete blood count [1] and blood tests deemed the initial stage of detection and diagnosis of malaria, leukemia and anemia, are involved. In addition, during a full physical test a number of tests are carried out. The complete blood count (CBC) test is used for the structure calculation and distribution of all cell blood components. The count on white blood cells (WBC), hemoglobin (HB) levels and platelet is often in CBC.

CBC and blood smears scans help to differentiate between and diagnose and track health conditions such as anemia, leukemia, infections and allergy [3]. For blood disorders, such as HB-dependent anemia, the development and deterioration of red blood cells have been measured. Further experiments are conducted in order to confirm iron deficiency anemia (IDA), if IDA is reported in red cell indexes. Red blood cells (RBCs) differ from 4.2 to 5.9 million cells of natural blood in a cm^2 range. Extreme heart, lung or kidney disorders can, for example, mean high RBC numbers. HB also increased with high numbers of RBC due to bone marrow disorders [2]. HB also increased. Normal blood WBCs are between 4, 500 and 10,000 [4]. A blood smear examination is carried out to examine leukemia morphology, along with bone marrow scans, when leukemia is suspected [6-10]. For platelets, small blood cells that assist with blood coagulation, normal numbers vary from around 150,000 to 450,000 platelets perμ-liter. In patients with decreased platelet levels, such as patients suffering from Dengue fever, their platelet count is closely tracked and their gain is very limited and the patient needs transfusion [2]. An irregular blood smear read typically entails inflammation or disease [11].

The thin-blood smear research continues to be the gold standard for this condition [5]. Malaria is an RBC-infected parasite. Microscopic photographs are also used for early diagnosis, examination and count of such blood disorders as anemia and leukemia before confirmation by other laboratory studies. However, a highly probable, repeated, arbitrary and time-consuming task is a manual or visual quantification in thin-blooded films and WBCs of leukemia. A powerful counting mechanism, which collects information on the microscopic distribution of particles, may help detect clinical anomalies [15]-[20].

An algorithm is developed and validated in this paper which classifies and counts red and white blood cells in the microscope image. In this paper, an automated blood image processing technique is developed with Multi Support Vector Machine Classifier (MSVM) that accurately finds the RBC, WBC and platelet count from a microscopic blood sample image. The detection of these three parameter provides an effective analysis on dengue symptoms from human body.

2. Related Work

Many researchers have been studying blood cell segmentation and counting. Some scientists used morphological operations and thresholds for classification [5] [14] [15].

In [5], the researchers suggested a method-based morphological approach with iterative threshold approaches. RBC cells that contained clumping cells were used to create a triangulation of the Delaunay. They used actual images produced in the laboratory by microscopy and a laboratory expert detected the reality on the ground. There was a 2.8% difference between manual and automatic red blood cell counts. They tolerated some overlap, but in cases with a high degree of overlap cells the cells could not be identified. In comparison, iterative threshold method did not differentiate between faint red cells.

In [8], the researchers used Zack's thresholding threshold technique on HSV colour models S-and-V image components. Thresholds have been used to improve segmentation accuracy in combination with a sequential algorithm. The Dhruv Pathology Lab and CDC-DPDx obtained research results and images of blood cells and determined the truth of the ground through experts. The dataset's size was limited. Holes were present for most of the RBCs found. More pre-processing steps were required to increase the accuracy.

In [9], the researchers suggested an automated survey in thin blood stream samples [9] which counted the red blood cells and detected parasites of malaria. Both RBCs and WBCs are processed in order to count the green colour sheet and for segmentation on the infected RBC using the Otsu thresholding. A histogram was used to assess the optimal threshold. The basic details were calculated by a pathologist who mixed their observations with manual statistics. However, because of the use of morphology and thresholds the technique does not distinguish clumping and overlapping cells.

