Analysis of Medical Slide Images Processing using Depth Learning in Histopathological Studies of Cerebellar Cortex Tissue

Xiang-yu Zhang[1], Xiao-wen Shi[2], Xing-bo Zhang[3*]
Artificial Intelligence, School of Information Science and Technology,
Shandong Agriculture And Engineering University, JiNan, 250100, China[1]
Government Economic Management, School of Government,
Beijing Normal University, Beijing, 100875, China[2]
Department of Internet of Things Engineering, School of Information Science and Technology,
Shandong Agriculture and Engineering University,
No. 866, Nongganyuan Road, Licheng District, Jinan District, JiNan, 250100, China[3]

Abstract*—Today, with the advancement of science and technology, artificial intelligence evolves and grows along with human beings. Clinical specialists rely only on their knowledge and experience, as well as the results of complex and time-consuming clinical trials, despite the inevitable human errors of diagnosis work. Performing malignant and dangerous diseases, the use of machine learning makes it clear that the ability and capacity of these techniques are beneficial to help correctly diagnose diseases, reduce human error, improve diagnosis, and start treatment as soon as possible. In diseases, image processing and artificial intelligence is widely used in medicine and applied in stereological, histopathology. One of the essential activities for diagnosing the disease using artificial intelligence and machine learning is the fragmentation of images and classification of medical images, which is used to diagnose the disease with the help of images of the patient obtained from medical devices. In this article, we have worked on classifying medical histopathological images of brain tissue. The images are not of good quality due to sampling with standard equipment, and an attempt is made to improve the quality of the images by operating. Also, all images are segmented using the U-NET algorithm. In order to improve performance in classification, segmented images are used to classify images into two classes, normal and abnormal, instead of the images themselves. The images in the data set used in this study have a small number of images. Due to the use of a convolutional neural network algorithm to extract the feature and classify the images, more images are needed. Therefore, the data amplification technique to overcome this problem is used. Finally, the convolutional neural network has been used to extract features from images and classify fragmented images. Experimental results shown that the proposed method presented better performance compared to other existing methods.

Keywords*—Image processing; fragmentation of images; machine learning; image classification; stereological; histopathology

I. INTRODUCTION

Today, with advances in various fields such as engineering and medicine, organizations produce and collect large amounts of data every day. Hence, the need for data analysis to improve an organization's processes, advance goals, speed things up, and reduce possible errors is felt. With the development of technology, there are significant advances in medicine that have increased data and information, so one of the topics in data analysis is to improve the quality-of-life process and community health, which is medical data. Machine learning can be used to improve performance and conclusions in medicine and reduce diagnostic errors. There are different types of medical data. Data can be text, image, video, and audio. In this article, the data used are medical images of the brain area taken from slides. In this way, brain cells are placed on a slide, one of the accessories of laboratory equipment, as an example for observation under a microscope. Then, microscopic observations are taken, and these images are used as data in this study.

One method of data analysis for medical images (brain area) is machine learning. Machine learning is the scientific study of algorithms and statistical models that computer systems use to perform a particular task without explicit instructions, patterns, and inference. This is known as a subset of artificial intelligence. Machine learning algorithms create a mathematical model based on sample data, known as "training data," to make predictions or decisions without explicitly planning for the task [1-4]. Using the built model, the machine learns that if new data enters the machine, the machine can use the built model to predict the new data and specify the desired label for each data. The purpose of this paper is to identify image tags using a machine [5-7].

The purpose of this study is to develop a method to perform malignant and dangerous diseases using machine learning techniques which the ability and capacity of these techniques are beneficial to help correctly diagnose diseases, reduce human error, improve diagnosis, and start treatment as soon as possible. In diseases, image processing and artificial intelligence is widely used in medicine and applied in stereological, histopathology. One of the essential activities for diagnosing the disease using artificial intelligence and machine learning is the fragmentation of images and classification of medical images, which is used to diagnose the disease with the help of images of the patient obtained from medical devices.

Types of machine learning methods include supervised learning, semi-supervised learning, and unsupervised learning [8,9]. The data that will be used in this study are images of brain cells, all of which are labeled. So, learning that can be used for them has supervised learning. On the other hand, these data have two types of labels (normal and abnormal). As a result, the type of problem will be a binary classification problem. To learn, the machine must be able to extract features from photographs. An essential part of this study is the extraction of features from photographs and the fragmentation of photographs to examine microscopically the changes made by cerebellar cortex images in which the body changes [10,11]. The cellular neurons are comparable in different groups. The data used is raw and real, so that they will have some inconsistencies and problems. Most images are not of good quality and will confuse the machine. So, these problems must be fixed to improve performance and efficiency. On the other hand, it is necessary to prepare the data according to the conditions and the problem to the appropriate data to be injected into the desired algorithms. In general, it means that the data should be transformed in a way that the algorithm is acceptable and permissible for the implementation of algorithms, and the data should be cleared of any unnecessary errors and information to have the desired output. Data processing needs to be preprocessed. That will be the first step in this study. The most critical data preprocessing techniques include data cleansing, data integration, data reduction, and data transformation [12-15].

The next step is to segment the images. Fragmentation is a very related task in the analysis of medical images. Automatic separation of organs and structures of interest is often necessary to perform tasks such as visual augmentation, computer-aided detection, interventions, and the extraction of quantitative indicators from images [16-18]. Image segmentation, also called tagging, is the process of dividing an individual element of an image into a set of groups so that all the elements in a group have a common feature. In medicine, this common feature is usually that the elements belong to the same type of tissue or organ [19-23]. Different algorithms and methods can be used for segmentation. The purpose of segmentation is to simplify and change the representation of an image into something more understandable and easier to analyze. By segmenting the images, the borders and lines of the images will be determined, leading to better performance for the next step, which is to extract the features.

After preprocessing and segmentation, the feature extraction operation is performed on the data. Feature extraction is a process in which, by performing operations on data, it is obvious and determining features are determined. Feature extraction is done on the data used in this article to extract the features that are in the images. The machine is trained in these features, and based on the learning it has from these features, any other image except these images is provided to the machine so that the machine can correctly predict the label of the image without the label. There are different algorithms for feature extraction, which in this research will use a convolutional neural network algorithm. Deep learning algorithms, especially convolutional neural networks, have quickly become a method for analyzing medical images. Deep network learning algorithms consist of many layers that input data while learning higher-level features. For example, it converts images to output (for example, the type of disease).

The most successful models for image analysis to date are convolutional neural networks [24-26]. In deep learning or hierarchy, several different layers are used to learn features. The more (deeper) this hierarchy of layers is, the more nonlinear properties are obtained. For this reason, this article has tried to use more layers. Of course, this statement has its limitations. After a certain number of layers, the system's performance does not improve, and new and more features are not trained. On the other hand, it is impossible to work directly on the input image to obtain or produce features containing more information. For this reason, deep learning with layers and hierarchies has been used.

