RMIT

RMIT International University Vietnam
School of Science and Technology
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NUCLEI CLASSIFICATION OF COLON CANCER HISTOLOGY IMAGE

Team name:	DacLoc
Team members:	Tran Minh Quang – s3757281
	Ngo Quang Trung – s3742774
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Lecture:	Dang Pham Thien Duy

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Introduction

In recent years, the world is witnessing a rapid development of computer-aided diagnosis (CAD) to support the doctor in the decision-making process. The age of technology nowadays has shown unlimited potential of Artificial Intelligence (AI) and the application of AI on CAD systems have shown a positive impact on the healthcare system with decision support, image detection, and patient triage [1]. One of the most well-known applications of AI in CAD is the classification and detection of tumors in histology Images.

Nucleus image classification for histology image is applied in various medical applications in diagnosis of cancer, bone metastases, coronary artery disease or diabetic retinopathy. The main advantage of applied CAD in the above is that it can produce a quick investigation about the image and the doctor can quickly analyze the abnormality in a short amount of time compared to traditional methods in which doctor and medical practitioner have to spend a lot of time in diagnosing histology images.

There are several image classification techniques such as Support Vector Machine (SVM), K-nearest neighbour (KNN) and convolutional neural network (CNN). The SVM is a supervised learning algorithm, so we need deep biological knowledge to preprocess data and extract features from it before training the model and it does not perform well in explaining non-linear relationship of features. In contrast, KNN is an unsupervised machine learning algorithm that does not require labelled data but in tradeoff with accuracy. The CNNs using fully connected layer and SoftMax regression is considered the most suitable technique for this problem, the data preprocessing does not need prior knowledge on biological, the neural network with leaky-RELU activation can have a good explanation of non-linear relationships especially in case of histopathology image and the CNNs model is also well known for its high performance with diversity of architectures. In this project, we will apply computer vision techniques to build nucleus detection models of colon cancer histology images and a binary classification model predict whether the cell type is cancerous or not.

Related work

There are several published research papers which proposed CNN architectures to tackle this problem. K. Sirinukunwattana and his colleagues proposed a Softmax-CNN with Neighboring Ensemble Predictor (NEP) for nucleus classification. The proposed model has a weighted average F1 score is 0.784, AUC scores are 0.917 and the testing accuracy is 71.15% which is a decent performance. In addition, S. Shabbeer et al have published a new efficient CNN architecture for classification nucleus in histology images which have deeper layers than the previous one and the results show that there is improvement in the accuracy and F1 score which are 81% and 0.789 respectively.

Convolutional network architecture

In this project, we applied 3 CNNs architecture to classify whether a cell image is cancerous or not and cell types of the cell image which are VGG16, ResNet50v2 and MobileNetv2. Besides these above-mentioned models which will be initialized and trained with the data set, we will take the result of two models that also use a similar data set which are Softmax-CNN proposed by K. Sirinukunwattana et al [2] and RCCnet by S H Shabbeer and his colleagues [3].

1. The VGG16 or can be called OxfordNet is a CNN architecture that was used to win the Large-Scale Visual Recognition Challenge in 2014 conducted by Karen Simonyan and Andrew Zisserman of the Visual Geometry Group Lab of Oxford University [4]. At the moment, VGG16 is still well known as one of the excellent computer vision architectures. The models contain different convolutional layers and max pool layers, at the end, it has three fully connected layers and a softmax regression for classification. The main advantages of VGG16 are it has very good performance with a high accuracy score, however, the training time is high, and it needs a lot of memory.

2. The ResNet50v2 model is a modified version of the ResNet50 CNNs model which has 48 convolutional layers, 1 max pooling layer and 1 average pooling. ResNet50v2 is the winner of the Image Net competition 2015, the noticeable thing about the model is it is capable of training CNNs model with extremely deep layers with greater accuracy. Hence, because of that performance, ResNet computation time is very slow with an enormous number of parameters.