The WBC, RBC, and platelet counting method has been introduced by the authors in [10]. Several preprocessing steps were taken before the image was converted into binary. Segmentation and cell count are based on an optimal threshold value calculated by the histogram. They reached 95% accuracy for their proposed method compared with manual numbers and hematology analyzers. However, it cannot distinguish alternate cells. By using iterative thresholds, the danger of losing useful image information is high, reducing segmentation accuracy.

The authors in [12] also introduced the circular detector method for the identification of image characteristics such as the circulation of the Gabor wavelet filters. The wraps will be stripped from the source and the plane wave will radiate from the centre of this filter. They are testing the potential solution on simulated images and real microscopic images, which overlap cells with one another.

The researchers in [13] established a method that was not Hough Turn to classify white blood cells. By combining circular detection with electro-magnetism, they used an optimisation of the corner maps image. In comparison to the red cells, the number of white cells in blood smear images was limited; hence, overlapping white cells are observed in a small degree. The technique was not tested for clumping cells. They compared the results and demonstrated good consistency in the process.

3. Methodology

The suggested methodology for processing microscopic blood streaming images was developed by dividing and counting both WBC and RBC. The segmentation is focused on threshold and morphologic operations and then is based on the circular properties of the blood cells derived from an iterative MSVM of circle detection and classification of RBC, WBC and platelets.

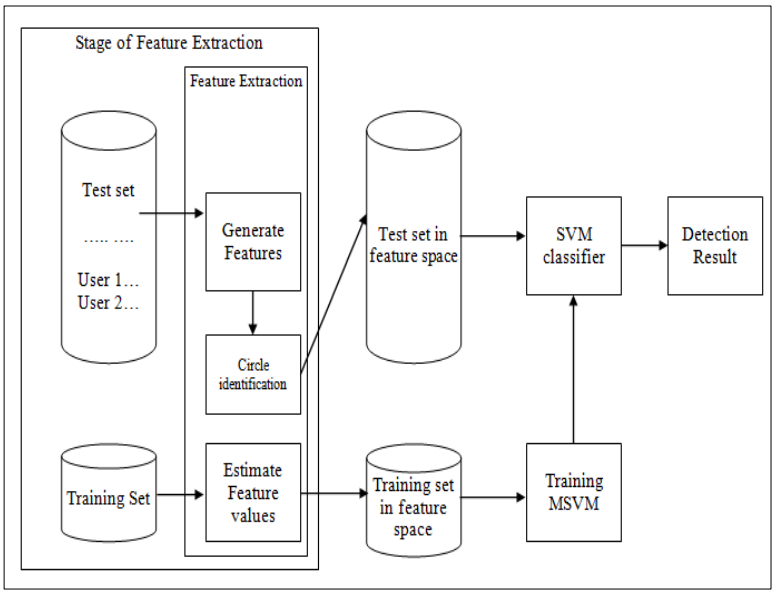


Figure 1 Proposed MSVM classification

A modern technique has been proposed and used for RBC and WBC counting for binary images based on the RCD fundamentals. The first image contains only RBCs and the second image contains WBCs; this step has been taken using thresholding. Thus, the original image is split into two images, where the histogram is investigated for 20 grey samples, and it indicates the optimal threshold values for removing WBCs and RBCs. Each image is prepared by morphological operators following cell separation to obtain the edge image using canny operator. Then it is used to count the cells of each image by an iterative MSVM. The proposed classification engine is illustrated in Figure 1.

Preprocessing

The suggested cell segmentation approach works with boundary images. The blood smears microscopy is a vivid image, and the image has to be prepared several measures before the edge image is extracted. The cells were segregated by form and separate preprocessing steps for WBCs and RBCs were established in our proposed system. White blood cells are collected as a separate image at this point, and the density of the red blood cells varies. Thus, separate pre-processing steps are preferable for each type of cell.

Proposed Method for Counting

The Hough Transform method implemented MSVM algorithm ignores the accumulator power. Several improvements to the simple RCD algorithm have been made to address the issue of initialization when using large pixel images. The methods were changed to detect irregular circles, to choose the optimum circle of the candidate circles, to evaluate the number iterations in a totally dynamic form in order to improve identification and runtime of the algorithms and to improve cell overlap.