Most dangerous diseases, such as cancer and the presence of tumors in the body's organs, are well diagnosed by examining and analyzing images obtained from sampled tissue samples. Therefore, it is possible to prevent the disease's progression and treat it as soon as possible by diagnosing it as quickly and accurately as possible. Therefore, a better and more accurate analysis of histological images can be beneficial to doctors and patients and can even be said to reduce the risk of death. Generally, histology specimens obtained in the operating room are processed by formalin and then embedded in paraffin to diagnose the disease. The tissue is then cut with a high-precision device and mounted on glass slides. The slides are stained with hematoxylin and eosin (H&E) to see the nucleus and cytoplasm. Finally, pathologists complete the diagnosis by visually examining histological slides under a microscope. However, in breast cancer diagnosis, histologists agree in 75% of cases and disagree in other cases [27-29]. Therefore, due to the complex nature of visible structures, traditional manual detection of tissue microstructure and general organization of nuclei in histological images is very time-consuming and can be subjective. As a result, computer-aided automation systems are essential to reduce specialists' workload by improving diagnostic efficiency and reducing the mentality of disease classification [30-33].

In this article, images of cerebellar tissue are used, the images used are of low quality, and the quality of the images should be normalized and then analyzed. In addition to the low quality of the images, when coloring the images, unfortunately, some color deposits are created in the image, which is quite similar to the cells in the texture and distorts the process. The color of the cells, on the other hand, is very similar to the background color of the tissue, slowing down the analysis. The challenges for segmentation and image classification are that the number of images is about 91, which is a minimal number and not enough to use deep learning to analyze images, and solutions had to be devised. On the other hand, an algorithm for segmentation should be selected that can perform well on histopathological images and has acceptable and good accuracy with low images. Regarding the classification algorithm, an algorithm that works well for histopathological medical images should be selected. It is expected that the quality of the images can be increased and the accuracy of the work can be improved, and also that the images can be segmented with high accuracy. Most importantly, the results obtained by extracting features from the images using machine learning are better and more accurate than the physicians' manual method. The classification error can also be significantly reduced until new data or a histological image of the new patient can be presented. Correctly predict whether the new image has a normal or unnormal texture.

II. PROPOSED ALGORITHM

Fig. 1 shows a flowchart of the general process and the proposed algorithm. In the first step, the image quality is improved, including two parts: color change and removing color deposits. Then, the images are divided into two training sets and experiments in the second step. In the third step, the images are segmented by the U-net algorithm. In the fourth step, due to the lack of images, data amplification technique training is applied to the images. In the fifth step, all images are pre-processed. Finally, feature extraction is performed on fragmented and amplified images using the convolution neural network algorithm and using these features. The convolution neural network classifies the images. In the following, each of these sections is examined.

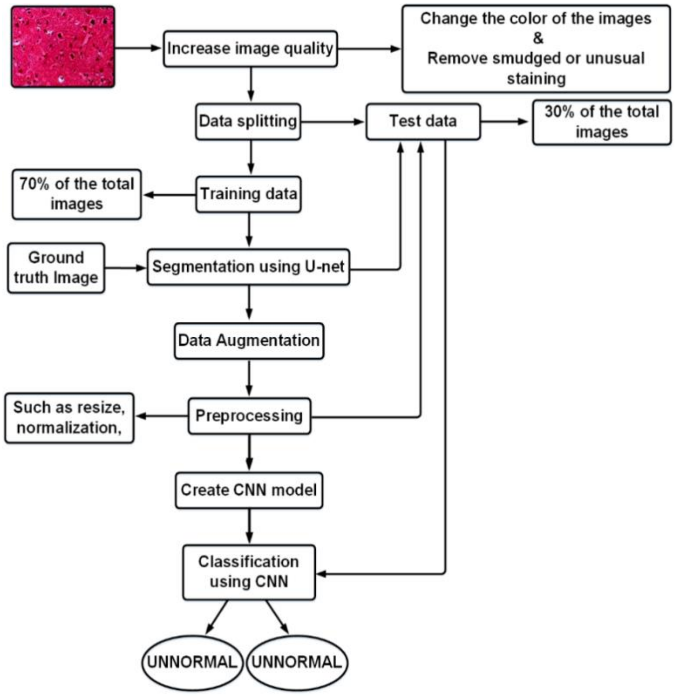

Fig. 1. The proposed algorithm

III. PROPOSED PROCESS

In this section, the solution of the article is described in detail. According to the explanations in the previous chapters, the primary purpose of this article is to present a process for improvement in the classification of histopathological images of brain tissue using deep learning. Also, the following is a general introduction to the data set to understand the process better.

A. Data Set

The data used in this article are brain tissue images. This dataset contains 91 histological images. All available images have labels, and there are two types of labels that are normal and abnormal. Each available image is only a member of one of these two tag classes. Class images do not overlap, meaning that an image can be a normal and non-normal class member and belongs to only one class. On the other hand, the number of images in these two classes is balanced, i.e., the number of images in the two classes is not much different from each other and is relatively evenly distributed in the two classes. For more familiarity with the available data, normal and unnormal image samples are shown in Fig. 2 and 3, respectively. As shown in the figures above, both images are very similar, and it will not be easy to distinguish between them. In histological images, in order to analyze the images, the cells in the histological images should be analyzed. These images have been used for the first time in this article, and no analysis has been done on these images before. Brain tissue is first sampled to image the data, then placed on a slide, a laboratory device, then stained by specialists to identify the cells better, and placed under a microscope and photographed. All the equipment used for sampling and photography is standard laboratory equipment, and no advanced and high-quality equipment is used because this sampling and imaging are done in a simple laboratory in the university. For this reason, the images are not of good quality.