3. The MobileNetV2 which is developed by Google is a compact CNNs model specialized for mobile devices or devices with low computational power. The model has two blocks with 3 layers in each block. Since the model size of MobileNetV2 is relatively small, it will have faster computation time compared to VGG16 and ResNet50v2 but as a result, the accuracy is lower than the other models.

Set up phase

Data set

The data set we used in this project is a modified version of the “CRCHistoPhenotypes” data set published by K. Sirinukunwattana et al [2]. The data set consists of 9896 27x27 colon cell images from 99 patients. The cell is categorized into 4 types: fibroblast, inflammatory, epithelial or others (miscellaneous). The first 66 patients cell histology image is classified into four above mentioned types and stored in the data_labels_mainData.csv file, while the other cell images of the remaining 33 patients do not contain the cell types information and are saved in file "data_labels_extraData.csv". In addition, all of the cell images have a binary label “isCancerous” which points out the tumor necrosis cell is epithelial.

Training detail

Training data augmentation

Before data modelling, data preprocessing is an important step to increase the accuracy of the model and avoid overfitting and underfitting problems. The cell histology image will be flipped and randomly rotated to extend the variations and diversity of the data set, thus, could improve the model accuracy. In addition, the cell image's size of the data set is 27x27 which is not suitable for training with the convolutional neural network from the Keras framework, so we have resized the image to 32x32. Finally, we split the data into three parts training, testing and validation with the ratio of 80/10/10 respectively.

Initialization and training of the network

The deep learning framework we applied in this project is Keras - which is one of the most popular frameworks for constructing neural networks at the moment. When training our model, the loss function is categorical cross-entropy (log loss) and the evaluation metrics are accuracy, f1 score, recall and precision. Our model optimizer is Adam which is an optimized algorithm based on stochastic gradient descent and adaptive estimator, the benefits of the Adam optimizer are computational and memory-efficient which is suitable for models that have to deal with large amounts of data and parameters. Finally, the model is trained with 500 epochs. In addition, to reduce the computation time of convolutional neural networks, we set up our environment to train the model using the power of our GPUs.

Evaluation Metrics

The model will be evaluated based on two criteria: performance of CNNs model and training time. The performance of the model is based on the accuracy score and F1 score. The F1 score represent both of the recall and precision score of the model which illustrate how well model in imbalance data set. There exists a tradeoff between accuracy and training time, the higher training time is, the better performance. However, since this is not a competition, we need a model with low training time but can produce appropriate accuracy.

Result and Analysis

Cell type classification

After perform data preprocessing and finished setting up the model and evaluation framework, we will train the model on our computer with the train and validation data set. The three CNN model that are trained with the given data set are VGG16, ResNet50v2 and MobileNetv2. We also use the result from two research papers as mentioned above for comparison.

Model name	Trainable params	Trainning time (second)	Accuraccy score on test set	F1 score on test set
VGG16	14.714.688	**699**	**82,14%**	**0.7978**
Resnet50v2	23.564.800	1569	81.23%	0.7786
MobileNetV2	2.257.984	1052	77,39%	0.7374
SoftmaxCNN-NEP	899.200	x	71,15%	0.784
RCCnet	1.512.868	x	80,61%	0.789

Table 1: Cell types classification model comparison

From the table above, we can see that the VGG16 neural network has outperform others models in every aspect, it has the shortest training time with highest accuracy score and F1 score. Hence, it is reasonable to conclude that the VGG16 CNN model is the best model for this problem. It is also noticeable that the performance of Resnet50v2 model is almost as good as VGG16, while the MobileNetv2 can not perform as well as the others which showed that the complexity of the model affect the accuracy.

Cancerous cell classification

The cancerous cell classification is a binary classification problem and since there are not exist any prior work about this problem, we just train our three CNN models which are VGG16, ResNet50v2 and MobileNetv2.

