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Advancing Glioblastoma Diagnosis through Innovative Deep Learning Image Analysis in Histopathology

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Abstract: It has been the practice of human pathologists to diagnose pathology by examining stained specimens in a slide using a microscope for decades. Recently, several technologies have been developed to digitize the full pathological slide in order to streamline the labor-intensive process of manual labeling and categorization of pathological slides. Machine learning algorithms have been used to examine these digital slices for applications such as diagnosis in many cases. Many digital pathological image analysis algorithms rely on generic image recognition technologies, such as face recognition. A number of specific processing techniques are often required because digital pathological images and tasks differ greatly from facial features. Because of this, a new machine-learning technique has been developed specifically for histopathological images in order to differentiate glioblastoma slices from non-glioblastoma slices, thereby improving pathology diagnosis efficiency and labor intensity.

Keywords: Deep Learning; Machine Learning; Healthcare Innovation; Artificial Intelligence in Pathology.

1. Introduction

Cancer is the world's second leading cause of death, accounting for 9.6 million deaths in 2018, or around one out of every six deaths, according to the World Health Organization [1]. Every year, around 100,000 Malaysians are diagnosed with cancer [2]. When cancer is diagnosed early, it is more likely to react to therapy, increasing the likelihood of survival and lowering treatment expenses. However, around 60% of cancer cases recorded at the time of diagnosis in Malaysia are in the late stages [3]. Cancer has a tremendous economic impact that rises year after year; in 2010, the total yearly economic cost of cancer was estimated at $1.16 trillion [1]. Thus, there is an urgent need to develop a more efficient pathology diagnosis that can screen cancer cases earlier and quicker.

Histopathology is the current gold standard of a cancer diagnosis. Traditionally, a human pathologist makes this diagnosis by physically checking the stained specimens on the sliding glass and then using a microscope to examine each one individually. This method necessitates labor-intensive human labeling and categorization of pathological slides [4-7], increasing the likelihood of missing key cancer signals, particularly in the early stages, and is subject to inter-observer variability.

The research aims to

- Develop a machine-learning approach for diagnosing glioblastoma using histopathology images.
- Validate the developed model with publicly available histopathological image datasets.
- Building an automatic pipeline for the detection of glioblastoma to automate the process.

2. Related Work

Recently, many developments have been deviated to focus on capturing the entire slide of the biopsy tissues/cells with a scanner and then converting the slides to digital copies so that advanced image

processing analysis techniques can be applied to highlight the important features or patterns to assist the pathologists in the diagnosis [8-11 Computerized technologies provide quicker and more repeatable image processing, freeing clinician-scientists and pathologists from tedious and repetitive routine tasks [12-13]. More importantly, it can significantly minimize bias and give accurate disease characterization, although pathology and microscopy are very complex [14].

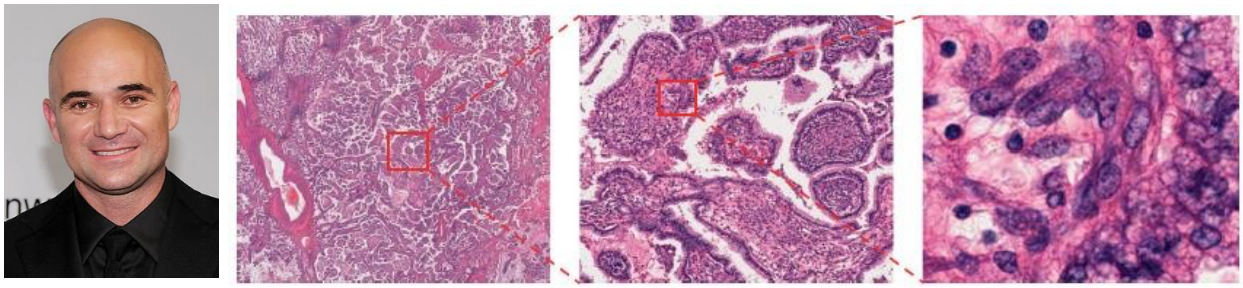

Figure 1. Digital pathological images are very different from facial features and have some unique characteristics.

Digital pathological image analysis frequently relies on generic image identification technologies, such as face recognition, as its foundation. However, digital pathological pictures differ significantly from face features and exhibit several distinct properties, as seen in Figure 1. It is not the best solution to use general facial recognition techniques on these images, and special processing techniques are often required.

The literature has several machine learning algorithms for histopathological image interpretation, such as support vector machine (SVM) and neural network (NN) [5-8]. Typically, these proposed techniques need to perform some pre-processing as shown in Figure.2 before applying the machine learning algorithms.