Initialization Problem

In order to solve the initialization problem in simple MSVM, the proposed technique divides the edge image on 8 nearby linked components. Finally, we split the entire image in small partitions and handle each partition as an input image before entering our standardised iterative circle detection algorithm that uses local randomisation steps.

As far as this initialization issue is concerned we have previously stressed that the global option of four pixels (in the full image) will minimise the likelihood of finding true circles, time consumption and the need for several iterations in order to find true circles. The four pixel choices in the RBC labelling can be conveniently, if cell A is to be detected. This method is also streamlined by adding 4 pixel local selections.

Irregular Circle Detection

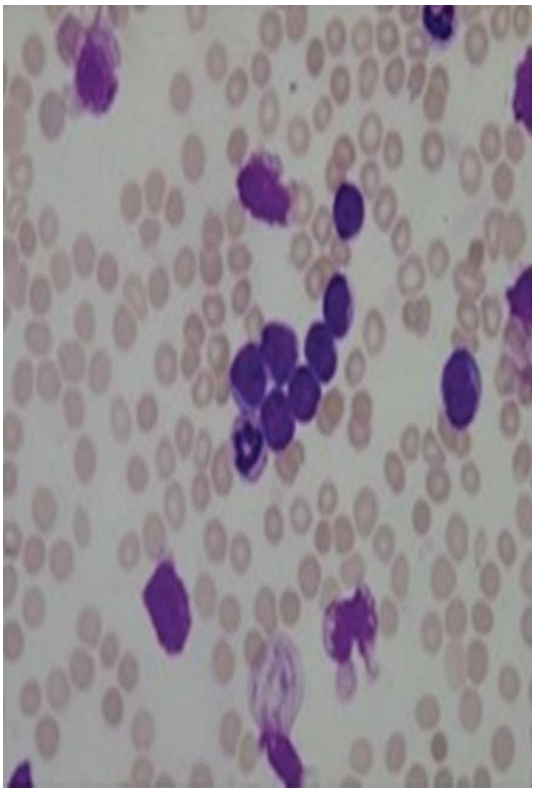
Approximately oval are normal red and white blood cells; but not all blood cells are regular blood cells. So,

if a potential circle was identified, we observed irregular circles. If a potential cycle can be found by the algorithm, these two circles are superimposed on the grid and all edge pixels in the section are tracked. Red pixels do not appear in the candidate circle boundaries. We raise the distance between the two circles by partitioning the image dependent on related components.

Proposed Classification using MSVM

To find all circles in the partition image, the number of iterations is extremely significant. Therefore, for many reasons calculating the number of iterations is not a simple feat. Second, the number of iterations depends primarily on two factors: the number of edge pixels on a image and the distance from the edge pixels needed for each iteration to form a circle. As a consequence, large numbers of iterations can be seen in the image. The approach suggested is a way to determine dynamically for each partition image a number of iterations. Two other considerations are introduced: the .