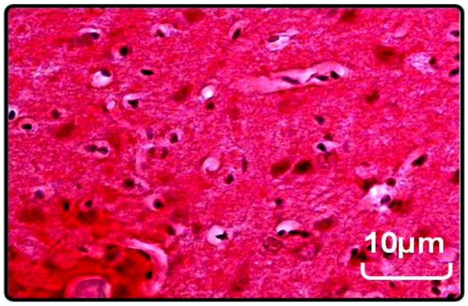

Fig. 2. Sample normal image

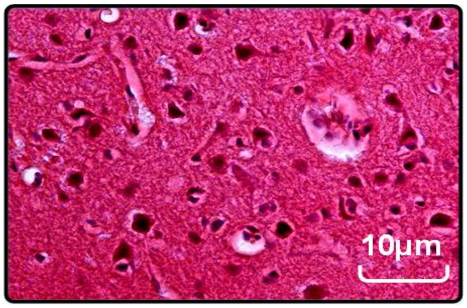

Fig. 3. Sample unnormal image

B. Improve Image Quality

As shown in the previous images in Fig. 1 and 2, the background colors and the cells in the images are very similar. This may confuse the process, so to avoid this problem to increase the images' transparency and better distinguish the cells from the background, the color of the images has been changed using the Icy program. Fig. 4 shows an example of an image before and after a color change. The sediments in the images are very similar to the actual cells. This causes many errors in the work process. For this purpose, the colored deposits in the images must be removed. To remove these sediments, Icy software and a paint program are used, and the sediments are removed. Fig. 5 shows an example of images (a) before and (b) after sediment removal.

Due to a large number of images, all the steps performed in this step are applied to all images in the data set.

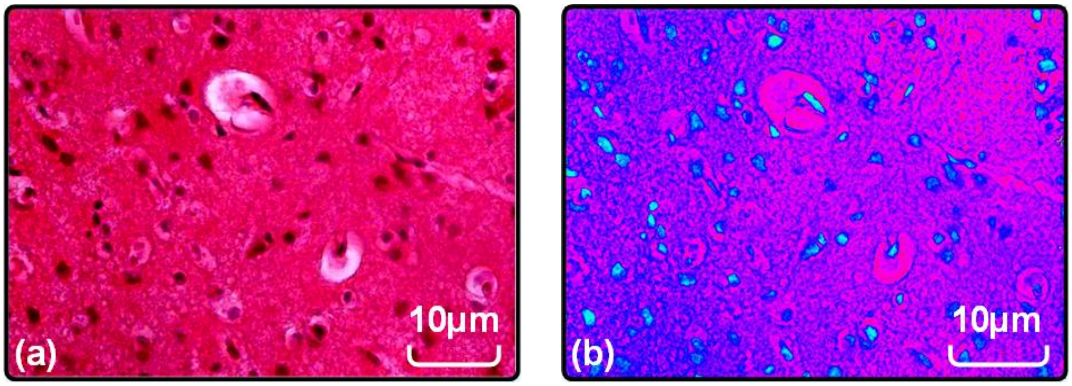

Fig. 4. Sample images, (a) before applying the color change, (b) after applying the color change

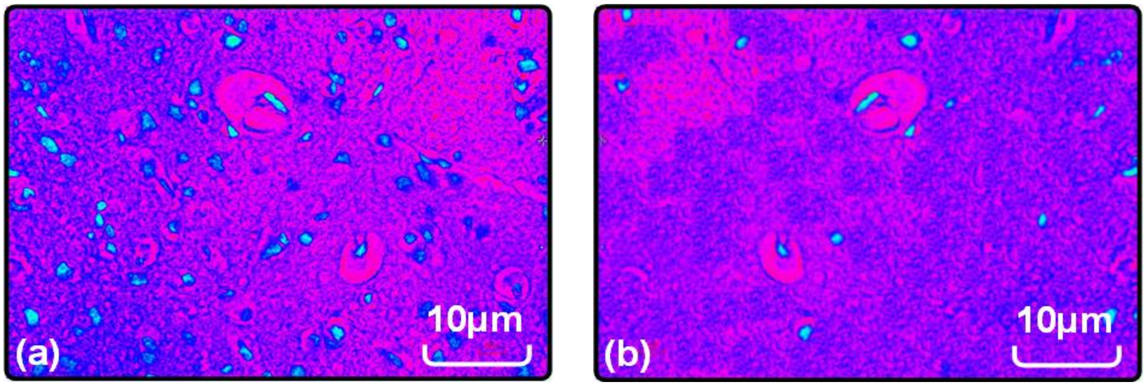

Fig. 5. Sample images, (a) before sediment removal, (b) after sediment removal

C. Data Separation

After changing the color and removing color deposits, the images should be divided into two parts: training and testing. In all processes, the ratio of the number of training to the test is about 7 to 3, i.e., 70% of the normal data and 70% of the unnormal data are related to the training section, and the remaining 30% are related to the test section. The following is the number of data assigned to each class. The total images are equal to 91 images, of which 50 images belong to the normal class, and 41 images belong to the unnormal class. Out of a total of 91 images, 64 images are allocated to the training set and 27 images to the test set. Out of 64 images related to the training set, 34 are for normal class, and 30 are for unnormal class. Also, out of 27 images assigned to the test set, 16 are for normal class, and 11 are for unnormal class. As it turns out, there is a balance between the number of images in both classes, meaning that the distribution of images in the classes is relatively equal.

$$\text{Overall Image} \to 91 \begin{cases} Normal \to 50 \\ Unnormal \to 41 \end{cases},$$

$$\text{Training Data} \to 64 \begin{cases} Normal \to 34 \\ Unnormal \to 30 \end{cases},$$

$$\text{Teste Data} \to 27 \begin{cases} Normal \to 16 \\ Unnormal \to 11 \end{cases}$$

D. U-Net Algorithm

This algorithm has a specific architecture, which is used in this article. The architecture is briefly described below. In 2015, Ronberberger et al. Proposed architecture for the segmentation of biomedical images [34]. This architecture is called U-net because of its U-shape. It is also called hourglass architecture. Convolution neural networks and deep learning techniques are not yet widely used because they have limitations due to the need for large amounts of data to teach complex models. However, the U-Net architecture does not require a large number of images due to the beneficial use of data amplification techniques. Fig. 6 shows the architecture of this algorithm. This architecture has two contracting paths on the left and a Symmetric expanding path on the right. The contracting path is to extract the feature, and the expansion path is symmetrical to obtain the feature map. In general, this architecture has 23 layers of convolution. The contraction path follows the typical architecture of a convolutional network. This path involves repeated use of two 3×3 convulsions, each modified using a linear function (ReLU) and a maximum aggregation operation of 2×2 max using step 2 for downsampling. At each step of the descent, the number of feature channels doubles. Each step in the symmetric expansion path involves a mapping of the feature map, followed by 2×2 up sampling that halves the number of channels and two 3×3 convulsions with the ReLU linear function for correction. Also, at each stage, the feature maps are concatenated in the opposite stage of the contraction path. Cutting at any stage is necessary due to the loss of boundary pixels in each convolution. In the last layer, a 1×1 convolution is used to map all 64 attribute vector components to the number of available classes. Data reinforcement is essential when the amount of data is small. Since there is often little data in medicine, the need for data reinforcement becomes sensitive in these cases. This is present in the U-Net architecture itself, and this has made U-Net work well for low-data datasets. All images are fragmented using this algorithm, and then the images generated by the output of the U-Net algorithm will be used.