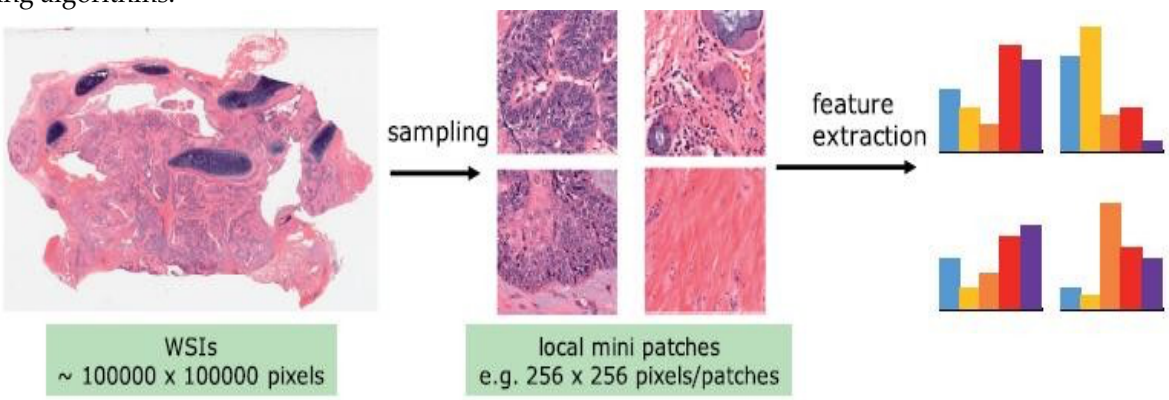

Figure 2. Machine learning steps in digital pathological image analysis.

It usually starts from the whole slice image (WSI) which has high resolution then splits the WSI into various small local patches to detect the cancer regions. The primary purpose of feature extraction is to collect valuable information for training a machine learning algorithm, such as SVM or NN, to distinguish between normal and malignant cells/image patches.

Several local feature extraction approaches, such as gray level co-occurrence matrix (GLCM) and local binary pattern (LBP), have been utilized for histopathology image analysis, however they all suffer from the same difficulty. Computationally expensive search of local features because these methods have to first split the high-resolution WSI into many small image patches for training and cancer detection, and they have high false-positive results and do not generally have high. Geometric Deep Learning can also play its role in developing a robust model [23-24].

In this paper, we aim to mitigate the above-mentioned problem by using deep learning algorithms such as convolutional neural networks [15-16], which can optimize feature selection and classifiers at the same time. The deep learning algorithm has been shown to outperform other traditional methods, which require some form of pre-processing before machine learning algorithms, in various computer vision applications.

3. Methodology

This The most suitable model and architecture of deep machine learning for the histopathological images using the collected data will be selected. In general, deep machine learning has the architecture as shown in Figure 3, where the first part is the feature extraction part in which multiple convolutions and subsampling/pooling processes will be performed and followed by the classification section to decide whether the input image is normal or glioblastoma slice.

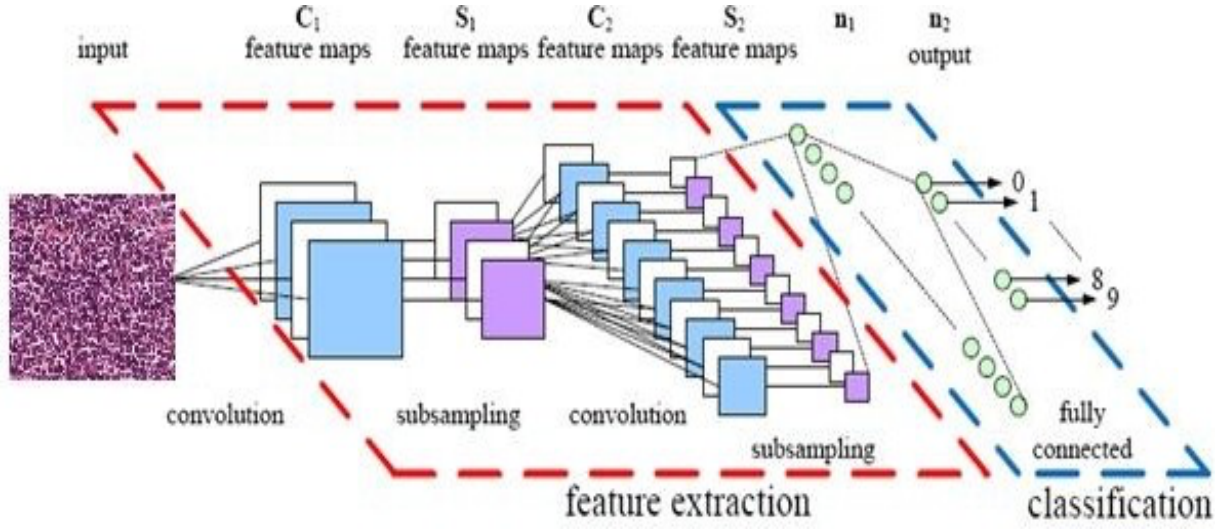

Figure 3. A general proposed framework for the deep machine learning model for histopathological image analysis.

