

ORIGINAL PAPER

Using Deep Learning for Blood Cells Detection

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Abstract

The complete blood count is one of the most important and most performed exams in the medical field. Through it, it is possible to discover important alterations in the organism and it is used in the assessment of patients health. Although it is a common practice, the performance of exams is difficult in laboratories because of the high cost of purchase and maintenance machinery. As an alternative to that, this project develops a computational model of Deep Learning capable of detecting cells automatically through images of blood samples. Through the use of object detection libraries, it was possible to train a model aimed at this problem and capable of detecting cells in images with satisfactory precision. Considering the identification of cells in images of blood samples in the best results obtained, it was possible to count white cells with 100% accuracy, red cells with 89% and platelets with 96%, generating subsidies to elaborate the main parts of a blood count. The elements aimed at classifying types of white cells were not carried out due to the limitations of the dataset used. However, as it showed good results, the research can be expanded to future works that address this problem.

Keywords: Blood Test; Complete Blood Count; Deep Learning; Neural Networks

Resumo

O hemograma é um dos exames mais importantes e mais realizados no âmbito médico. Através dele é possível descobrir importantes alterações no organismo e geralmente é utilizado na avaliação da saúde dos pacientes. Embora seja uma prática comum, a realização dos exames é dificultada nos laboratórios por utilizar um maquinário de alto custo de compra e manutenção. Como alternativa a isso, este projeto desenvolve um modelo computacional de *Deep Learning* capaz de detectar células automaticamente através de imagens de amostras de sangue. Através da utilização de bibliotecas de detecção de objetos, foi possível realizar o treinamento de um modelo voltado para essa problemática e capaz de detectar células em imagens com precisão satisfatória. Considerando a identificação de células em imagens de amostras de sangue nos melhores resultados obtidos, foi possível realizar a contagem das células brancas com 100% de acurácia, as vermelhas com 89% e das plaquetas com 96%, gerando subsídios para elaborar as partes principais de um hemograma. Os elementos voltados a classificação de diferentes tipos de células brancas não foram realizados devido à limitações do *dataset* utilizado. Porém, como apresentou bons resultados, a pesquisa pode ser expandida para futuros trabalhos que abordem esse problema.

Palavras-Chave: Deep Learning; Exames de Sangue; Hemograma; Redes Neurais

1 Introduction

Human health is always a central area of research, bringing benefits for all society, being vital to guarantee disease treatment, fast recovery, and longevity for all people. Considering the problems faced with the COVID-19 pandemic, such as the lack of professionals and the

overloaded health system, it is necessary to think of ways to automate tasks to speed up the work of health workers, allowing them to focus on urgent problems. With the advances in technology and communication systems, automation is already present in the life of everyone, becoming indispensable in all areas.

This work aims, as its main objectives, to seek methods

to assist in the production of blood count exams for detecting blood cells, providing a tool to help health workers in this task. Currently, blood counts are performed by specialized machines, which have high costs for purchase and maintenance. We hypothesize that this process can be automated using Deep Learning algorithms by applying computer vision techniques on microscopic images of blood samples as an alternative to current specialized machines.

Deep Learning algorithms have been used in many areas, such as medicine (Krittawong et al., 2019), economy (Akanbi et al., 2020), education (Offir et al., 2008), e-commerce (Ha et al., 2016), even in video games (Greengard, 2017). Therefore, Deep Learning provides an alternative way to traditional methods to realize tasks and automate processes. Furthermore, other works are found in the literature, which present techniques to help health workers in their decision-making process (Ravi et al., 2017; Zhao et al., 2019).

Deep Learning techniques depend upon large and well-prepared datasets to achieve good results. These data must be collected and adapted in a pre-processing phase so that the learning process can be the best possible. A Deep Learning model goes through the training process and then techniques are applied for testing and checking the quality of the results. Reaching satisfactory results, the model can be used by a person in an information system, where the results are post-processed to show human-readable information through graphical user interfaces (Zocca et al., 2017; Giancarlo and Md. Rezaul, 2018).