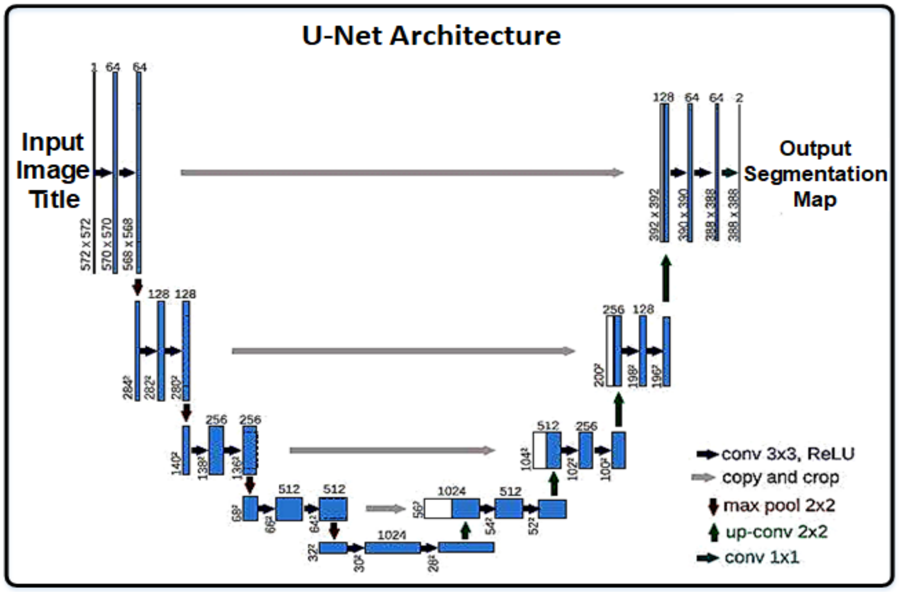

Fig. 6. U-Net architecture [34]

E. Generate Mask Images

In order to segment images, there must be a tag for the images. The label in the segmentation is different from the label in the classification. In segmentation for system training, the system must be told which goal in the main image is to select and segment which part of the images. In image segmentation with the U-Net algorithm, the required tags are images called masks, which are given to the system to compare the image and the mask corresponding to determine the purpose, segmentation, and selection. The real and mask sample images extracted by the excerpt are shown in Fig. 7.

As mentioned, these tags did not exist for this dataset. In this study, mask images are extracted using Icy software, a mask extraction program. This is done under the supervision of an expert so that the selection of essential areas would not be mistaken and the system could be properly trained.

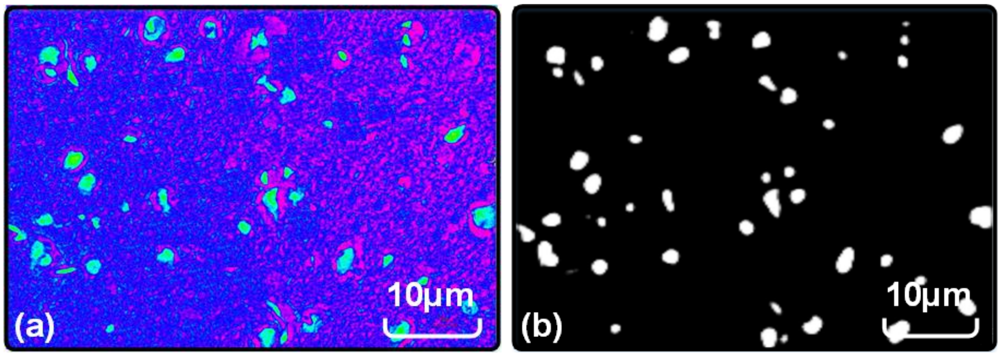

Fig. 7. Sample image (a) real, (b) mask

F. Data Augmentation

Improving the performance of deep neural networks is often directly related to the data available for training. In convulsive neural networks, if the amount of data is small, the system learning operation will not work well. More data is needed to improve the network. On the other hand, due to the lack of data in medical imaging, especially tissue imaging, due to complex sampling and imaging, and not much data collection is possible, the image enhancement technique will be beneficial. This technique allows the data to be amplified and the data set to be strengthened without requiring new images. This data will be based on the images in the current data set. By learning new properties from those images and the original images, the network gains the power to understand a broader range of each object and becomes so-called Generalized.

Therefore, it is clear that the selection of settings for the data amplification technique must be made carefully and follow the content of the data and the type of problem. Applicable trial and error enhance data enhancements for selected images. In this way, new images are generated by the data amplification technique using different settings. Then the convolutional neural network is trained, and user settings in the data amplification technique are selected according to the improvement or non-improvement of the network. Modern deep-learning algorithms, such as convolutional neural networks, can learn features independent of their location in the image. However, amplifying and adding data by changing rotation, light, and color can further aid in learning independent features in the image. Eventually, the grid learns to recognize the object correctly if it is turned from left to right in the image or has little light and clarity. The critical point here is that data amplification should only be applied to training images, not test data, as this would compromise network performance. Fig. 8 shows the main figure. Fig. 9 also shows (a) the vertical flip and (b) the horizontal flip.

By applying the above changes to the entire tutorial images, about 50 images are added to each of the normal and unnormal image groups. The above changes do not pose a problem histologically because histologists can analyze images from any angle and direction.