Figure 2 shows the results of input image,

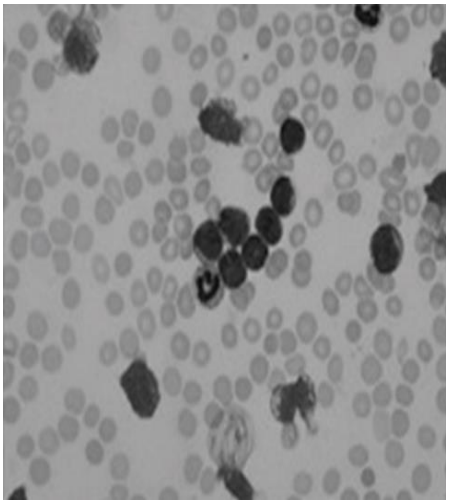


(a)Original blood image

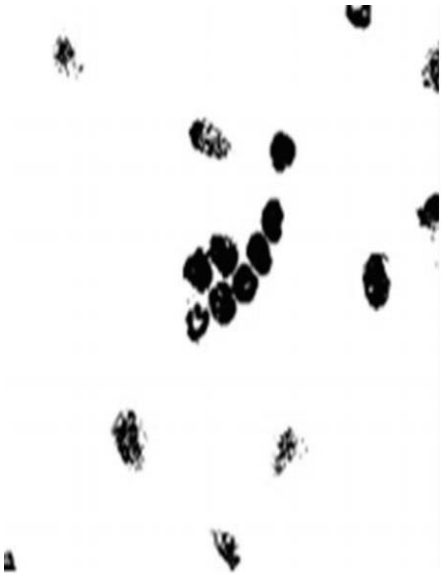
number of pixels on the partition and the radius of the cell. Although the approach suggested involves a certain size of the random boundary pixels in the same circle, the number of iterations has been marginally increased to tolerate the conditions proposed and to ensure that all alternatives can be taken into account. In this case, for every partition there are no fixed number of iterations. The number of iteration is based entirely on the relation between the number and cell radius of the edge pixels in the partition.

4. Results and Discussion

The experiments are conducted on 100 different blood image samples and the simulation is conducted in Matlab. The proposed method is compared with other existing machine learning classifiers like Random Forest (RF), K-Nearest Neighbor (KNN), Naïve Bayes (NB) and Support Vector Machine (SVM). The MSVM and other existing classifiers are tested in terms of sensitivity, specificity and accuracy of the classifiers



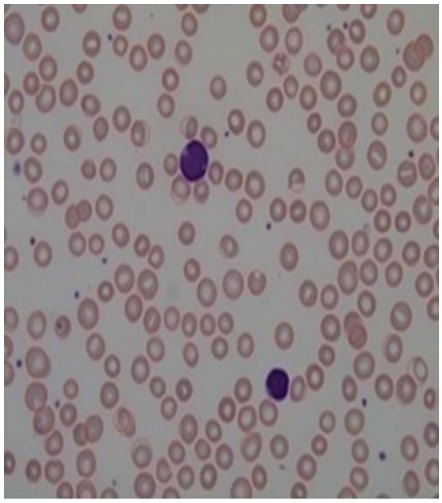
(b) gray scale image



(c) thresholding the binary image

(d) Canny edge detection after noise removal and filling holes

(e) Removal of WBC and displays RBC



(f) RBC detected in classification for a test image

Figure 2: Processing results at each stage

The Fig.2-Fig.3 shows the results of sensitivity, specificity and accuracy with existing machine learning classifiers.

The Figure 4 shows sensitivity of the classifier, where the proposed MSVM obtains higher sensitivity than the other existing classifiers. This is due to accurate detection of true positive samples and reduced false positive rate than other classifiers.