This work uses Convolutional Neural Networks (CNNs) to automate the detection and counting cells of blood sample images. Usually, the manual process verifies and analyzes samples with glass slides and a microscope. Then the cells count happens, to elaborate blood tests with this information. As mentioned, in more structured labs, specialized machines are applied to automate this task, which brings its associated costs. More specifically, this work uses a blood sample dataset to detect and count different types of cells, to assist health workers in elaborating the results of blood tests.

The developing process of this project considered the following steps:

- We performed a systematic mapping on the topic to find relevant works in the literature about Deep Learning techniques in the health area.
- We searched and found datasets containing blood sample images to be applied in the context of this work.
- We pre-processed the chosen dataset to prepare it for the computational model training.
- We chose a pre-trained network by performing tests and measuring the empirical results of cell counting.
- We trained a Convolutional Neural Network model to detect and count blood cells present in blood sample images.
- We developed a functional prototype that provides a human-usable interface for the presented Deep Learning model.

This work shows an alternative way to analyze blood samples for the elaboration of blood count tests. Therefore,

the main focus is to assist health workers in repetitive tasks, bringing agility to their decision-making processes without losing accuracy in producing laboratory exams. This is even more important in times of health crisis, such as the one we are facing with COVID-19, where the health system is overloaded. Besides, the results of this work can be further explored by other researchers in future studies.

This work has been organized as follows: [Section 2](#) explains literature mapping, which begins the process. [Section 3](#) explains all theoretical research used in this work. [Section 4](#) explores the methods used throughout the process. In [Section 5](#), the results of this work are presented. In [Section 6](#), works related to this are mentioned. Finally, in [Section 7](#), the conclusion of this work is made.

2 Systematic Literature Mapping

The process of research and selection of related works was based on a systematic mapping of projects with proposals to assist in the identification and interpretation of blood count exams. This mapping resulted in the identification and selection of the main research works in the same area of this paper. Another objective of this systematic mapping was to verify methods to apply Deep Learning on images of blood samples to obtain information to automate the generation of the complete blood count exam.

The systematic literature mapping was developed by searching for articles with a search string¹ in the main digital libraries and research repositories. These articles were analyzed and selected considering the research area and topic to be included as a related work. To manage the systematic mapping, we used Parsifal², a tool that implements and manages the protocol of systematic mapping and reviews.

We defined two research questions for this project: (1) “How Deep Learning Algorithms can be used to interpret exams?”; and (2) “How to treat images to be able to recognize by Deep Learning Models?”. From these questions, words and terms were extracted to form a useful search string. The words and their synonyms can be seen in [Table 1](#).

Table 1: Keywords and Synonyms

Keyword	Synonym
Blood Analysis	Blood Sample
Classification	Interpretation, Recognition
Deep Learning	Artificial Intelligence, Computer Vision, Machine Learning

[Table 2](#) lists the digital libraries where the articles were collected, the quantity of each one, and the search string used in the selection. The same search string was used for all libraries, and the articles found are from the last five years (2016–2021).

¹The search string is a set of keywords organized to facilitate a search.

²<https://parsif.al/>

Table 2: Databases and Number of Articles Selected

Database	Articles
ACM Digital Library	37
IEEE Digital Library	13
Scopus	114
Search String	
("classification" OR "interpretation" OR "recognition") AND ("deep learning" OR "artificial intelligence" OR "computer vision" OR "machine learning") AND ("blood analysis" OR "blood sample")	

2.1 Exclusion Criteria

The articles collected in our search were verified against some exclusion criteria, removing the paper that matches any of them, as shown in [Table 3](#).

Table 3: Exclusion Criteria

Exclusion Criterion	Nº
The work does not belong to the research area	101
The work shows results outside the area of computing	29
The work is not a primary work	6
The work is duplicated	16

The selection process began with 164 articles from three digital libraries. After applying exclusion criteria, only 12 articles were retained. This was due to 101 articles being eliminated using the criterion “The work does not pertain to the research area”. This means that these articles had some relation to the topic, but were developed for other areas outside of the scope of blood count exams. An additional 29 articles were eliminated using the criterion “The work presents results outside the field of computing”. This means that these articles were related to blood count exams, but had no connection to the field of computation. Additionally, six articles were eliminated using the criterion “The work is not a primary source”, meaning that these articles were literature reviews or similar. Ultimately, 16 articles were eliminated due to duplication among the digital libraries.

