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Detection of Lung and Colon Cancer from Histopathological Images: Using Convolutional Networks and Transfer Learning

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Abstract Analyzing histopathology images to detect the presence of cancer cells is a very important task during cancer treatment. This task has traditionally been largely done by manual methods. Therefore, the results of these analyzes are highly dependent on the pathologist's skills and professional experience, wasting time and manpower. Automating this task using deep learning techniques will speed up the early detection of cancer cells. Interestingly, these techniques have led to impressive advances in image processing in various fields, including the medical field. In this paper, we first attempt to highlight the importance of using deep learning techniques to classify histopathological images, and have cited studies using LC25000 datasets to accomplish this task. We then compared twelve models based on pretrained VGG-16, ResNet, DenseNet and NasNet models. The overall accuracy in this study ranged from 95.99% to 99.98%, reaching 100% for some categories. The purpose of this article is to compare pretrained models, examine the impact of the number of layers on the performance of built models, and highlight the importance of using transfer learning techniques.

Keywords: Histopathological images, Deep learning, Classification, Convolutional neural networks, VGG, ResNet, DenseNet, NasNet, Lung cancer detection, Transfer learning, Colon cancer detection, Image preprocessing

1. INTRODUCTION

Colon and lung cancers are the second most frequent cancers worldwide, with unacceptably high mortality rates. According to World Health Organization statistics, in 2020, these two types of cancer caused 2.21 and 1.93 million deaths respectively [1] .

According to the Moroccan Ministry of Health, lung cancer accounted for 11.4% of cancer cases recorded between 2008 and 2012, followed by colorectal cancer with a proportion of 6.7% [2].

Cancer results from the transformation of normal cells into cancerous ones. This process sometimes leads to the formation of malignant tumors. Finding these cells early can keep them under control and greatly increase the chances of recovery.

Cancer diagnosis involves several key steps to detect the cancer cells and then determine the stage and type of cancer [3]. If cancer is suspected, a physical examination is usually performed by a physician. Imaging tests such as mammography, computed tomography (CT), MRI, ultrasound or radiography can then be performed to visualize internal tissues and organs. If suspicious areas are identified, a biopsy may be performed to remove a tissue sample for examination in the laboratory. Analysis of this tissue, known as histopathological analysis, involves examining a tissue sample under a microscope to look for cancer cells and determine the type and stage of cancer.

Histopathological analysis is performed by expert pathologists by viewing slides from several biopsies. The aim of this examination is to detect patterns, shapes and dimensions of relevant structures present in the tissue, or other features specific to certain diseases. To detect the presence of cancer in a tissue, the expert must differentiate between healthy and cancerous cells.

Given that a histopathological image may contain a large number of cells, and that the characteristics used to classify them are also numerous, this visual evaluation is necessarily time-consuming, fastidious and subjective.

To overcome this issue and improve the accuracy and speed of diagnosis, a number of studies have attempted to automate the task of processing and analyzing histopathological images using deep learning algorithms.

Deep learning is a subcategory of machine learning that exploits artificial neural networks. In the last decade, it has achieved impressive performance in the automatic processing of text [4] [5] and images [6], particularly in

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the medical field [7] [8]. In contrast to machine learning, deep learning does not require a pre-processing step for feature extraction [9] and hypothesis domain selection. But it can also be used to create models that learn from scratch based on large amounts of data.

Convolutional networks are the most dominant and successful deep learning models for image processing and recognition.

In this paper we present a comparative study of the convolutional networks VGG-16 [10], ResNet [11], DenseNet [12] and NasNet [13], and their performance in classifying histopathological images of lung and colon cancer in the LC25000 dataset [14].

The histopathological classification of many different types of cancer has attracted a great deal of interest. Various research studies have used the LC25000 dataset, either to compare the pre-trained models' performances or to propose new classification models for histopathological images. The accuracy achieved in these studies ranged from 88% to 100%. The details of these researches will be presented in section 2.

The rest of this paper is organized as follows: Section two presents related work, section three is a brief description of convolutional networks and the concept of transfer learning, as well as the structures of our models. The dataset will be presented in section four, followed by models and results in section five. These results are discussed in section six. Section seven is the conclusion.

2. RELATED WORK

Several studies have attempted to classify histopathology images in the LC25000 dataset, using machine and deep learning techniques. In this section, we focus on works that have achieved the best performances, from the most recent to the earliest.

Wahid et al. [15] proposed a computer-aided diagnosis system using ShuffleNet V2, GoogLeNet and ResNet18, as well as a customized CNN model. ResNet18 achieved the highest accuracy for lung cancer, while ShuffleNet V2 was the fastest. For colon cancer, ShuffleNet V2 performed best, with an accuracy of 99.87%. The customized CNN model showed promising results, with an accuracy of 93.02% for lung cancer and 88.26% for colon cancer.

Kumar et al. [16] compared two approaches in this dataset, using deep convolutional neural networks and handcrafted feature extraction techniques. The results showed a significant improvement in the performance of classifiers with deep features, in particular the RF classifier with DenseNet-121, achieving 98.60% precision, 98.63% recall, an F1-score of 0.985%.

Talukder et al. [17] presented a hybrid model integrating deep feature extraction and ensemble learning, achieving remarkable accuracy rates: 99.05% for lung cancer, 100% for colon cancer and 99.30% for combined detection.

Mehmood et al. [18] have developed a highly accurate and efficient model. It is an alternative to current detection methods. By fitting a pre-trained neural network (AlexNet) and applying a contrast enhancement technique to poorly performing images, overall accuracy was increased from 89% to 98.4%.

Abbas et al. [19] studied the use of convolutional neural networks in this dataset. Six CNN architectures were evaluated, with outstanding F1 scores of 0.997 for VGG-19, 0.999 for ResNet-50 and 0.999 for ResNet-101 on the test set.