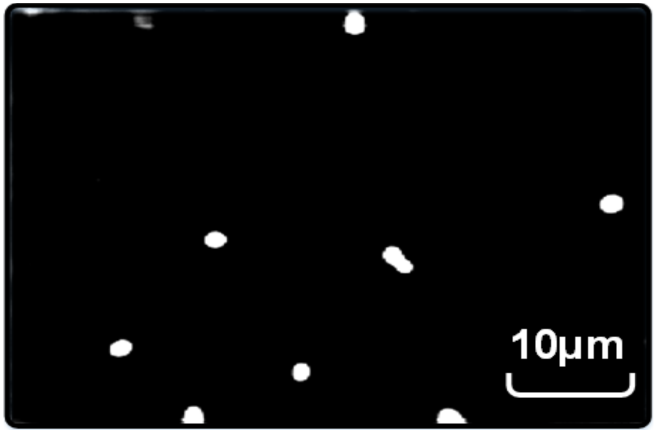

Fig. 8. The main figure

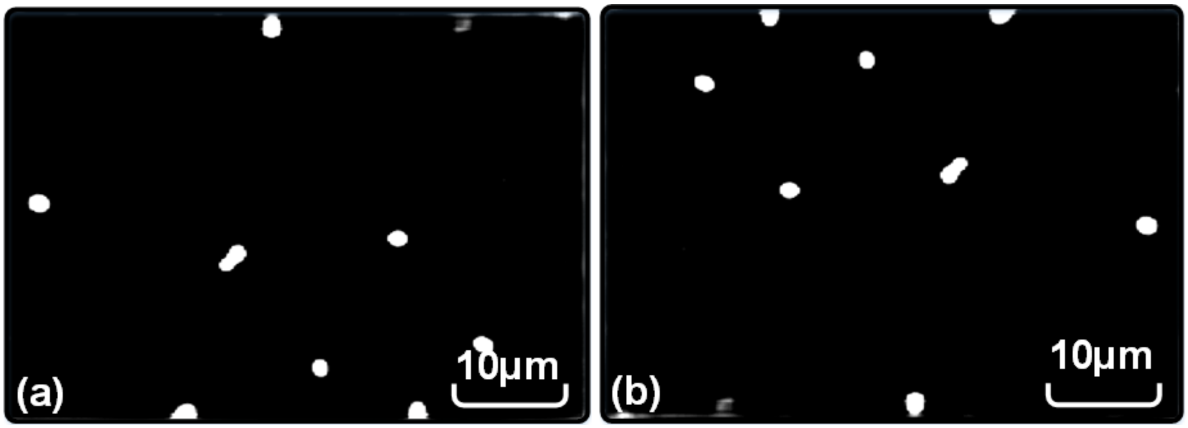

Fig. 9. Shows (a) the horizontal flip, (b) the vertical flip

IV. CONVOLUTION NEURAL NETWORK ARCHITECTURE

When a computer receives an image as input, it sees it as an array of numbers. The number of arrays depends on the size of the image (in pixels). For example, suppose a color image in JPG format with a size of 1280×960 pixels is given to the computer. In that case, its replacement array will have 3×1280×960 cells. The number 3 goes back to RGB and means that the image is in color. Each of these houses also has a number between 0 ~ 255. This number indicates the pixel intensity. The only available tools in the category of images using convolutional neural networks are such numbers. To understand and recognize complex images, such as the image of a cell, the computer first recognizes the simpler features of that image, such as edges and curves.

The design of network layers can be different for each data, depending on the purpose pursued. The architecture designed in this article gave the best results for the data at hand. This architecture has 6 layers of convolution, and 5 layers of aggregation applied between the layers of convolution. In the last layer, a fully connected layer is used. The fully connected layer is responsible for calculating the score of categories (classes) to classify images. The filters used for the convolution layer have dimensions of 5×5, which include weights. The ReLU activator function is also used for the activator function. ReLU applies an activation function to each neuron, such as max (0, x), which sets the threshold at 0 (i.e., values x for negative values and 0 for negative values). This does not change the mass size from the previous step, i.e., the size of the output in this layer equals the output dimensions of the previous layer. This function does not change the dimensions of the output. The input layer is 3×224×224 images. The value of 3×224×224 are the dimensions of the images, and 3 also refers to the fact that the images are 3 channels, i.e., color images. Images enter the convolution neural network through the feed-forward stage. In the feed-forward stage, each filter is slid along the inlet's width and height, creating an Activation Map for that filter. As the filter slides across the inlet width, multiplying the point between the filter inputs by A stream is also performed. The result is passed through an activation function, and output is generated. In other words, at this stage, the input is multiplied by the weights, added to the bias, and entered into an activation function. This process continues until the end.

The initial weight of the grid is randomly weighted. Then Adam's reverse optimization algorithm is used to update the weights. The reverse algorithm is used to adjust the parameters based on their impact on the final result. This algorithm calculates the error from the last layer. In order, layer by layer, the parameters are adjusted based on that error. That is, the weights and deviations are changed in such a way as to produce a result closer to the actual output with less error in the next iteration. CROSS ENTROPY is used as a loss function to determine the amount of error in the reverse algorithm, which aims to minimize the error. Optimizers and other activators can be used, each of which can be tried and tested. If each of these items is accurate, that item will be selected for use, but in most cases, they are not much different. In this study, it is concluded by trial and error to use the ReLU activator function and Adam optimizer. Fig. 10 shows the general structure of the architecture used.

As shown in the architecture shown in Figure 10, the first 224×224 images enter the network. In the first layer, a convolution layer with a 5×5 filter is applied to the image. The ReLU activator function is used, and the output is given to the aggregation layer with a 2×2 filter and step 2, in which the dimensions of the images are halved. Then the output from the first aggregation layer is given to the second convolution layer again, and the same cycle continues. In designing convolutional neural network architecture, an important question is how many layers and what kind of sex is needed. Because the performance of architectures and layers is different for different data, like the other stages, trial and error have been used in this stage. Increasing the number of layers to a range improves neural network performance. After a range, increasing the number of layers reduces performance. This point can only be found by trial and error. The number of layers is also increased by trial and error. After this number of layers, as shown in Fig. 10, it is observed that the network performance does not improve. Even after the following few layers, it reduces the network performance. That is why the network is trained with 6 layers of convolution and ReLU, 5 layers of aggregation, and one fully connected layer.