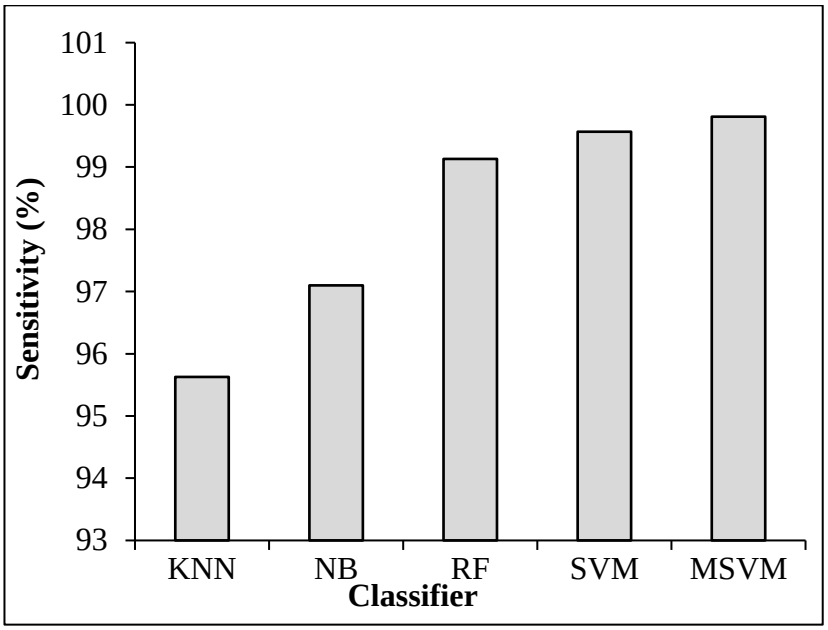


Fig.3. Sensitivity

The Figure 5 shows specificity of the classifier, where the proposed MSVM obtains higher specificity than the other existing classifiers. This is due to the reduced detection of false positive rate and optimal improvement in finding the true positive RBCs, WBCs and platelets than other classifiers.