Garg et al. [20] used eight pre-trained CNN models to detect lung and colon cancer from histopathological images, focusing on data augmentation techniques. The models were evaluated on this dataset achieving remarkable performance with accuracy ranging from 96% to 100%. They also used GradCAM and SmoothGrad to visualize the CNN models' attention images, highlighting their ability to distinguish between malignant and benign images.

In this paper, we aim to highlight the importance of transfer learning and the impact of the depth of fully connected layers on the classification performance of histopathological images in the LC25000 dataset.

3. CONVOLUTIONAL NEURAL NETWORKS AND TRANSFER LEARNING

A. *Convolutional Neural Networks*

Convolutional networks are a deep learning technique widely used for computer vision tasks [21]. In 1988, Yann LeCun successfully trained the LeNet model, Figure 1, for handwriting recognition using gradient descent and backpropagation algorithms [22].

The general architecture of a convolutional network consists of many different types of layers:

- The convolution layers generate a feature map containing the characteristics of the input image.
- Polling layers reduce the size of the feature map to improve computational capabilities.
- Fully connected layers that combine the values of the last feature map.
- The decision layer, which uses these combinations to determine the image category.

To overcome underfitting and overfitting problems, additional layers can be added, such as normalization and dropout layers.

Several models have succeeded in improving this architecture and achieving higher performance. In The ImageNet

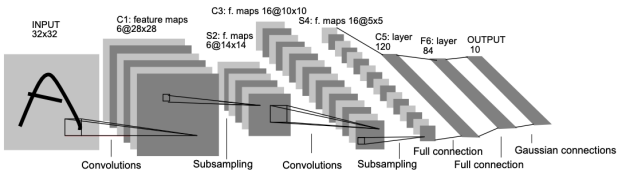


Figure 1. The first CNN architecture, LeNet from [22]

Large Scale Visual Recognition Challenge (ILSVRC), AlexNet [23] , GoogleNet [24] and ResNet [11] took first place in 2012, 2014 and 2015 respectively.

To explore the performance of convolutional networks in the classification of histopathological images, we applied transfer learning techniques to four pre-trained models: VGG-16, ResNet, DenseNet and NasNet. The details of these models' architectures will be briefly presented in the next sub-section.

B. *Transfer Learning*

In deep learning, a high-performance model needs to be trained, then validated and tested on a considerable amount of data. training these models from scratch requires significant computational and storage resources. However, acquiring this data is not always easy, particularly in fields where data is scarce or its acquisition and preparation are very expensive, such as the field of histopathological image processing.

Transfer learning and data augmentation are the two most popular solutions to these challenges.

Transfer learning is a machine learning technique that transfers the knowledge of a pre-trained model, which is trained on a sufficiently large dataset, to perform a similar task in another domain where there is a shortage of data. This technique is based on the fact that the first layers of convolutional networks always learn the same features. These features are combined in the last decision layers to give the probability of belonging to one category or another.

For a classification task, we use a CNN pre-trained model and replace the last completely connected layers with those that meet the objective of our classification task. The weights of the pre-trained model are fixed, and determining the weights of the fully connected layers will be the goal of the training.

In this study, we trained 12 models. These models can be grouped, based on the pre-trained model, into 4 categories: VGG, ResNet, DenseNet and NasNet. Each category contains 3 models, which we have named model (1), model (2) and model (3).

In model (1) we replaced the fully connected layers of the pre-trained model with a fully connected layer of 128 neurons followed by a decision layer of five classes. In model (2), we have replaced these layers with a layer of 256 neurons, followed by the same layers used in model (1). The structure of model (3) as it is illustrated in Figure 2, we have replaced these layers with a layer of 1024 neurons, followed by a layer of 512 neurons and followed with the same layers used in model (2). The activation function used in these fully connected layers is the Relu function.

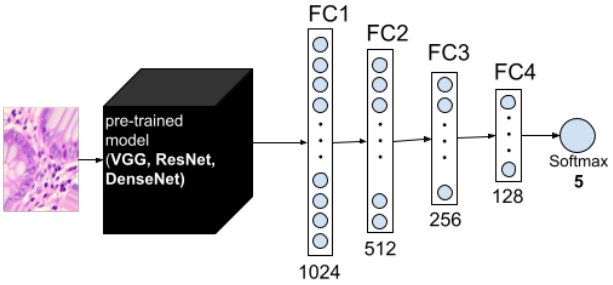


Figure 2. the structure of model (3) using a pre-trained model and four fully connected layers.

All dataset images are normalized and resized before being used in models training and testing. To regularize our models and avoid overfitting, a dropout operation has been added to the fully connected layers except for the FC4 layer and the decision layer.

The training and testing of these 12 models will enable us to explore the performance of these pre-trained models in the classification of histopathological images, as well as the impact of the number of fully connected layers on their performances.

4. DATASET

A. *Description*

The dataset used in this study is the Lung and Colon Cancer Histopathological Image Dataset (LC25000) . It consists of 25,000 histopathological images that are divided into 5 classes, namely, colon adenocarcinoma (colon_aca), benign colonic tissue(colon_n), lung adenocarcinoma (lung_aca), lung squamous cell carcinoma (lung_scc), and benign lung tissue(lung_n). All images have a size of 768 x 768 pixels. Each class contains 5,000 images of histological features. Figure 3 shows a sample of these images.

This dataset was generated on the basis of 750 images of lung tissue and 500 images of colonic tissue, and using various data augmentation techniques such as rotation, displacement, horizontal and vertical flipping, zooming, brightness modification and cropping. This dataset was cited more than 132 times between 2020 and 2023, as shown in Figure 4 .