The main part of this work is to train the machine learning method to find the optimal weights, biases, convolution sizes, and layers needed to differentiate a normal and abnormal histopathological image input using the collected data. In the classification part, the obtained features will be flatted and converted to a fully connected layer before using the Sigmoid function to perform the classification. The main difference between conventional machine learning and deep machine learning is the feature extractions are performed separately from the classification for the previous, meaning pre-processing has to be performed first to extract as many useful features from the images before feeding them to the machine learning for training. Since the two processes are separated, it is not easy to extract the most relevant and useful features for the classification. In the deep learning approach, feature extractions and classification are simultaneously trained and optimized, leading to better feature extractions and thus better classification.

Basically, instead of seeing the histopathological image from a single view, we extend it to multiple 'views' using image processing techniques as shown in Figure.4.

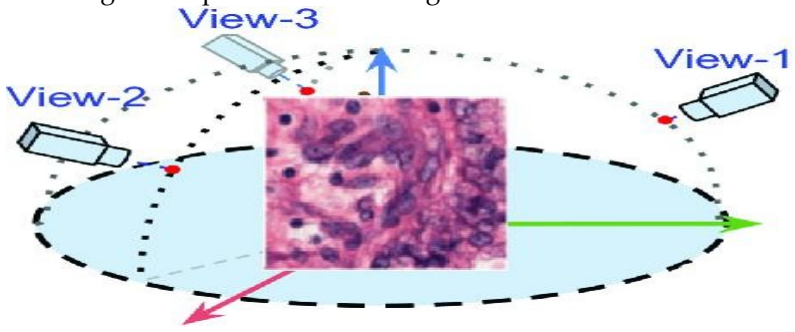

Figure 4. The proposed multi-view approach to improving the deep machine learning algorithm.

The advantage of MVCNN is it allows the designed algorithm to 'see' the images from multiple 'angles' like how a human sees an object. These extra 'views' have contributed to better accuracy for another work we did recently for document classification. It will be interesting to study how the added information can contribute to histopathological image analysis.

Once the deep learning model architecture has been designed, a few publicly available datasets such as TCGA and GTEx will be used to check the performance of the designed model. Cross-validation and

multiple random mixing of the images will be used to test the developed model. The current design is to use 80% of the available data to train the deep learning algorithm and the remaining 20% for validation.

The primary performance criterion considered is accuracy. The accuracy is determined as the ratio of correct predictions to total input samples. Montalto and Edwards [21] compared their proposed deep-learning classification model against three pathologists who assessed the test pictures independently. Their study compared one pathologist to another and found that the agreements varied from 0.52 to 0.78, while the deep-learning model ranged from 0.64 to 0.77, indicating that the model exhibited similar inter-reader agreement with individual pathologists. This study will compare the proposed model to the existing literature in terms of inter-reader agreement and accuracy for 10 particular driver mutations in non-small cell lung cancer, such as STK11, EGFR, SETBP1, TP53, FAT1, and KRAS.

4. Conclusions

The main goal of this work to enhance histological glioblastoma diagnosis with deep machine learning image processing. The proposed deep learning model architecture is built around a fundamental framework that incorporates various stages for feature extraction and classification. Notably, the research presents a multi-view convolutional neural network (MV-CNN) approach that expands on the conventional single-view viewpoint. MV-CNN evaluates histopathology pictures from several perspectives, similar to way people perceive objects, potentially increasing accuracy.

The primary objective was to train the machine learning method to distinguish between normal and abnormal histopathological images using collected data. Unlike conventional machine learning, the deep learning approach integrates feature extraction and classification, optimizing both simultaneously for improved accuracy. The model's architecture involves convolutional layers for feature extraction, followed by a classification section utilizing a sigmoid function.

In conclusion, the research achieved notable advancements in histopathological glioblastoma diagnosis, leveraging the innovative MV-CNN approach. The multi-view strategy demonstrated potential benefits, offering a more comprehensive understanding of histopathological images. The study discussed unexpected findings and potential challenges, paving the way for future research directions and model refinements. The intention is to submit the research outcomes to a distinguished scientific journal or conference, contributing to the evolving landscape of deep learning applications in medical diagnostics.

The proposed model based on deep learning models could be used to detect glioblastoma and non-glioblastoma based on classification results. It could be used to develop an automatic system and may deploy this model in public hospitals for automatic evaluation of patients without the intervention of doctors. This system will be used in the biomedical industry.

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