Classification of Leukaemic Cancer Cells from Normal Cells Using a Convolutional Neural Network

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***Abstract*—Acute Lymphoblastic Leukaemia (ALL) is a type of malignant cancer of the lymphoid line of blood cells. ALL most commonly occurs in children and it has generally good prognosis. It is vital that ALL be detected early and treated promptly. Therefore, a system capable of diagnosing potential patients by analysing images of their blood smear may facilitate in earlier diagnosis. In this report, it is proposed that a Convolutional Neural Network (CNN) be used to classify malignant cells (B-ALL) from normal cells. The method presented in this paper yields mediocre results; the accuracy of the model in question does not exceed 68%.**

I. Introduction

Acute Lymphoblastic Leukaemia (ALL) is a malignancy of blood cells. It is characterised by uncontrollable hyperplasia of lymphoblasts in the bone marrow with little to no cell differentiation. Lymphoblasts then migrate to other organs of the body, through the bloodstream, causing tissue death.

ALL is the most common type of leukaemia in children; comprising 80% of total leukaemia cases. Children with Down syndrome or other genetic disorders are more likely to develop ALL. Adults over the age of 60 may also develop ALL due to chromosomal and molecular discorders.

There are many variants of ALL. All of which have one common characteristic, namely the presence of lymphoblasts in the bone marrow and blood. There are three ALL groups, specifically:

- B-lymphoblastic leukemia/lymphoma without specific genetic characteristics,
- B-lymphoblastic leukemia/lymphoma with specigic genetic disorders and
- T-lymphoblastic leukemia/lymphoma.

[1]

Symptoms of ALL are mainly caused by cytopenias (anaemia, thrombocytopenia, leukopenia and/or neutropenia). Some of these include, but not limited to:

- fever (60%),
- pallor (40%),
- excesive bleeding (50%) due to thrombocytopenia,
- ostalgia (bone pain) (25%),
- lymphadenopathy (50%) and
- hepatosplenomegaly (70%) among others.

[2]

II. Related Work

Researchers have employed a wide variety of machine learning techniques to approach this problem [3], [4], [5], [6]. A common pattern observed in many studies is the use of image processing techniques to enhance important features of input images. In particular, cell segmentaion has a vital role in the appropriate classification of input images [4]. Other techniques, such as normalisation, contrast enhancement and noise removal have been used to improve the overall quality of input images. As for the classification algorithm, K-means clustering has been used widely to classify blood cells, showing a significant accuracy rate of 98% [3]. Convolutional Neural Networks (CNNs) are increasingly getting more popular as a means of classifying images. Researchers have used models such as Mobilenet, ResNet, AlexNet, DenseNet and VGG16 with accuracy rates reaching up to 99.39% [4], [5].

III. Proposed Method

In this report, a CNN is used to extract features from the C-NMC dataset [7], [8], [9], [10], [11], [12] and perform classification. The dataset contains **15.135** images from **118** patients. There are two classes: normal and leukaemia blast. The images have already been processed by the authors of the dataset. The authors performed cell segmentation and noise reduction from the microscopic images using their "own in-house method of stain color normalisation" [7].

Further image processing is conducted to input data. While the initial images use the RGB colour profile, the processed images use the grayscale profile instead. Additionally, the images are resize to 128 by 128 pixels. By reducing the amount of data needed to be processed, the model becomes more performant. This is crucial as the hardware resources used to perform the experiments were limited. Next, histogram equalisation is used to increase the contrast of the images in order to enhance its features. Finally, the image in converted into an array and then normalised to further reduce numeric complexity.

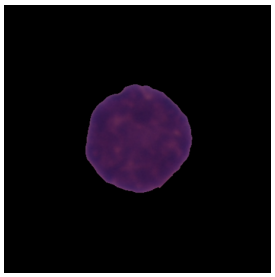

Fig. 1: Dataset image: UID_H12_24_5_hem.bmp

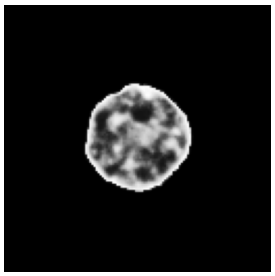

Fig. 2: Processed image used by model

Only a part of the dataset is used in this project. Specifically,

- 4.800 images are used for training the model
- 1.200 images are used as validation set and
- 1.200 images are used for testing the model.