B. *Dataset Preparation*

In this study, we have divided this dataset into three parts. The first part, representing 80% of the data, was dedicated to training the model, while 10% was dedicated

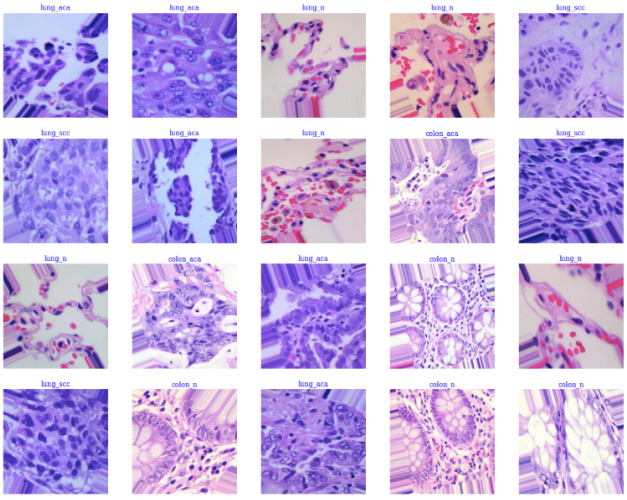


Figure 3. A sample of histopathological images from dataset LC25000

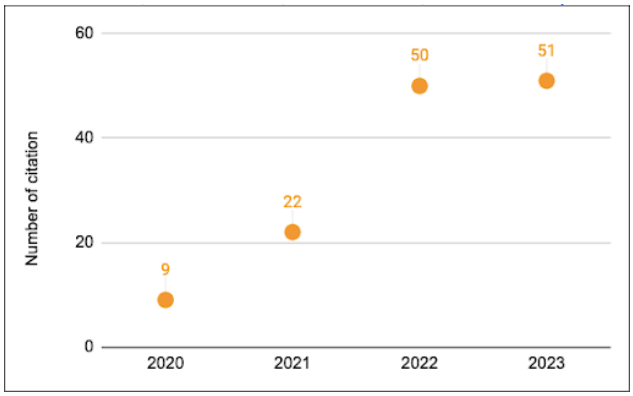


Figure 4. The number of citations of the LC25000 dataset between 2020 and 2023

to validating it during training, and the final 10% represents the test dataset. This last part of the data is used to test the model's performance on images that are not used to train or validate the models.

The images in this dataset are resized and normalized before being used for model training.

5. MODELS AND RESULTS

A. Metrics

Before describing our models and their performances, we present the metrics that are used to compare them, which are : accuracy, precision, recall and f1-score.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (1)$$

$$Precision = \frac{TP}{TP + FP} \quad (2)$$

$$Recall = \frac{TP}{TP + FN} \quad (3)$$

$$F1 - Score = \frac{2 * Precision * Recall}{Precision + Recall} \quad (4)$$

TP: True Positive

TN: True Negative

FP: False Positive

FN: False Negative

B. Proposed Models

In this section, we present the general structure of the pre-trained models used, as well as their main contribution to the evolution of convolutional neural networks [25] . For each CNN architecture, we present the results achieved for models (1), (2) and (3).

To verify and confirm the results achieved in this study, we ran the training of these models several times over several weeks in Kaggle Notebooks, a cloud computing environment that enables reproducible and collaborative analysis. This environment offers 32 hoursweek of use of a machine with 16 Gigabyte memory and NVIDIA T4 x2 GPU. Model training stops when accuracy is no longer in progress for several successive epochs, or if the number of epochs reaches 40. As previously mentioned, we have chosen the VGG, ResNet, DenseNet and NasNet models for this study.

1) VGG

VGG stands for Visual Geometry Group and is one of the most popular pretrained models for image classification. Its main contribution is to increase network depth in order to improve performances. Thanks to this contribution, VGG16 won first place in the 2014 ILSVRC competition, achieving 92.7% accuracy on the ImageNet dataset.

VGG's architecture is mainly inspired from the AlexNet one, but replaces the traditional method of using high-dimensional filters with lowdimensional filters (3x3 and 1x1) and increasing the number of layers.

There are two types of VGG architecture: VGG16 and VGG19. The difference is that VGG19 has 19 convolutional layers, 3 more than VGG16. In this study, we have chosen VGG16.

By using the VGG16 pretrained model, we have obtained the results shown in Tables I and II, Figures 5 and 6.

Analyzing the results in these tables and Figure 5, we note that:

- Compared with model (1), the accuracy of model (2)

has improved, and the accuracy of the validation data has reached 98.5% at epoch 22, and the accuracy of the test data has also reached 98%. This confirms the effect of adding the FC3 layer to the model's performances.

- As more layers are added to the model (3), performance on validation and test data starts to degrade. This can be explained by the vanishing gradient phenomenon.

Analyzing the confusion matrix in Figure 6, we note that :

- Models (2) and (3) are a little confused when detecting lug_aca and lug_scc images.
- Model (1) performs poorly when detecting colon_n and lung_scc images. Its accuracy for these two classes did not exceed 70%.

2) ResNet

In theory, the more layers you add to a neural network architecture, the better its performance. But in practice, performance starts to degrade when a given number of layers is exceeded. This is due to the vanishing gradient problem, which is mentioned in the performance analysis of model (3) based on VGG-16.

To solve this problem, the authors of Residual Neural Networks (ResNet) proposed a new technique called "identity skip connections" or "residual connections", as shown in Figure 7. Using this proposal, ResNet successfully trained a 152-layer neural network and won (ILSVRC 2015) with a top-5-error of 3.57% and an accuracy of 95.29% , outperforming human performance in this dataset.

There are many variants of ResNet, varying in the number of layers used. In this study, we chose Resnet-50, which trains 50 neural network layers.