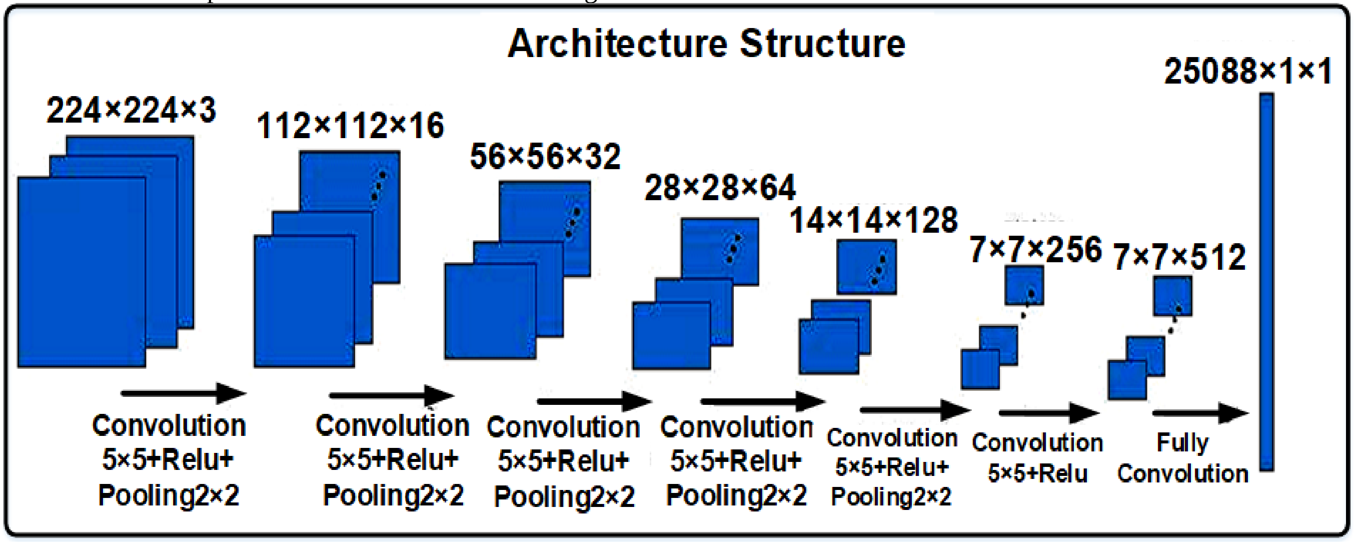

Fig. 10. General structure of architecture

VI. RESULTS AND EVALUATION

In this section, evaluations and comparisons are provided to prove the efficiency of the proposed algorithm. For this purpose and to provide comprehensive results, the proposed method is reviewed in stages. In the following, the obtained results are discussed using evaluation criteria to measure the performance of the proposed process. The knowledge generated in the model learning stage should be analyzed in the evaluation stage to determine its value and then determine the efficiency of the model learning algorithm. These criteria can be calculated for the educational data set in the learning phase and the set of experimental records in the assessment phase. Evaluation of experimental data is often used because it shows the performance of the process. So, one of the most critical steps after designing and building a model or an algorithm is to evaluate its performance. Different evaluation criteria are used based on the existing algorithm and purpose. In this dissertation, two essential algorithms have been used, each with a separate evaluation. First, a brief description of the evaluation criteria used is given.

The results of the convolution neural network are described. In most previous works, the images entered the convolutional neural network directly after initial preprocessing. Alternatively, extracted through the neural network and then classified by another algorithm. The images are classified in several stages using a convolutional neural network, and the classification results are evaluated. All the results of these several stages are compared. The last step is related to the proposed process. The goal is to raise the standards of accuracy and reminder; the more these three criteria, the better the network performance. The criterion of accuracy obtained in all stages is in percentage.

On the other hand, the criteria of accuracy and numerical recall are between 0 and 1, which is closer to 1, i.e., the better the performance of that class. The data are randomly isolated six times for evaluation, and then all steps are performed. Finally, the results obtained from the repetition of six steps are averaged.

A. *Evaluation of Convolution Neural Network with Raw Images*

In a reference study [24], the images entered the convolutional neural network for further analysis after applying techniques to reduce the number of images and select images. Because the data set, they used to have a lot of similar images. This study does not need to reduce the number of images because the data set used has few images. According to the reference, the images then entered the convolutional neural network [35]. First, the raw images entered the convolution neural network without any changes. Raw images are primary images without applying the segmentation algorithm and without applying the sediment removal and color change steps. The evaluation is performed 6 times on random data. Table I shows the accuracy, precision, and recall obtained in all these six steps. Also, in the end, the average of six steps will be considered.

In this table, the rows represent the evaluation steps, and the columns represent the evaluation criteria, which is the same as the overall accuracy of the convolution neural network. Precision and Recall are also provided for each normal and abnormal class. Because both classes are equally important. Convulsive neural network in these conditions has an accuracy of about 76.14%. The normal class has a Precision of approximately 0.739 and a Recall of approximately 0.76. Also, the unnormal class has a Precision of approximately 0.76 and a Recall of approximately 0.73.

B. *Evaluation of Convolutional Neural Network with Fragmented Image*

As mentioned before, in previous works, most images are classified using a convolutional neural network after a series of preprocessing to classify the images, especially histopathological images. In the solution proposed in this article, all images are segmented before the images are classified. Then, fragmented images are classified using a convolutional neural network. This step discusses the results obtained from the classification of fragmented images. The results for this process are according to Table II, in which also in this step, 6 random data are evaluated and finally averaged.

In this process, the accuracy is equal to 87.61%. Also, the precision and Recall of the normal class are equal to 0.871 and 0.91, respectively, and the precision and Recall of the unnormal class are equal to 0.915 and 0.846, respectively. As it is known, all the evaluation criteria in this process have improved compared to the previous process.

C. *Figures and Tables Evaluation of Convolution Neural Network with Segmented Image and Use of Data Amplification*

In this series of evaluations, the quality of the images is first improved using the scale removal step and color change. The improved images are then segmented using the U-Net algorithm. Due to the lack of several images and in order to improve the performance of the convulsive neural network, the data amplification technique is used. The results obtained from the classification of this step of the images are according to Table III, also this step is repeated 6 times, and the average is taken.

The accuracy of this process is equal to 93.825%. Also, the precision and recall of the normal class are 0.912 and 0.978, respectively. On the other hand, the precision and recall of the unnormal class are equal to 0.979 and 0.9.

D. *Overall Evaluation Results*

The following Table IV shows all the results of the evaluated steps. There is also a comparison chart in Fig. 11 to measure the accuracy of all steps.

Fig. 12 also provides a comparison chart for all steps and precision and recall criteria for each normal and abnormal class.

According to the diagram in Fig. 12 and Table IV, it can be seen that the accuracy obtained from the classification stage of fragmented images and the use of the data amplification technique has the highest percentage, approximately 93.82%. Also, according to Fig. 12 and Table IV, it is clear that the precision and recall of both normal and unnormal classes in the classification of fragmented images and the use of data amplification are more than the other steps. Therefore, using the segmentation and data amplification technique in histological medical images will have a good performance on the convolutional neural network.

TABLE I. RESULTS FROM THE CLASSIFICATION OF PRIMARY RAW IMAGES

-	Accuracy (%)	Precision (n)	Recall(n)	Precision(un)	Recall(un)
1	70	0.675	0.75	0.719	0.64
2	77.37	0.791	0.57	0.664	0.85
3	77.77	0.835	0.71	0.745	0.85
4	80.76	0.774	0.86	0.842	0.75
5	76.92	0.772	0.86	0.827	0.67
6	74.07	0.636	0.86	0.815	0.62
AVG	76.148	0.793	0.768	0.767	0.73
STDEV	3.69	0.074	0.116	0.07	0.102

TABLE II. RESULTS FROM IMPROVED AND SEGMENTED IMAGE CLASSIFICATION

-	Accuracy (%)	Precision (n)	Recall(n)	Precision(un)	Recall(un)
1	92.59	1	0.88	0.892	1
2	85	0.851	0.86	0.858	0.85
3	85.18	0.763	1	1	0.69
4	88.88	0.813	1	1	0.77
5	88.88	1	0.79	0.826	1
6	85.18	0.801	0.93	0.916	0.77
AVG	87.618	0.871	0.91	0.915	0.846
STDEV	3.05	0.103	0.82	0.72	0.129