2.2 Inclusion Criteria

The inclusion criteria were defined as follows:

- It should contain proposals for new technologies to analyze blood counts;
- It should detail the process, method, or technique to count blood cells;
- It should develop systems to elaborate blood counts with Deep Learning;

In [Table 4](#), it is possible to note that all 12 selected articles match the inclusion criteria since they fit at least one criterion.

All the selected articles are related to resources to assist

Table 4: Selected Articles

ID	Title
A1	Analyzing microscopic images of peripheral blood smear using deep learning (Mundhra et al., 2017)
A2	Automatic detection and classification of leukocytes using convolutional neural networks (Zhao et al., 2017)
A3	Automatic white blood cell classification using pre-trained deep learning models: ResNet and Inception (Habibzadeh et al., 2018)
A4	Classification of Human White Blood Cells Using Machine Learning for Stain-Free Imaging Flow Cytometry (Lippeveld et al., 2020)
A5	Blood cell classification using the hough transform and convolutional neural networks (Molina-Cabello et al., 2018)
A6	White Blood Cells Image Classification Using Deep Learning with Canonical Correlation Analysis (Patil et al., 2021)
A7	Image processing and machine learning in the morphological analysis of blood cells (Rodellar et al., 2018)
A8	Improving blood cells classification in peripheral blood smears using enhanced incremental training (Al-qudah and Suen, 2021)
A9	Corruption-Robust Enhancement of Deep Neural Networks for Classification of Peripheral Blood Smear Images (Zhang et al., 2020)
A10	Convolutional neural network and decision support in medical imaging: Case study of the recognition of blood cell subtypes (Diouf et al., 2019)
A11	Combining Convolutional Neural Network With Recursive Neural Network for Blood Cell Image Classification (Liang et al., 2018)
A12	Blood diseases detection using classical machine learning algorithms (Alsheref and Gomaa, 2019)

the interpretation of blood counts using Deep Learning and Machine Learning concepts.

2.3 Analysis of Selected Articles

In the end, having the articles selected and classified, the data extraction of these works was performed as a final step for this mapping. It is possible to notice that the most used algorithms and approaches are indeed Deep Learning techniques for this kind of task. For example, the use of Convolutional Neural Networks (CNN) (A1, A2, A3, A4, A5, A6, A8, A9, A10, A11) and Recurrent Neural Networks (RNN) (A6, A11), where neural network approaches for the classification of blood cells are between the most used.

Other works use traditional Machine Learning algorithms for classification. For example, Random Forests or Decision Trees appeared in some of the selected papers (A2, A4, A7). Some works resorted to Support Vector Machine (SVM) (A7), K-Means, and K-Nearest Neighbors (KNN) (A12), which make the classification considering the nearest neighbors approach.

3 Background Reading

The complete blood count (CBC) exam is simple, but extremely important for human health. With these exams, one can obtain several information about the patient's body, including detecting diseases and problems early. For example, it can diagnose anemia, dietary deficiencies,

blood parasites, and autoimmune diseases. It can also identify infections, diseases, drug effects, and other disorders in the human body (Lokwani, 2013; Longo, 2013).

The exam can be requested by a doctor or by the patient himself and performed in a clinical analysis laboratory, which is responsible for collecting the blood, sending it to specific analysis, and delivering the results for the patient. The machinery used to perform the blood count is expensive for both acquisition and maintenance. Additionally, it can be time-consuming since sometimes the blood needs to be sent from one place to another to be processed.

3.1 Blood

The blood is an element of the human body, which circulates in a liquid state throughout the circulatory system, being important for the correct functioning of cells through the entry and exit of substances that can modify its composition (Vivas, 2017). The blood can be divided into two parts: the plasma (or serum) and the cellular part.

The plasma is responsible for transporting substances through the system, which is formed by the ingestion of water and food. It can also be called serum, and it is possible to differentiate them by the presence or absence of anticoagulants used depending on the type of analysis and research intent (Vivas, 2017; Paulo Cesar Naoum, 2007).