Using Resnet as a base model, we obtained the results shown in Tables III and IV. Analyzing the results in these tables and Figure 8, we note that:

- Model (2) slightly outperformed model (1) on the validation data, reaching 99.24%. But the accuracy of the test data decreased. This means that the model is overlearning.
- By adding more layers, the accuracy of model (3) decreases on both validation and test data. This may be due to the vanishing gradient problem.

Analyzing the results of the confusion matrix in Figure 9, we observe that:

- Models (1) and (3) make a small confusion in the detection of lung_acc and lung_aca classes.
- Model (2) is the best of the three, and although it also creates some confusion in these two categories, the number of classification errors is twice as low as models (1) and (3).

3) DenseNet

DenseNet is a type of convolutional network that uses so-called Dense Blocks , as shown in Figure 10. These are inspired from the idea of ResNet, but instead of summing the input and output of the previous layer, the input of a DenseBlock layer is made up of the concatenation of the outputs of all its previous layers. This small modification enabled DenseNet to achieve an accuracy of 93.88% in the ImageNet dataset in 2016.

Using DenseNet as a base model, we obtained the results shown in Tables V and VI.

Analyzing the results in these table and Figure 11, we note that:

- The model (1) reached a good accuracy of 99.98% on the validation data, but it takes 29 epochs for the model to reach this result.
- The model (2) has the best accuracy of the three, 99.35%. It slightly surpassed the accuracy of model (2) without degrading the accuracy achieved in the test data, which is 99.98%.
- While model (3) maintained the same accuracy on the test data, it degraded on the validation data, failing to exceed 98.53%.

Analyzing the results in Figure 12:

- we can only observe that the accuracy of model (3) has degraded. This is due to confusion in the classification of lung_aca and lun_acc images.

4) NasNet

In the field of neural network architecture research, the Google ML group has introduced a new learning method called Neural Architecture Search (NAS). This approach aims to automate the design of neural network architectures. In other words, it enables artificial intelligence to generate neural architectures itself.

NASNet is a convolutional neural network created automatically using Neural Architecture Search. In this study, we used a specific version of NASNet called NASNetLarge. This version is designed for large-scale image classification tasks and was trained on the ImageNet dataset.

Using NASNetLarge as a base model, we obtained the results shown in Tables VII and VIII.

Analyzing these results in these tables and Figure 13, we note that:

TABLE I. Accuracy of models using VGG-16

		Model 1	Model 2	Model 3
Validation Dataset	best accuracy %	97.5	98.5	96.36
	epoch	19	22	16
Test Dataset Accuracy %		95.99	98	95.99

TABLE II. precision, f1-score and recall, in the validation dataset, of models using VGG-16

	Model 1			Model 2			Model 3		
	precision	f1-score	recall	precision	f1-score	recall	precision	f1-score	recall
colon_aca	0.76	0.98	0.86	0.99	0.99	0.99	0.96	0.99	0.97
colon_n	0.99	0.70	0.82	1.00	1.00	1.00	1.00	0.99	0.99
lung_aca	0.73	0.96	0.83	0.91	0.97	0.94	0.94	0.88	0.91
lung_n	0.99	0.95	0.97	1.00	1.00	1.00	0.99	1.00	1.00
lung_scc	0.94	0.70	0.80	0.97	0.91	0.94	0.92	0.94	0.93

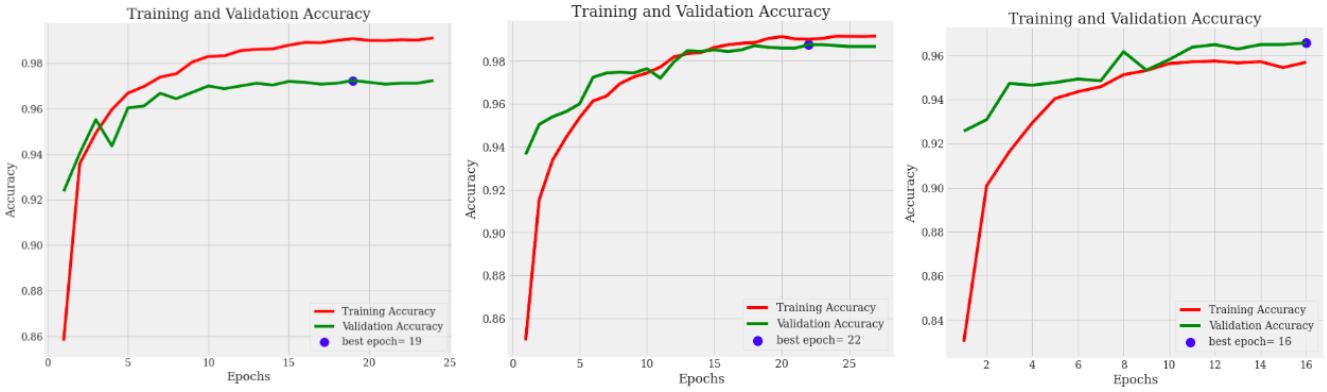
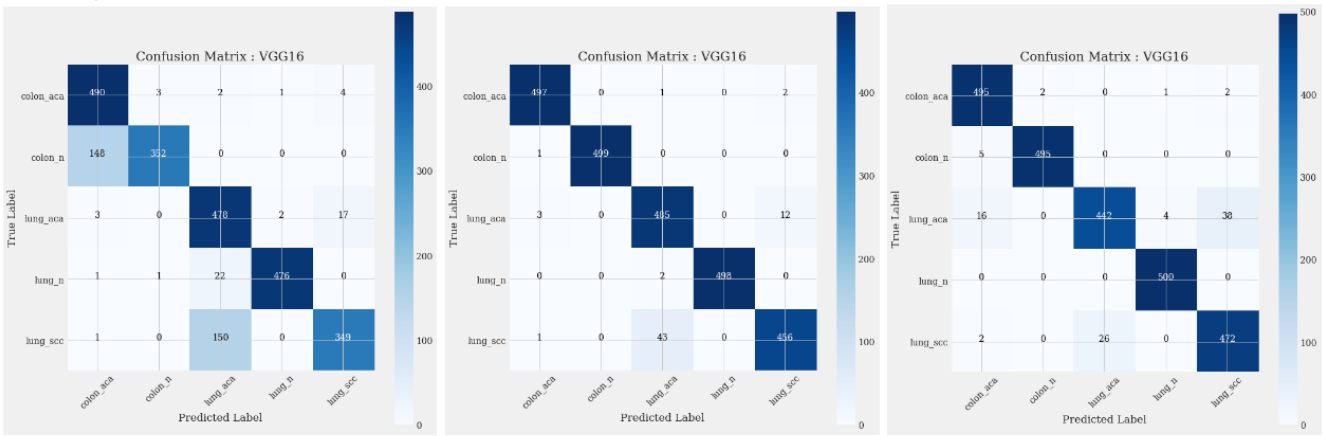