TABLE III. RESULTS FROM THE CLASSIFICATION OF FRAGMENTED IMAGES AND THE USE OF DATA AMPLIFICATION TECHNIQUES

-	Accuracy (%)	Precision (n)	Recall(n)	Precision(un)	Recall(un)
1	96.3	1	0.94	0.943	1
2	92.59	0.869	1	1	0.85
3	92.59	0.869	1	1	0.85
4	92.59	0.869	1	1	0.85
5	92.59	1	0.93	0.934	1
6	92.59	0.869	1	1	0.85
AVG	93.825	0.912	0.978	0.979	0.9
STDEV	1.913	0.067	0.033	0.031	0.77

TABLE IV. OVERALL RESULTS OF ALL EVALUATION STEPS

-	Accuracy (%)	Precision (n)	Recall(n)	Precision(un)	Recall(un)
CNN	76.148	0.739	0.768	0.768	0.73
UNET+CNN	87.618	0.871	0.91	0.915	0.846
UNET+ Data augmentation+ CNN	93.825	0.912	0.978	0.979	0.9

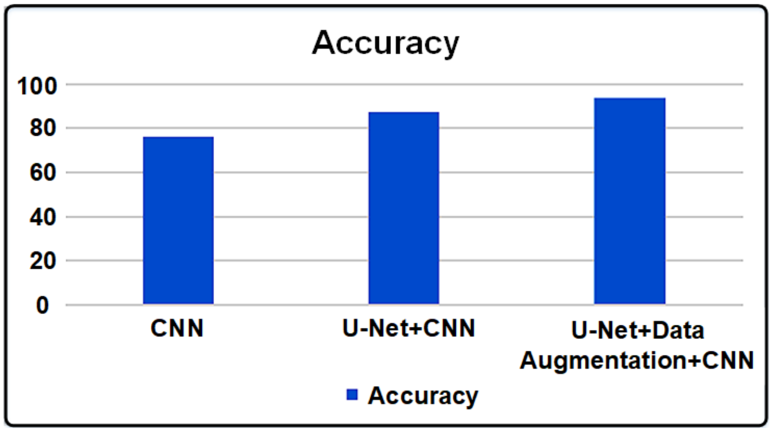

Fig. 11. Diagram related to the accuracy criterion of all evaluated steps

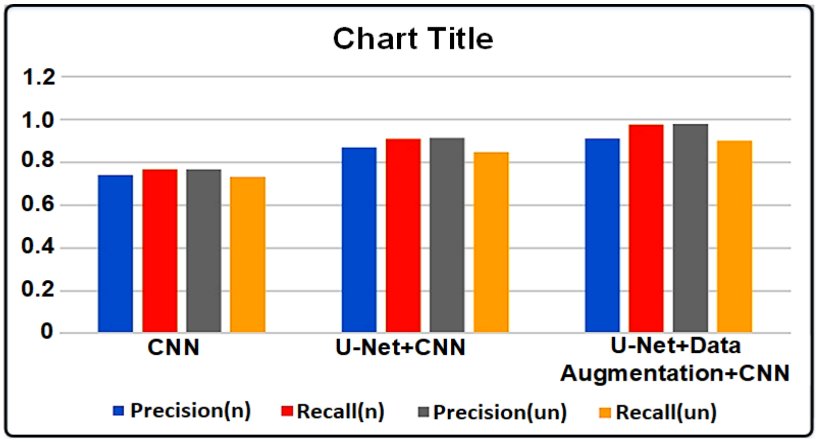

Fig. 12. Diagram of precision criteria and recall of all assessed steps

VII. DISCUSSION

The accuracy, precision, and recall attained over the course of six steps are shown in this study's experimental results. To show the convolution neural network's overall accuracy, the evaluation process and evaluation standards are represented. Precision and Recall are also supplied for each normal and abnormal class. Because both classes are equally important. In these circumstances, the accuracy of the convulsive neural network is roughly 76.14%. Precision and Recall for the typical class are respectively 0.739 and 0.76. Also, the Abnormal class has a Precision of roughly 0.76 and a Recall of approximately 0.73.

According to the presented results, it can be seen that the accuracy obtained from the classification stage of fragmented images and the use of the data amplification technique has the highest percentage, approximately 93.82%. Moreover, the results of performance measurements indicates that the precision and recall of both normal and unnormal classes in the classification of fragmented images and the use of data amplification are more than the other steps. Therefore, using the segmentation and data amplification technique in histological medical images will have a good performance on the convolutional neural network.

VIII. CONCLUSION

Today, deep learning has become one of the main techniques in the field of machine learning. They have solved many problems by using deep learning, and the use of deep learning has helped to improve the performance of many problems. For example, they use in-depth learning to diagnose various diseases, process medical images, social networking issues, etc. In this paper, deep learning is used to classify histological images. Images in different stages are classified using a neural network, as is clear from the results of the implementations. Improved image quality improved the performance of the U-Net segmentation algorithm. The U-Net algorithm also performed well for histopathological imaging.

On the other hand, the U-Net algorithm for small medical data sets can produce satisfactory results. The results obtained from the classification of fragmented images show that the segmentation of histological images improves the function of the convolutional neural network. The data amplification technique is also effective in this study because the number of images for training convolutional neural networks is minimal. Using the data amplification technique has led to better network learning. More images will ultimately help the process perform better. So, in general, it can be concluded that using segmented images and data amplification technique is helpful for histological images and causes better performance of the convolution neural network.

REFERENCES

[1] S. Penchikala, Big data processing with apache spark, Lulu. com2018.

[2] M. Juez-Gil, Á. Arnaiz-González, J.J. Rodríguez, C. López-Nozal, C. García-Osorio, Approx-SMOTE: Fast SMOTE for big data on apache spark, Neurocomputing, 464 (2021) 432-437.

[3] V. Ankam, Big data analytics, Packt Publishing Ltd2016.

[4] H. Kadkhodaei, A.M.E. Moghadam, M. Dehghan, Big data classification using heterogeneous ensemble classifiers in Apache Spark based on MapReduce paradigm, Expert Systems with Applications, 183 (2021) 115369.

[5] A. Arooj, M.S. Farooq, A. Akram, R. Iqbal, A. Sharma, G. Dhiman, Big data processing and analysis in internet of vehicles: architecture, taxonomy, and open research challenges, Archives of Computational Methods in Engineering, (2021) 1-37.