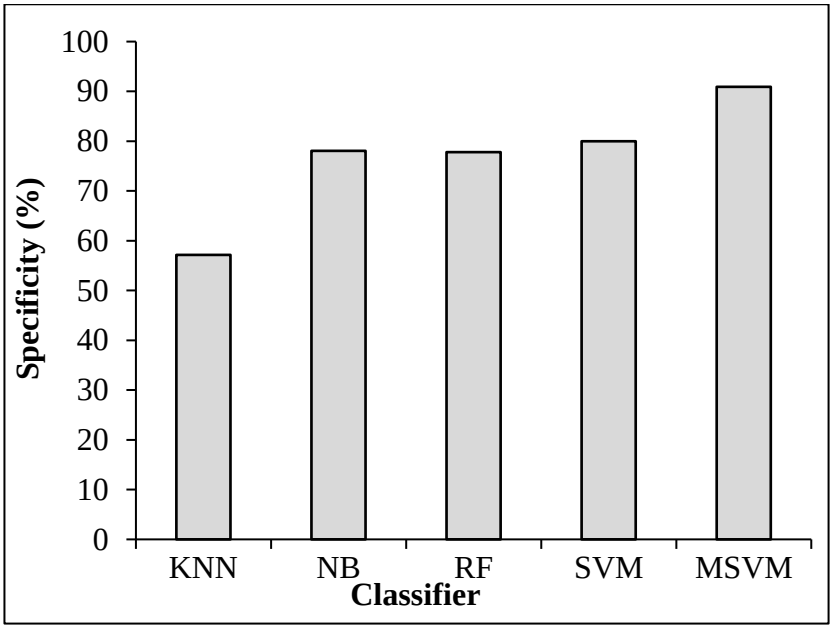


Fig.4. Specificity

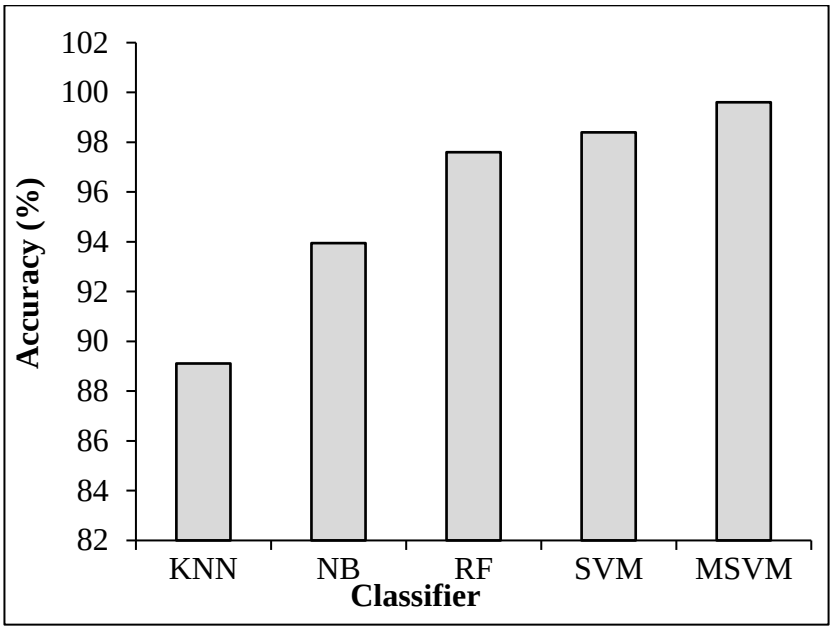


Fig.5. Accuracy

The MSVM shows higher accuracy than other methods with its circular detection model on finding the RBCs, WBCs and platelets. Such extraction of features from the blood image samples helps the classifier to obtain higher rate of classification accuracy than other methods.

5. Conclusions

In this paper, we developed an automated blood cells counting that includes counting of RBC, WBC and platelets using MSVM. The MSVM helps in identification of RBC, WBC and platelets individually that regulates the diagnostic system to identify the presence of dengue in a human. Thus this system provides an effective counting of these parameters to accurately identify the symptoms of dengue. The simulation with existing machine learning classifiers showed that the proposed MSVM offers improved classification of blood samples than SVM, RF, NB and KNN. The proposed method yields an average accuracy of 99.6% that shows higher level of FPR than other machine learning classifiers.

References

[1] M. Habibzadeh, A. Krzyzak, and T. Fevens, "Application of pattern recognition techniques for the analysis of thin blood smears images," Journal of Medical Informatics & Technologies, vol. 18, 2011.

[2] M. M. Osman, "Normal reference value of blood cell count, red, white and platelet of Khartoum North Area," Al Neelain Medical Journal, vol. 3, no. 8, 2013.

[3] Kousik, N., Natarajan, Y., Raja, R. A., Kallam, S., Patan, R., Gandomi, A. H. (2021). Improved salient object detection using hybrid Convolution Recurrent Neural Network. Expert Systems withApplications, 166, 114064.

[4] Yuvaraj, N., Srihari, K., Chandragandhi, S., Raja, R. A., Dhiman, G., Kaur, A. (2021). Analysis of protein-ligand interactions of SARS-Cov-2 against selective drug using deepneural networks. Big Data Mining and Analytics, 4(2), 76-83.

[5] H. Berge, D. Taylor, S. Krishnan, and T. S. Douglas, "Improved red blood cell counting in thin blood smears," in Proceedings of the 8th IEEE International Symposium on Biomedical Imaging: From Nano to Macro (ISBI '11), pp. 204–207, Chicago, Ill, USA, April 2011.

[6] Yuvaraj, N., & Vivekanandan, P. (2013, February). An efficient SVM based tumor classification with symmetry non-negative matrix factorization using gene expression data. In 2013 International Conference on Information Communication and Embedded Systems (Icices) (pp. 761-768). IEEE.

[7] Gowrishankar, J., Narmadha, T., Ramkumar, M., Yuvaraj, N. (2020). Convolutional Neural Network Classification On 2d Craniofacial Images. International Journal of Grid and Distributed Computing, 13(1), 1026-1032.

[8] L. B. Damahe, P. G. Student, R. G. College, and R. G. C. Engg, "Segmentation based approach to detect parasites and RBCs in blood cell images," International Journal of Computer Science and Applications, vol. 4, no. 2, 2011.

[9] L. B. D. Panchbhai and V. Vishal, "RBCs and parasites segmentation from thin smear blood cell images," International Journal of Image, Graphics and Signal Processing, vol. 10, no. 10, pp. 54– 60, 2012.

[10] S. Khan, A. Khan, and A. Naseem, "An accurate and cost effective approach to blood cell count," International Journal of Computer Applications, vol. 50, no. 1, pp. 18–24, 2012.