Figure 5. Accuracy evolution during training for models based on ResNet-50



Model 1 Model 2 Model 3

Figure 6. Confusion matrices for models based on VGG-16 on Test dataset

TABLE III. Accuracy of models using ResNet

		Model 1	Model 2	Model 3
Validation Dataset	best accuracy %	99.08	99.24	98.4
	epoch	17	13	12
Test Dataset Accuracy %		99	98	98

TABLE IV. precision, f1-score and recall, in the validation dataset, of models using ResNet

	Model 1			Model 2			Model 3		
	precision	f1-score	recall	precision	f1-score	recall	precision	f1-score	recall
colon_aca	0.99	1.00	0.99	1.00	1.00	1.00	0.99	1.00	1.00
colon_n	1.00	0.99	0.99	1.00	1.00	1.00	1.00	1.00	1.00
lung_aca	0.96	0.98	0.97	0.99	0.98	0.99	0.97	0.96	0.96
lung_n	1.00	0.99	1.00	1.00	1.00	1.00	1.00	1.00	1.00
lung_scc	0.98	0.97	0.98	0.98	0.99	0.99	0.96	0.96	0.96

TABLE V. Accuracy of models using DenseNet

		Model 1	Model 2	Model 3
Validation Dataset	best accuracy %	99.32	99.35	98.52
	epoch	29	10	10
Test Dataset Accuracy %		99.98	99.98	99.98

TABLE VI. precision, f1-score and recall, in the validation dataset, of models using DenseNet

	Model 1			Model 2			Model 3		
	precision	f1-score	recall	precision	f1-score	recall	precision	f1-score	recall
colon_aca	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
colon_n	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
lung_aca	0.99	0.98	0.98	0.99	0.98	0.99	0.97	0.96	0.96
lung_n	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
lung_scc	0.98	0.99	0.99	0.98	0.99	0.99	0.96	0.97	0.96

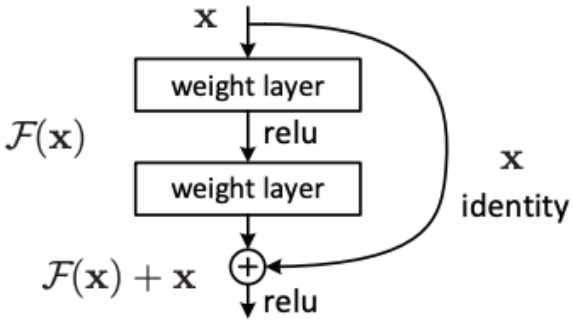


Figure 7. Residual learning: a building block [11]

- The accuracy of model (2) has improved slightly, but after the 17th epoch, this improvement has no effect on the accuracy of the test data.
- The accuracy of model (3) decreases on the validation data, but this has no effect on the accuracy on the test data.

Analyzing the confusion tables in Figure 14, we observe that:

- Models (1) and (2) classify the majority of images correctly.
- Model (3) performs poorly in classifying lung_aca