Model name	Trainable params	Trainning time (second)	Test set Accuraccy	Test set F1 score
VGG16	14.714.688	**943**	92.36%%	0.9225
Resnet50v2	23,519,360	1569	**93.19%**	**0.9308**
MobileNetV2	2,223,872	1254	92.80%	0.9265

Table 2: Cancerous cell classification model comparision

All of the three model have really good performance, the accuracy score and F1 score of three models do not show huge different, although the ResNet50v2 CNN model has the best performance out of three model. However, in term of training time, VGG16 need lowest time but can still produce good performance, therefore, for the cancerous cell classification, the VGG16 is the best model while still produce

Overall, the VGG16 CNN model have the best performance for cell types classification and cancerous cell classification which illustrated good accuracy score and low training time. However, in the second classification, if we need more accuracy, the ResNet50v2 should be considered and the MobileNetv2 can also be considered if we need compact CNN model. In addition, the accuracy of the cancerous classification model shows better accuracy than the cell type classification which because the latter model is a binary classification compared with multilabel classification in the latter one. Furthermore, the amount of data for the cancerous classification model is higher than the other which also resulted in the different of performance.

Improve the model performance by contrastive learning

From the given data set, we have train three CNN models for cell type classification, and the VGG16 show the best performance with over 80% accuracy and 0.79 F1 score. However, in this project we also have another data set which only show whether it is a cancerous cell type or not and not labeled the cell type. Hence, their exist a technique called contrastive learning to improve the accuracy of the model by utilize these unlabeled data. Ting Chen et al proposed a paper "A Simple Framework for Contrastive Learning of Visual Representations" which present SimCLR framework which is a contrastive self-supervised learning algorithm [5]. The idea of SimCLR is taken two random augmentations of an image encoded and pass it two a fully connected layer to get a representation of the augmented image. Then, the model will try to maximize the similarity between two representations. This technique will give the model the ability to see the similarity with a pair of images without any label. Thus, this method can utilize the unlabeled data in the given data set to increase the accuracy of the model.

Since our team do not have time to construct the entire framework especially the encoder function for model with high complexity such as VGG16, we construct a simple CNN model with 4 convolutional layers and a fully connected layer. Then we train a baseline model with labelled data, a contrastive model with both labeled and unlabeled data and finally a finetuning model which inherit from the pretrained contrastive model.

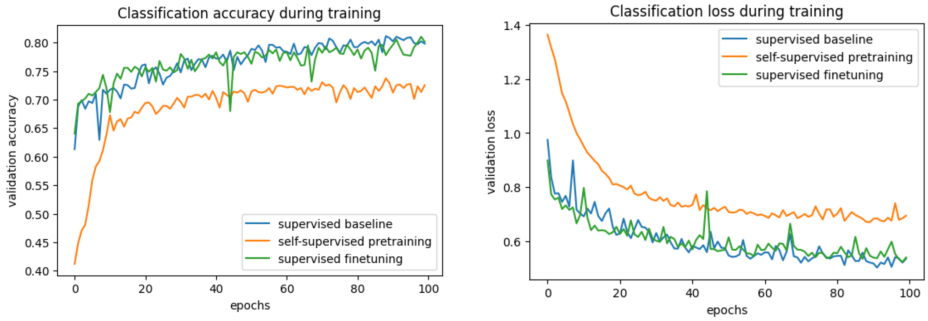

Figure 1: The classification accuracy and loss with respect to epoch

As we can see from the graph, the finetuning model perform better with higher accuraccy and lower loss which illustrated the model with unlabelled data generalize better than baseline model.

Conclusion

In conclusion, several CNN models have succefully constructed with good performance especially in comparision with model in published paper. The VGG16 CNN model show the best performance in both of classification problems, which lead to the conclude that the VGG16 architecture is the best model for colon cancer image classification. In addition, our team also implemented a constructive self-supervise learning algorithm which use the unlabelled data to improve the performance of cell types classification model. However, we only implemented SimCLR methods for an simple CNN

architecture, In the future, out team will try to implement it on VGG16 model to achieve higher accuracy.

Reference

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