The cellular part contains all the cells that belong to the blood, and they can be classified into red cells, white cells, and platelets. The red blood cells are small and round and carry hemoglobin, which is a very important protein for the transport of oxygen and carbon dioxide through the blood system, allowing the necessary gas exchanges (Lokwani, 2013; Longo, 2013). The white blood cells are responsible for organism defense against the main threats to the human body present in the blood system. The platelet cells are the smallest blood components and have a great responsibility in hemostasis, participating in the maintenance of blood vessels (Lokwani, 2013).

3.2 Complete Blood Count

A complete blood count (CBC) is a common and widely used exam in which a blood analysis is performed, including counting different types of blood cells. Analyzing this data and comparing it to normal ranges makes it possible to reach various conclusions about a patient's health and even identify certain diseases or problems (Vivas, 2017; Lokwani, 2013).

A CBC is generally performed in two main steps. The first step is related to the erythrocyte analysis, which refers to the analysis of red blood cells and can reveal certain pathological changes in the erythropoietic system. This system is responsible for the production of red blood cells, such as an increase in the production of red blood cells and anemia. The second step is related to the leukocyte analysis, which includes the overall and specific count of leukocytes, also known as white blood cells. Finally, the overall count of platelets is performed (Vivas,

2017; Lokwani, 2013).

3.3 Machine Learning and Deep Learning

The goal of Artificial Intelligence (AI) concepts is to find ways to teach machines to learn incrementally, similar to how humans do. Currently, specific algorithms are used to solve problems, but this approach is not always sufficient. More and more cases are arising where applying a fixed method for solving a problem is not enough, and as an alternative to this, one can implement computational models of Machine Learning and Deep Learning (Faceli et al., 2021; Ethem, 2016).

To prepare a supervised AI model, three steps are necessary: data pre-processing, the training phase, and finally, the testing phase. In the pre-processing phase, data is analyzed and adapted for better understanding by the model (Raschka, 2015), and is also separated into two sets, the training set and the test set. In the training phase, the model will receive a large volume of data and the expected results for each one and training configurations. Finally, in the testing phase, the model will be tested against new data never seen by the model, and its performance will be evaluated using some evaluation or metric method (Raschka, 2015; Nick, 2018).

Neural networks are machine learning structures that seek an approach similar to the human brain, as they use a structure composed of perceptrons, which is a computerized version of something similar to a human neuron. A perceptron can receive inputs (input data) and produce an output. The performance of perceptrons can be improved by combining several of them, forming a network, and combining the processing power of each to achieve a more assertive result using less time. For this structure, the name artificial neural network is used, or as it is known, Artificial Neural Network (ANN) (Sugomori et al., 2017; Giancarlo and Md. Rezaul, 2018).

It is important to note that in addition to the information passed from one perceptron to another, there is another important factor for their operation, which is the weights. The weights are values defined for each piece of information received by the perceptron, and we can think of them as a priority criterion between one information and another, which will be adjusted to achieve the desired result (Giancarlo and Md. Rezaul, 2018).

Initially, the algorithm starts the artificial neural network with random weights and enters the training mode to perform the learning. During training, the algorithm can predict results compared to the correct values, to know if it is succeeding. The backpropagation algorithm then calculates the difference between the obtained result and the real result, and this error information is passed back to all previous layers to adjust the weights and minimize the error. This process is performed continuously during training and only ends when the adjustments lead to an increase in the error again, indicating that the weights have been adjusted to the limit (Giancarlo and Md. Rezaul, 2018).

Deep Learning is a branch of machine learning that focuses on developing deep neural networks, which are complex neural network architectures. These networks have a larger number of neurons, hidden layers, and

more complex configurations and specific connections between neurons (Giancarlo and Md. Rezaul, 2018). Due to the capabilities of deep neural networks, several specialized variants have emerged with the goal of more closely mimicking human nature. For example, variants that specialize in natural language processing, such as Recurrent Neural Networks, or those that specialize in image recognition and interpretation, such as Convolutional Neural Networks (CNNs).

3.4 Convolutional Neural Networks (CNNs)

A Convolutional Neural Network (CNN) is a neural network architecture specifically developed for image recognition, with the ability to interpret images by dividing them into important parts. This network works initially with three basic information, interpreting images as 3-dimensional matrices, being height, width, and color (Giancarlo and Md. Rezaul, 2018).