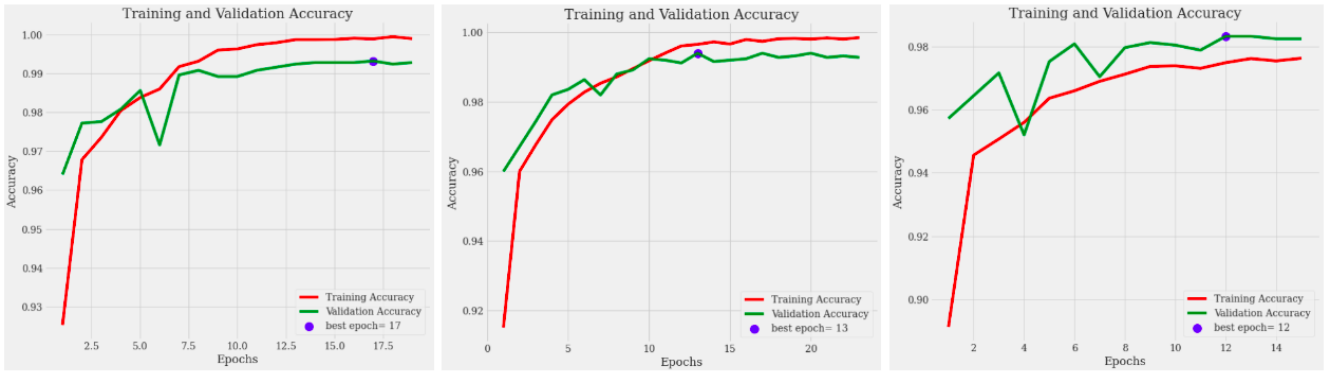


Figure 8. Accuracy evolution during training for models based on ResNet

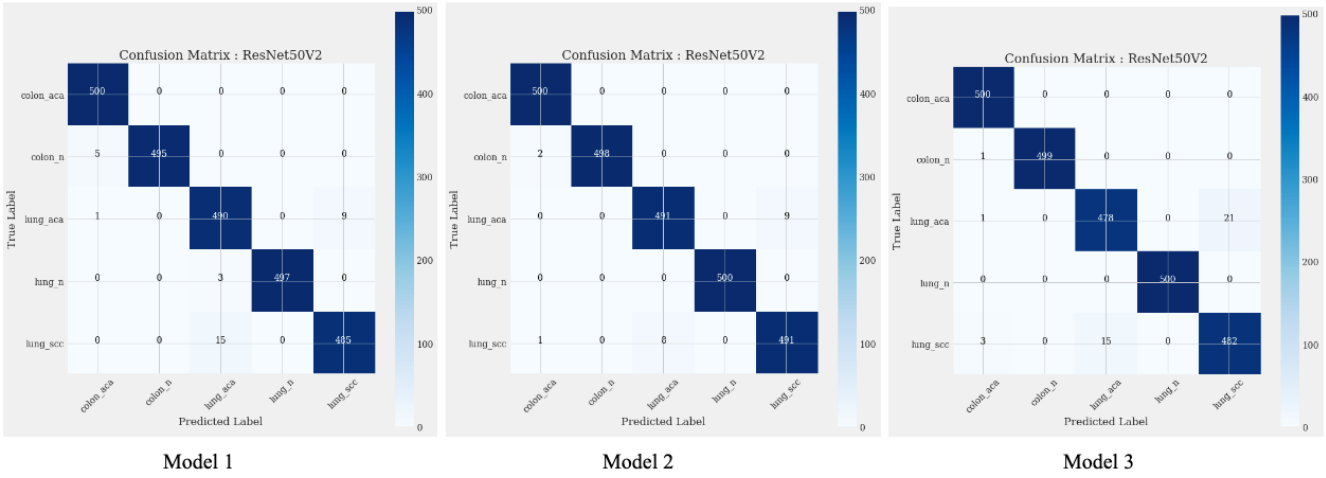


Figure 9. Confusion matrices for ResNet-based Models on validation dataset.

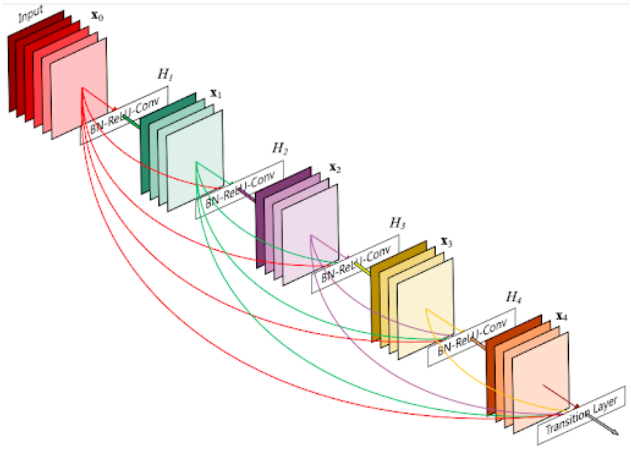


Figure 10. Residual learning: a building block [12]

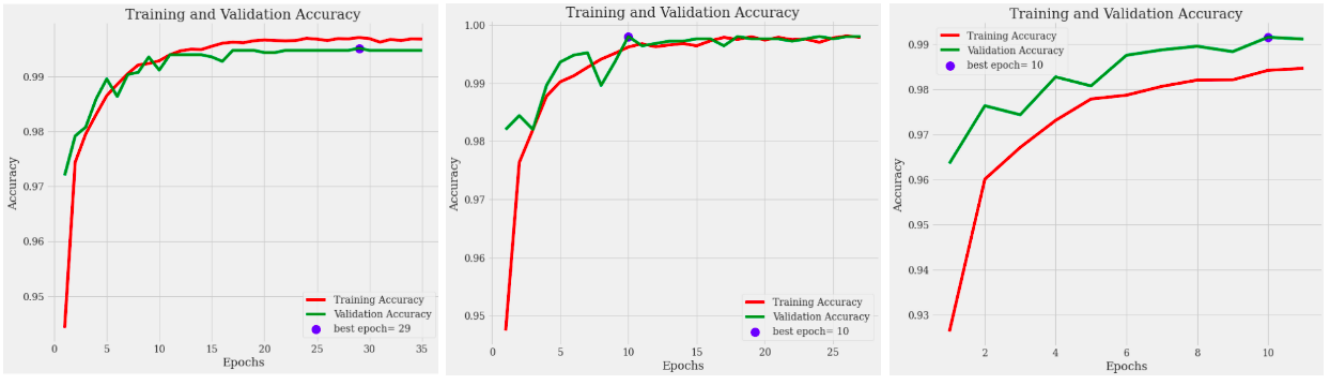
and lung_scc images.

6. DISCUSSION

The use of transfer learning techniques shows great promise for revolutionizing a number of fields, including healthcare. This technology could provide an answer to the problem of data scarcity, which is a major barrier to the use of artificial intelligence to process medical images, particularly histopathology images. The results of this comparative study confirm this conviction.