The images in all three sets are arbitrarily chosen. The images used for training are located in the training subdirectory. The images used for validating and testing are located in the validation subdirectory. Even though the dataset does have a set of images for the purpose of testing, the class labels are not available publicly [7]. For this reason, the author decided to pull additional images from the validation subdirectory to populate the testing set.

The model consist of 14 layers. Specifically:

1) a two-dimentional convolution layer which has 32 filters, a kernel size of 3 by 3, input size equal to 128x128x1 and uses ReLU as its activator function,
2) a batch normalisation layer,
3) a two-dimentional max pooling layer,
4) a dropout layer,
5) a two-dimentional convolution layer which has 64 filters, a kernel size of 3 by 3 and uses ReLU as its activator function,
6) a batch normalisation layer,
7) a two-dimentional max pooling layer,
8) a dropout layer,
9) a flattening layer,
10) a layer of 128 neurons,
11) a batch normalisation layer,
12) a layer of 64 neurons
13) a batch normalisation layer and
14) a single-neuron layer as the output layer.

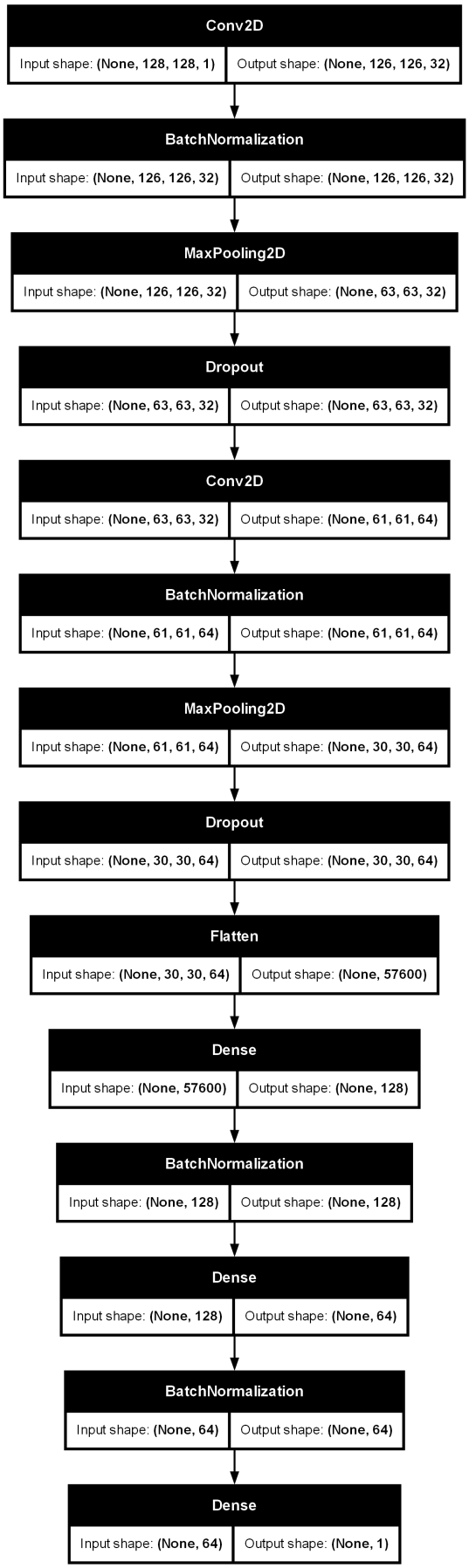

Fig. 3: Plot of model

The chosen batch size is 40 and the epoch number is 20.

Validation loss was monitored in order to ensure it remained minimal. Training is stopped when validation loss has not improved after 8 epochs. In addition, model checkpoints are used to keep the best-performing model at the end of the training. Once the training is complete, the weights from the best-performing model are saved for later use. Finally, binary cross entropy is used as the loss function.

IV. Experimental Result

The experiments conducted on Python Tensorflow showed suboptimal accuracy. In particular, the model the model predicted correctly 808 out of 1200 presented case images. Thus, making it only about 67,3% accurate.