[6] J. Qiu, Q. Wu, G. Ding, Y. Xu, S. Feng, A survey of machine learning for big data processing, EURASIP Journal on Advances in Signal Processing, 2016 (2016) 1-16.

[7] Q.-C. To, J. Soto, V. Markl, A survey of state management in big data processing systems, The VLDB Journal, 27 (2018) 847-872.

[8] Y. Reddy, P. Viswanath, B.E. Reddy, Semi-supervised learning: A brief review, Int. J. Eng. Technol, 7 (2018) 81.

[9] O. Chapelle, B. Scholkopf, A. Zien, Semi-supervised learning (chapelle, o. et al., eds.; 2006)[book reviews], IEEE Transactions on Neural Networks, 20 (2009) 542-542.

[10] C. Brasko, K. Smith, C. Molnar, N. Farago, L. Hegedus, A. Balind, T. Balassa, A. Szkalisity, F. Sukosd, K. Kocsis, Intelligent image-based in situ single-cell isolation, Nature communications, 9 (2018) 1-7.

[11] A.J. Perez, M. Seyedhosseini, T.J. Deerinck, E.A. Bushong, S. Panda, T. Tasdizen, M.H. Ellisman, A workflow for the automatic segmentation of organelles in electron microscopy image stacks, Frontiers in neuroanatomy, 8 (2014) 126.

[12] W. Sun, Z. Cai, Y. Li, F. Liu, S. Fang, G. Wang, Data processing and text mining technologies on electronic medical records: a review, Journal of healthcare engineering, 2018 (2018).

[13] Z. Guan, T. Ji, X. Qian, Y. Ma, X. Hong, A survey on big data pre-processing, 2017 5th Intl Conf on Applied Computing and Information Technology/4th Intl Conf on Computational Science/Intelligence and Applied Informatics/2nd Intl Conf on Big Data, Cloud Computing, Data Science (ACIT-CSII-BCD), IEEE, 2017, pp. 241-247.

[14] M.Z. Al-Taie, S. Kadry, J.P. Lucas, Online data preprocessing: a case study approach, International Journal of Electrical and Computer Engineering, 9 (2019) 2620.

[15] S. Singhal, M. Jena, A study on WEKA tool for data preprocessing, classification and clustering, International Journal of Innovative technology and exploring engineering (IJItee), 2 (2013) 250-253.

[16] F. Milletari, N. Navab, S.-A. Ahmadi, V-net: Fully convolutional neural networks for volumetric medical image segmentation, 2016 fourth international conference on 3D vision (3DV), IEEE, 2016, pp. 565-571.

[17] Z. Zhu, C. Liu, D. Yang, A. Yuille, D. Xu, V-NAS: Neural architecture search for volumetric medical image segmentation, 2019 International conference on 3d vision (3DV), IEEE, 2019, pp. 240-248.

[18] H.R. Roth, H. Oda, X. Zhou, N. Shimizu, Y. Yang, Y. Hayashi, M. Oda, M. Fujiwara, K. Misawa, K. Mori, An application of cascaded 3D fully convolutional networks for medical image segmentation, Computerized Medical Imaging and Graphics, 66 (2018) 90-99.

[19] E. Smistad, T.L. Falch, M. Bozorgi, A.C. Elster, F. Lindseth, Medical image segmentation on GPUs–A comprehensive review, Medical image analysis, 20 (2015) 1-18.

[20] A. Eklund, P. Dufort, D. Forsberg, S.M. LaConte, Medical image processing on the GPU–Past, present and future, Medical image analysis, 17 (2013) 1073-1094.

[21] T. Kalaiselvi, P. Sriramakrishnan, K. Somasundaram, Survey of using GPU CUDA programming model in medical image analysis, Informatics in Medicine Unlocked, 9 (2017) 133-144.

[22] I.R.I. Haque, J. Neubert, Deep learning approaches to biomedical image segmentation, Informatics in Medicine Unlocked, 18 (2020) 100297.

[23] H. Seo, M. Badiei Khuzani, V. Vasudevan, C. Huang, H. Ren, R. Xiao, X. Jia, L. Xing, Machine learning techniques for biomedical image segmentation: an overview of technical aspects and introduction to state-of-art applications, Medical physics, 47 (2020) e148-e167.

[24] G. Litjens, T. Kooi, B.E. Bejnordi, A.A.A. Setio, F. Ciompi, M. Ghafoorian, J.A. Van Der Laak, B. Van Ginneken, C.I. Sánchez, A survey on deep learning in medical image analysis, Medical image analysis, 42 (2017) 60-88.

[25] M.I. Razzak, S. Naz, A. Zaib, Deep learning for medical image processing: Overview, challenges and the future, Classification in BioApps, (2018) 323-350.

[26] J. Ker, L. Wang, J. Rao, T. Lim, Deep learning applications in medical image analysis, Ieee Access, 6 (2017) 9375-9389.

[27] Y.S. Vang, Z. Chen, X. Xie, Deep learning framework for multi-class breast cancer histology image classification, International conference image analysis and recognition, Springer, 2018, pp. 914-922.

[28] Y. Guo, H. Dong, F. Song, C. Zhu, J. Liu, Breast cancer histology image classification based on deep neural networks, International conference image analysis and recognition, Springer, 2018, pp. 827-836.

[29] M.B.H. Thuy, V.T. Hoang, Fusing of deep learning, transfer learning and gan for breast cancer histopathological image classification, International Conference on Computer Science, Applied Mathematics and Applications, Springer, 2019, pp. 255-266.

[30] S. Vesal, N. Ravikumar, A. Davari, S. Ellmann, A. Maier, Classification of breast cancer histology images using transfer learning, International conference image analysis and recognition, Springer, 2018, pp. 812-819.

[31] S. Khan, N. Islam, Z. Jan, I.U. Din, J.J.C. Rodrigues, A novel deep learning based framework for the detection and classification of breast cancer using transfer learning, Pattern Recognition Letters, 125 (2019) 1-6.

[32] C. Munien, S. Viriri, Classification of hematoxylin and eosin-stained breast cancer histology microscopy images using transfer learning with EfficientNets, Computational Intelligence and Neuroscience, 2021 (2021).

[33] H. Cao, S. Bernard, L. Heutte, R. Sabourin, Improve the performance of transfer learning without fine-tuning using dissimilarity-based multi-view learning for breast cancer histology images, International conference image analysis and recognition, Springer, 2018, pp. 779-787.

[34] O. Ronneberger, P. Fischer, T. Brox, U-net: Convolutional networks for biomedical image segmentation, International Conference on Medical image computing and computer-assisted intervention, Springer, 2015, pp. 234-241.

[35] M. Lorentzon, Feature extraction for image selection using machine learning, 2017.