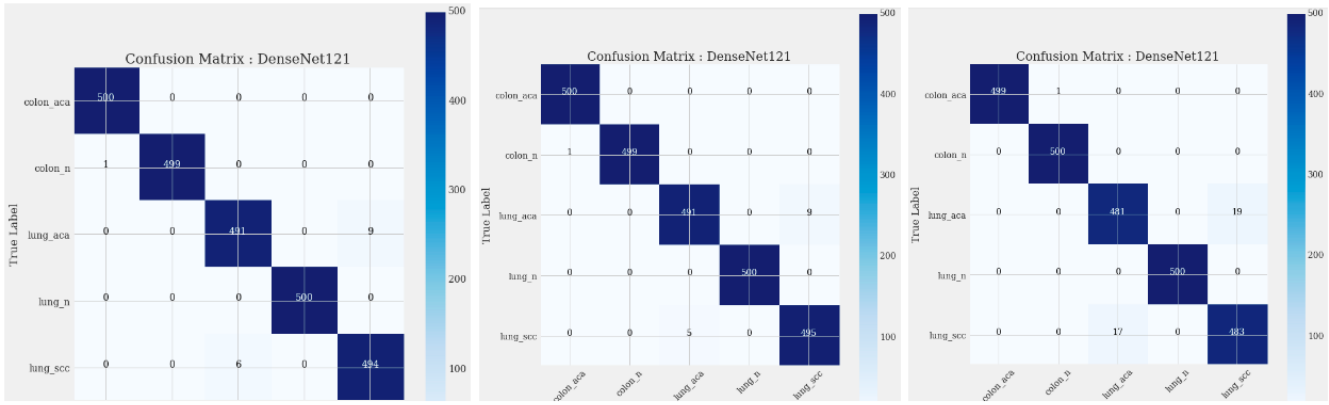
Analyzing the results obtained in this study and the evolution of accuracy and classification error on the validation datasets for all models, Figure 15, we note that:

- With the exception of the VGGbased model (1), the initial accuracy exceeds 70% and the error rate is less than 0.25 in most cases.
- Moving from model (1) to model (2), accuracy and error rate evolve continuously and converge rapidly towards the optimum value.
- Performance deteriorates in model 3, whatever the



Model 1 Model 2 Model 3

Figure 11. Accuracy evolution during training for models based on DenseNet



Model 1 Model 2 Model 3

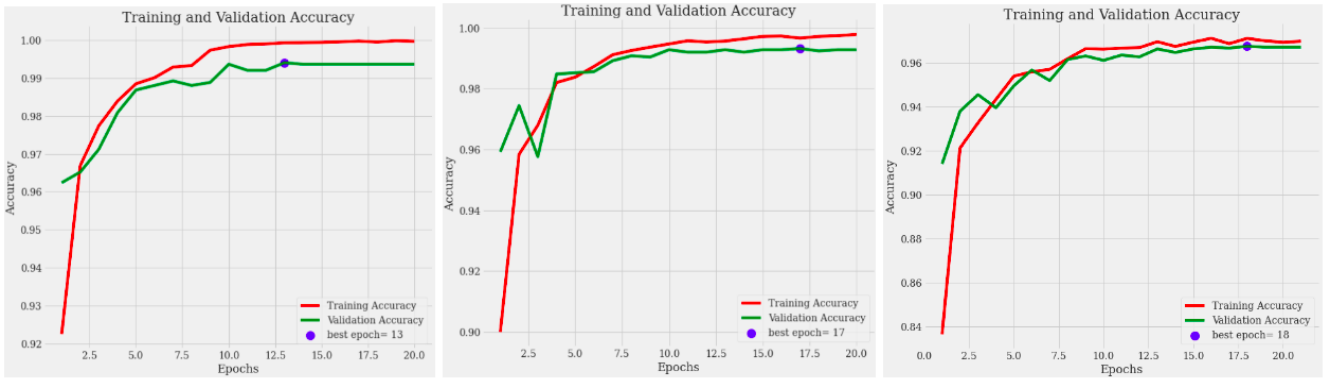
Figure 12. Confusion matrices for DenseNet-based Models on Test dataset

TABLE VII. Accuracy of models using NasNet

		Model 1	Model 2	Model 3
Validation Dataset	best accuracy %	99.24	99.36	96.64
	epoch	13	17	18
Test Dataset Accuracy %		95.99	95.99	95.99

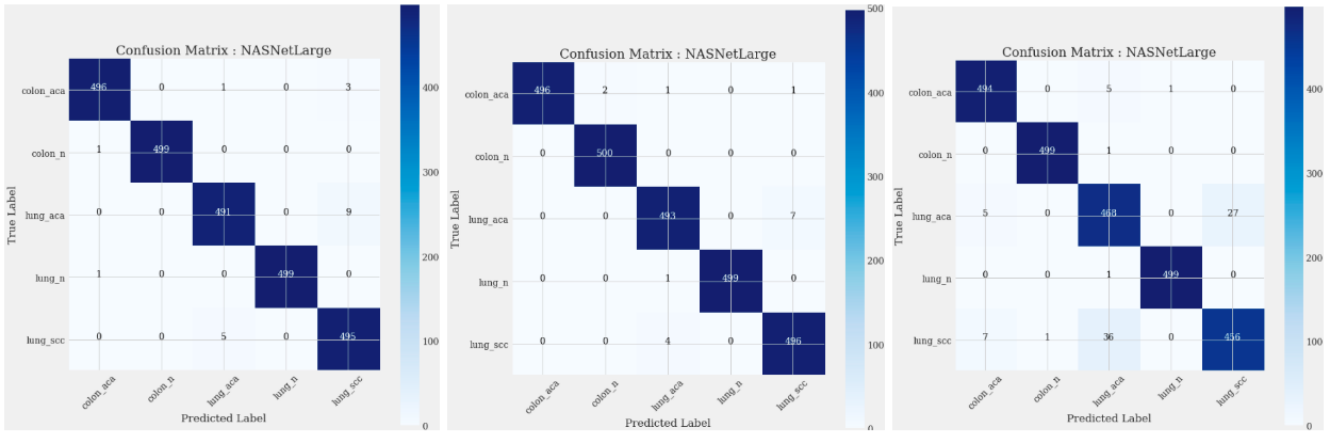
TABLE VIII. precision, f1-score and recall, in the validation dataset, of models using NasNet