Traditional neural networks work well for small images, but with a large volume of data, considering each pixel of the images, the model would have much difficulty in finding patterns, so the need for CNNs arose. To solve this problem, CNNs were developed to use partially connected layers and with great weight reutilization. In this way, there are fewer parameters to be interpreted and passed on, consequently, they are faster to train, having less risk of overfitting and requiring a smaller volume of training data (Giancarlo and Md. Rezaul, 2018).

This efficiency is also because a CNN, when learning to interpret a specific feature or element in an image, can identify that element anywhere in it, unlike traditional networks that only learn to recognize a feature in a fixed location. This shows the ability of CNNs to be more general compared to traditional networks (Giancarlo and Md. Rezaul, 2018).

This feature can be found in the convolutional layer, which is present at the beginning of the process and can be observed in Fig. 1.

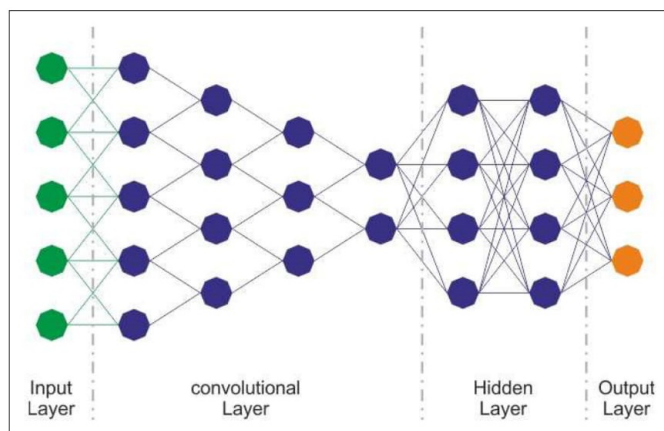


Figure 1: Convolutional Neural Network (Giancarlo and Md. Rezaul, 2018)

4 Methodology

4.1 Dataset

In the field of Artificial Intelligence (AI), the choice of the dataset is an extremely important task. For this work, we used the BCCD Dataset¹. This choice was based on the larger number of works referencing this source. Also, we observed that, compared to other available datasets in the literature, this was the most comprehensive and in-depth one for this research area (Shenggan, 2019).

Fig. 2 shows some examples of images present in the used dataset of images, containing the three types of cells.

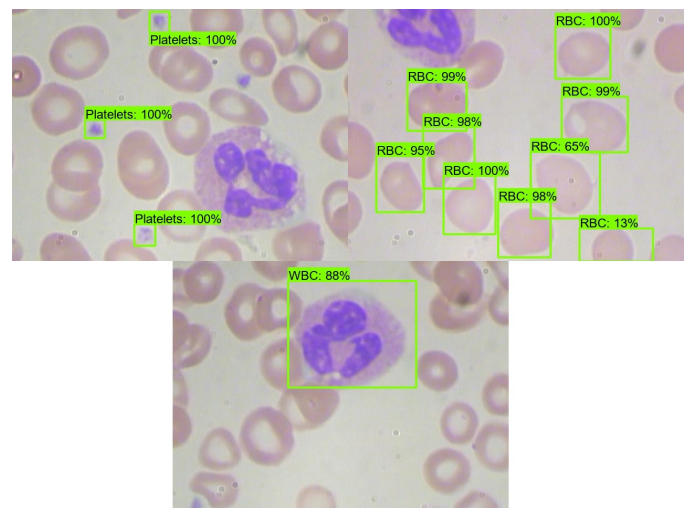


Figure 2: Detection of the three types of cell.

The dataset presents three categories of detection: White Blood Cell (WBC), Red Blood Cell (RBC), and Platelets. The files are separated into different directories, wherein in one of the folders, we have the whole set of images, and in another folder, we have XML files containing the coordinates of each cell in the images.

With the dataset in hand, the study of its content was performed, to point out its features and also its limitations. Initially, it was possible to notice that one of the limitations of the dataset was that not all the cells had coordinates in the images mapped. A large part presents the correct mapping, but some cells do not present any coordinates, which is a flaw of the dataset that can affect the training of the model.