Two common metrics used to measure a model's ability to provide correct results are sensitivity (TPR):

$$\mathrm{TPR} = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FN}} \tag{1}$$

which is the percentange of positive cases predicted as positive and specificity (TNR):

$$\mathrm{TNR} = \frac{\mathrm{TN}}{\mathrm{TN} + \mathrm{FP}} \tag{2}$$

which is the percentange of negative cases predicted as negative [13].

With (1) we get $\mathrm{TPR} \approx 0,664$ or about 66,4%.

With (2) we get $\mathrm{TNR} \approx 0,841$ or about 84,1%.

The numbers used to calculate the aforementioned metrics are given by the following confusion matrix:

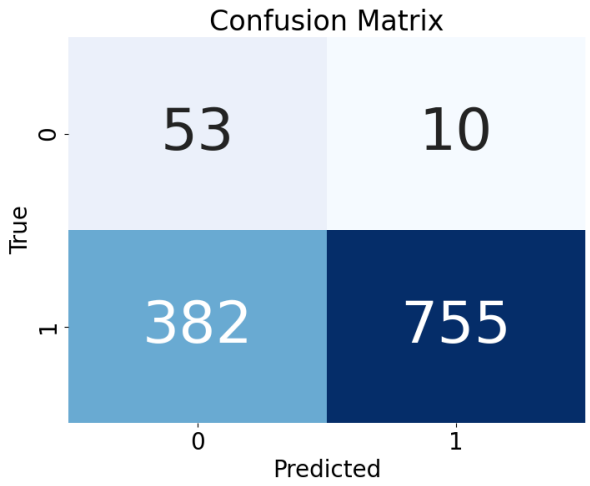

Fig. 4: Confusion matrix

Below is the accuracy and loss of the model during the training process:

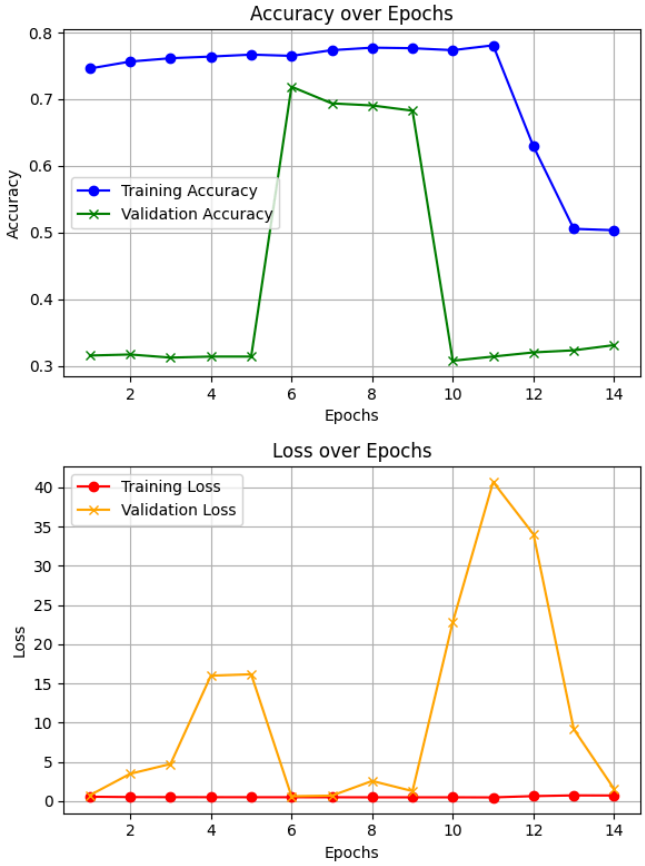

Fig. 5: Accuracy, loss, validation accuracy and validation loss using the provided sample weights

The model showed the lowest validation loss in epoch six and therefore the weights of that epoch were saved for later use.

V. Conclusions

The model presented in this paper is inadequate in diagnosing leukaemia patients correctly. This can be inferred from its mediocre accuracy of 67,3%. Even though the model is able to detect negative cases with relatively high precision ($\mathrm{TNR} \approx 0,841$) it is substantially worse in detecting positive cases ($\mathrm{TPR} \approx 0,664$). This is crucial as missing such a diagnosis may have devastating consequences on a patient's outcome. Therefore, it is unwise to use this model for diagnosing leukaemia patients in its current state.

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