	Model 1			Model 2			Model 3		
	precision	f1-score	recall	precision	f1-score	recall	precision	f1-score	recall
colon_aca	1.00	0.99	0.99	1.00	0.99	1.00	0.98	0.99	0.98
colon_n	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
lung_aca	0.99	0.98	0.98	0.99	0.99	0.99	0.92	0.94	0.93
lung_n	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
lung_scc	0.98	0.99	0.98	0.98	0.99	0.99	0.94	0.91	0.93



Model 1 Model 2 Model 3

Figure 13. Accuracy evolution during training for models based on NasNet



Model 1 Model 2 Model 3

Figure 14. Confusion matrices for NasNet-based Models on Test dataset

base model.

- The DenseNetbased model always performed best in this study: accuracy was consistently above 99% and error rate below 0.05.
- In the different models, the decrease in performance was always associated with classification confusion for the lung_aca and lun_scc classes.

Therefore, based on this analysis, we can draw the following conclusions:

- The number of layers and neurons added to a pre-trained model is a critical task in model design and can affect its performance. If there are too few layers, the model won't learn much. If the number of layers is too high, performance degrades, particularly on validation and test data. This is due to the vanishing gradient problem.
- The best pretrained model for classifying histopathological images is DenseNet.
- Classification confusion between two classes can impact all model performances. So, if we can find a way to reduce this confusion, performance will improve considerably.

Although we achieved good performance in this study, these results are relative because the size of this dataset is insufficient and it is itself based on data augmentation.

This study can be completed by:

- Adding other pre-trained models.
- Using another dataset.
- Improving the VGG-based model to achieve better performance.
- Use these models as base models for other tasks, such as the segmentation of histopathological images.

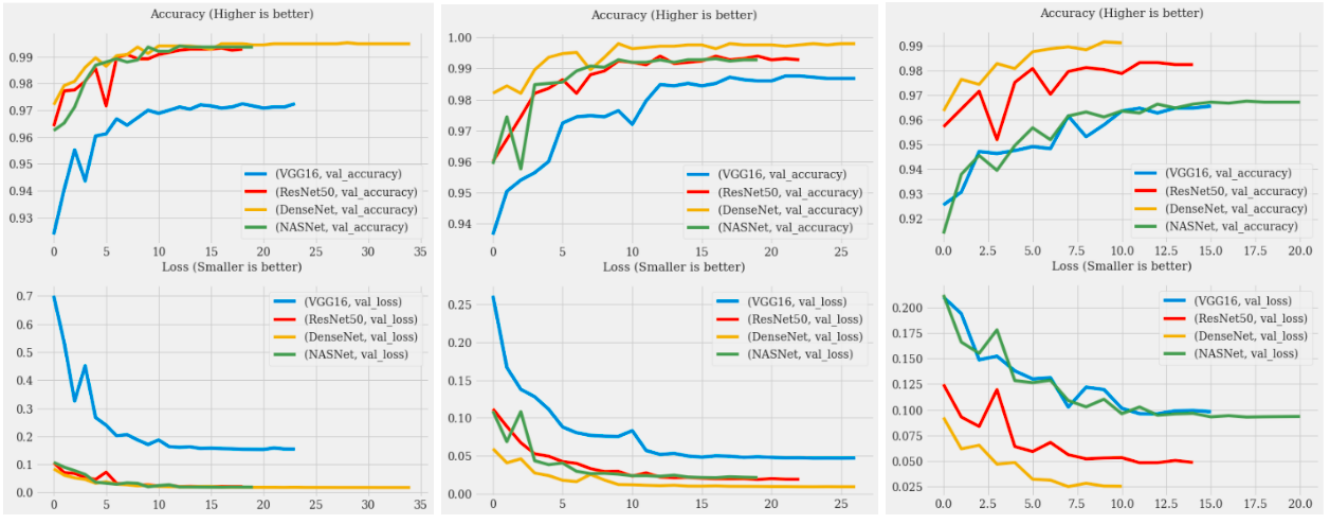


Figure 15. The evolution of accuracy and the error rate of models (1), (2) and (3) on validation data

- Use this dataset to test segmentation algorithms such as the sine-cosine algorithm [26] [27] and the fuzzy C-means and cuckoo search algorithms [28] or reinforcement learning algorithms [29].

7. CONCLUSION

By analyzing histopathology images, we can extract many features from tumor tissue. This can determine whether a tumor is benign or malignant and identify the need for treatment early on. This work requires a lot of expertise and time. With the number of new infections growing exponentially, the use of artificial intelligence to automate this task has become imperative.

In this article, we demonstrate the importance of using deep learning techniques, in particular convolutional networks, for the automatic classification of histopathological images of lung and colon cancer. We review a number of research papers that use the LC25000 dataset to detect and classify these images. We then test twelve models based on the VGG-16, ResNet, DenseNet and NasNet pre-trained models. The twelve models differ in the number of fully connected layers and the pre-trained model used. The accuracy achieved in this study ranged from 95.99% to 99.98%. DenseNet-based models showed the best performance, followed by ResNet-based models. These results highlight the importance of using transfer learning techniques and the impact of the number of fully connected layers added on overall model performances. However, to confirm these promising results, a crucial step is to train and test these models on a dataset comprising a significant number of histopathological images.

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