Another limitation of this dataset is the lack of classification of white blood cells. The dataset is only concerned about locating the cells in the image and categorizing them as white, red, and platelets. However, to develop a complete blood count, this is not enough. To make a complete blood count, it is necessary not only to count white blood cells but also to classify them (Neutrophils, Basophils, Eosinophils, Lymphocytes, and Monocytes, among others) so that a more concrete

¹https://github.com/shenggan/bccd_dataset

diagnosis about the patient can be made. Introducing detection of classes for white blood cells will be listed as possible future work.

With the acquisition of the dataset, the process of adapting the image set for detection by the model began. The dataset has 364 images with around 30 cells in each of them. The images were randomly split into two sets, where the training set contained 70% and the test set contained 30% of the images.

4.2 Object Detection

In order to develop the computational model, we used the Tensorflow¹ library, which has a large collection of functions and utilities for working with machine learning and also deep learning. In this work, we used the Object Detection module to find elements in image portions that were previously trained to be recognized.

In order to recognize the coordinates of the images, first, it was necessary to import and treat the XML files in variables that could be read by the model. In addition, it was necessary to create a function that could convert the XML coordinates into numbers in the scale of the model, thus allowing to import both the coordinates and the images successfully.

In this way, it was possible to perform the training and testing of the model with these resources. Configuring the model as follows and presenting the respective values in Table 5.

- **Batch Size:** Refers to the size of the batch used in training. Generally, the larger the batch, the better the learning, but it also requires more processing from the machine.
- **Learning Rate:** Refers to the model's learning rate. The higher it is, the faster the learning steps will be taken. If it is too large, the model begins to recognize cells where there are none. The model finds no cells in the images if it is too small.
- **Number of Batches:** Refers to the number of algorithm passes, it can also be described as epochs. Defines the range of executions the algorithm will have until it stops training.
- **Percentage of Accuracy:** Refers to the base number to be considered a correct hit, for example, if the algorithm has more than 50% certainty for a cell, it is considered a hit.

Table 5: Parameters defined for training.

	WBC	RBC	Platelets
Batch Size	24	24	24
Learning Rate	0.02	0.05	0.05
Number of Batches	500	500	500
Percentage of Accuracy	0.5	0.1	0.5

These parameters were configured based on tests performed, where for each execution of the code, we

verified and adjusted them as necessary. We repeated this process until we found a set of appropriate values yielding the best results. The complete code, along with the set of parameters used, is available online.

In addition to configuring these parameters, there is also another important and necessary aspect of this work, which consists of selecting an appropriate pre-trained neural network for use. Through a pre-trained network, many common parameters can be reused, using a technique known as transfer learning, to speed up the process of training new models. In addition, it can also impact the results, as if it was properly trained with basic information, such as contours and common elements, the results when training with more complex elements tend to be better.

For this work, the pre-trained ResNet-50 network was selected (He et al., 2015). Although there are many other pre-trained networks included in the documentation list and accepted by the object detection module of Tensorflow, this choice was made by separating the networks based on the image resolution of each one and using the one that presented the highest precision based on the score declared in the documentation.

The use of ResNet-50 helped in the model training phase, as it was not necessary to train the entire structure from scratch, but only train the last layers. As the initial layers of the model have already been trained with generalities, the entire workload focused on training only the last layers of the network with specific information. In this case, directing the learning towards images of blood samples.

The complete source code is available online². This allows the model to be reproduced by other researchers and developers interested in the field, facilitating result validation and promoting transparency in research.

5 Results

After training the model, we measured the prediction results using three metrics. The first was the standard accuracy, which allows for an overall view of the progress of the process. To calculate accuracy, we leverage the true positives (TP), false positives (FP), and false negatives (FN). We did not use true negatives (TN) since we are interested in object detection, and a true negative would correspond to anything other than the object of interest. From TP, FP, and FN, our standard accuracy can be calculated as: $Acc = \frac{TP}{TP+FP+FN}$. By measuring the standard accuracy, considering the number of real cells and the number of cells that the model should find, the values obtained can be found in Table 6.

Table 6: Results found by the model.