[11] N. Nguyen, A. Duong, and H. Vu, "Cell splitting with high degree of overlapping in peripheral blood smear," International Journal of Computer Theory and Engineering, vol. 3, no. 3, pp. 473–478, 2011.

[12] A. Rhodes and L. Bai, "Circle detection using a gabor annulus," in Procedings of the British Machine Vision Conference, pp. 108.1– 108.11, September 2011.

[13] E. Cuevas, D. Oliva, M. D´ıaz, D. Zaldivar, M. Perez-cisneros, ´ and G. Pajares, "White blood cell segmentation by circle detection using electromagnetism-like optimization," Computational and Mathematical Methods in Medicine, vol. 2013, Article ID 395071, 15 pages, 2013.

[14] Sangeetha, S. B., Blessing, N. W & Sneha, J. A. (2020). Improving the training pattern in back-propagation neural networks using holt-winters' seasonal method and gradient boosting model. In Applications of Machine Learning (pp. 189-198). Springer, Singapore.

[15] Alam, M. M., & Islam, M. T. (2019). Machine learning approach of automatic identification and counting of blood cells. Healthcare technology letters, 6(4), 103-108.

[16] Nassar, M., Doan, M., Filby, A., Wolkenhauer, O., Fogg, D. K., Piasecka, J., ... & Hennig, H. (2019). Label-free identification of white blood cells using machine learning. Cytometry Part A, 95(8), 836-842.

[17] Shirazi, S. H., Umar, A. I., Haq, N., Naz, S., Razzak, M. I., & Zaib, A. (2018). Extreme learning machine based microscopic red blood cells classification. Cluster Computing, 21(1), 691-701.

[18] Abdullah, E. L. E. N., & Turan, M. K. (2019). Classifying White Blood Cells Using Machine Learning Algorithms. Uluslararası Mühendislik Araştırma ve Geliştirme Dergisi, 11(1), 141-152.

[19] Abdullah, E. L. E. N., & Turan, M. K. (2019). Classifying White Blood Cells Using Machine Learning Algorithms. Uluslararası Mühendislik Araştırma ve Geliştirme Dergisi, 11(1), 141-152.

[20] Imran Razzak, M., & Naz, S. (2017). Microscopic blood smear segmentation and classification using deep contour aware CNN and extreme machine learning. In Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition Workshops (pp. 49-55).

[21] Manikandan, R and Dr.R.Latha (2017). "A literature survey of existing map matching algorithm for navigation technology. International journal of engineering sciences & research technology", 6(9), 326-331.Retrieved September 15, 2017.

[22] A.M. Barani, R.Latha, R.Manikandan, "Implementation of Artificial Fish Swarm Optimization for Cardiovascular Heart Disease" International Journal of Recent Technology and Engineering (IJRTE), Vol. 08, No. 4S5, 134-136, 2019.

[23] Manikandan, R., Latha, R., & Ambethraj, C. (1). An Analysis of Map Matching Algorithm for Recent Intelligent Transport System. Asian Journal of Applied

Sciences, 5(1). Retrieved from https://www.ajouronline.com/index.php/AJAS/article/view/4642

[24] R. Sathish, R. Manikandan, S. Silvia Priscila, B. V. Sara and R. Mahaveerakannan, "A Report on the Impact of Information Technology and Social Media on Covid–19," 2020 3rd International Conference on Intelligent Sustainable Systems (ICISS), Thoothukudi, India, 2020, pp. 224-230, doi: 10.1109/ICISS49785.2020.9316046.

[25] Manikandan, R and Dr.R.Latha (2018). "Map Matching Algorithm Based on a Hidden Markov Model for Vehicle Navigation" International Journal of Advanced Technology in Engineering and Science, 6(6), 36-42.

[26] Manikandan, R and Dr.R.Latha (2018). "GLOBAL POSITIONING SYSTEM FOR VEHICLE NAVIGATION" International Journal of Advances in Arts, Sciences and Engineering (IJOAASE), 6(13), 1-9.