Type	Model	Real	TP	FP	FN	Acc
WBC	74	74	74	0	0	100%
RBC	1007	908	908	99	0	90.17%
Platelets	57	59	57	0	2	96.60%

¹<https://www.tensorflow.org/>

²<https://github.com/anthonyleier/blood-detection>

The complementary and easy-to-use metrics Mean Square Error (MSE) and Root Mean Square Error (rMSE) were also calculated. These metrics refer to the performance of the computer model. While MSE works by calculating the mean squared error, rMSE is the square root of the value found by MSE. These metrics are interesting to use because they allow for a considerable visualization even of small errors. This scale does not present a maximum or ideal value, but the result should approach zero, the closer the better. In this way, it was possible to reach the relationship presented in Table 7.

	MSE	rMSE
WBC	0.383561	0.619323
RBC	14.3422465	3.787144
Platelets	0.904109	0.950846

Table 7: MSE e rMSE.

MSE was calculated based on the formula Eq. (1). First, the difference between the value found by the model y_i and the real value $\hat{y}_i$ for the n images was calculated, then the square of the obtained result was calculated. Finally, the average of these values for all images is made, generating the mean squared error.

$$MSE = \frac{1}{n} \sum_{i=1}^n (\hat{y}_i - y_i)^2 \quad (1)$$

The ideal value of this number is close to 0, as the higher the number, the higher the model's error. Since the result is always squared, predictions far from reality are easily perceived, making this metric interesting for problems where large errors are not tolerated.

The rMSE was calculated based on the formula Eq. (2). As MSE has already been calculated, it was possible to calculate the square root of the resulting value to find the final rMSE.

$$rMSE = \sqrt{\frac{1}{n} \sum_{i=1}^n (\hat{y}_i - y_i)^2} \quad (2)$$

This metric complements the normal MSE, allowing measuring the final result without changing the error scale, making some comparisons easier. While MSE is raised to the square, the rMSE does not have this problem, as the square root is extracted in the final process.

Although these metrics are generally used in regression tasks, in this case, they were used considering the number of cells found in relation to the actual number of cells in the image. This occurs because the hemogram is concerned with counting the cells, thus emphasizing the interpretation of the results (errors and successes) of the number of cells present in each image.

Through the relationship seen in Table 7, it is possible to notice that the best performance is in detecting white cells, which aligns with the definitions found by the

accuracy seen earlier. Following this, platelets also have good results, similar to the relationship of the model's accuracy. Finally, red cells show poorer results compared to the others. This may have happened because they are abundant in all images, having a much greater proportion compared to the others.

5.1 Discussion

The identification of the different types of cells was carried out gradually. First, the identification of white cells occurred due to their easy visualization, due to their sizes and contrast with relation to the others, being a great candidate to start the tests, and later develop the first version of the prototype. In addition, the dataset focused on one white cell per image. It was possible to notice that the model obtained a good accuracy rate, considering both performance metrics and visual analysis of the images. In this way, it is possible to perform the count of white cells with a good index of assertiveness.

After the detection of white cells, the next step was the identification and counting of red cells. These are differentiated in detection in relation to the others due to their quantity. Red cells appear in a greater proportion, presenting up to 20 cells per image. This was a challenge for the model due to the high quantity of cells. It is possible to conclude that although it does not have a performance as positive as the other classes, the results were also good, because they allow a satisfactory count of red cells, with a margin of error that can be considered small.

Finally, the detection of platelets was performed similarly to white cells. Although they are more present in the dataset than white cells, they are not in such a high number as red cells, presenting small sets per image. Another characteristic factor is their size, smaller and easy to identify just by looking at the image. Although they are easily identified, the overlap of cells can also occur in this case, hindering the performance of identification by the model.

In conclusion, the model adequately identified platelets, allowing a satisfactory count. Although not as positive as in the detection of white cells, it still surpasses red cells in terms of performance and criteria of assertiveness.

5.2 Elements of CBC

Based on the identification and counting of cells, as seen previously, it is possible to produce elements of the hemogram. A hemogram is essentially a statistical count of cells to compare these results with pre-calculated ideal values for each type of patient.

The initial values of the hemogram can be calculated by performing, after the identification of cells, the counting of each type. The units of measurement are important in this process, as they differ for each type of cell. The base unit for calculation is the cubic millimeter (mm^3), that is, a unit of volume. For the calculation of leukocytes, white cells, and also platelets, the counting is performed in proportion to one cubic millimeter. However, in the case of erythrocytes, red cells, they are in a greater quantity compared to other cells, so the calculation is done in

millions of cells per cubic millimeter.

The erythrocyte count can be made considering the number of erythrocytes in a ratio of millions/mm³. The leukocyte count can be made using the number of leukocytes found per/mm³. Finally, the platelet count can be made based on the number of platelets identified per/mm³.

This information is necessary to detect various diseases and imbalances in the patient's body. As, for example, the leukocyte count, the main examination to evaluate a person's immunity, through the number of leukocytes present in the body. The number of platelets also says a lot about the body, evaluating the patient's blood coagulation and predispositions to bleeding. The low number of erythrocytes could indicate anemia or associated disease, among many other cases. We can conclude that through the use of the proposed model, it is possible to elaborate important elements of the hemogram that, when applied to an image sample with volume values, can be useful to assist professionals in the analysis of samples.

5.3 Limitations

The limitations for producing a complete hemogram are related to the limitations of the dataset. First, to perform a complete hemogram, it would be necessary to have the classification of white cells in addition to the counting. Their classification into Monocytes, Leukocytes, Neutrophils, Eosinophils, Basophils, and Lymphocytes, among others, is necessary for the completeness of the examination. However, the dataset does not present these classifications, which focuses only on the differences between the three main types.

Other values related to volume calculations, such as the MCV (Mean Corpuscular Volume) and also the MCH (Mean Corpuscular Hemoglobin), are not possible to calculate due to lack of information. By using different datasets in future works, the aforementioned information can be calculated and provided during the data collection step.

6 Related Works

It is possible to reference some relevant articles in the literature related to the proposal of this work. This is the case of those dealing with the detection and classification of white cells using Deep Learning (Zhao et al., 2017; Habibzadeh et al., 2018; Patil et al., 2021). They differ from this work by seeking only the classification of white cells in a dataset that contains only images of this type of cells. While in this article, we seek to detect the three types of cells (red blood cells, white blood cells, and platelets) in a single image containing all of them. Other articles also perform this process of detecting white cells, but using traditional Machine Learning (Lippeveld et al., 2020).

In addition, articles that also seek the interpretation of blood cells, but use Machine Learning for this are also found (Rodellar et al., 2018; Al-qudah and Suen, 2021) and do not use computer vision like the one presented in this text. Finally, it is also possible to find some articles that use Deep Learning to analyze and interpret cells through images (Mundhra et al., 2017; Molina-Cabello et al., 2018)

but do not perform the detection and localization of multiple blood cells present in a single image.

In this way, it can be seen that the proposal of this work differs from others found in the literature. This article develops a Deep Learning structure with detecting, counting, and mapping various types of blood cells in a single image.

7 Conclusion

This project began with the interest of using Deep Learning techniques to assist health professionals in their daily activities by automating tasks, allowing more important tasks to receive more attention. It was realized that it would be possible to assist professionals in analyzing blood samples by identifying and counting cells, generating subsidies for generating elements of a complete blood count (CBC), an essential examination in the identification of many diseases.

To do this, it was necessary to understand the entire process of producing a CBC and also to find ways to associate the concepts of Deep Learning in this process. Through training an intelligent computer model capable of recognizing the different blood cells in an image, the count of all types of cells was developed with satisfactory precision.

The developed model shows potential to assist in the work of examination analysis professionals and also in cost reduction, since there is machinery involved in the current process for producing CBCs. However, with the current results, it is not possible to produce a complete CBC, because, due to the limitations of the dataset used, it was not possible to carry out the individual classification of the white cells, only performing the general count of them.

As future work, it is possible to use the concepts addressed in this text in different datasets, allowing the study for different types of examinations. In addition, it is possible to deepen the current study to also include the classification of white cells, supporting even more elements of a CBC. Finally, it would be interesting to improve the evaluation metrics used in this article, beyond the evaluation of the cell count, including the accuracy of the portion of the image identified with respect to each cell. With these improvements, it is possible to continue the approach adopted to estimate the cell count in relation to the volume and, subsequently, reproduce all the information present in a CBC.

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