RESEARCH PAPER

Comparative Analysis of Acute Lymphoblastic Leukemia Detection and Classification Using Deep Learning Techniques

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ABSTRACT

Leukemia (blood cancer) begins in the bone marrow and causes the formation of a large number of abnormal cells. The most common types of leukemia known are Acute lymphoblastic leukemia (ALL), Acute myeloid leukemia (AML), Chronic lymphocytic leukemia (CLL) and Chronic myeloid leukemia (CML). The objective of this research is to detect the presence of Acute lymphoblastic leukemia (ALL) and classify it into Early Pre-B, Pre-B and Pro-B categories. The performance of Deep CNN, Tuned CNN and Hypercomplex-Valued CNN for the classification are compared and the results are inferred, thus automating the detection and classification process. The traditional method used by doctors to detect ALL is tedious and time consuming. It consists of several methods such as blood testing, aspiration and biopsy to the bone marrow, image testing using CT scanning and MRI. The proposed approach uses image processing techniques to detect irregular blood cells in the microscopic images of the blood.

Keywords: Multiclass Classification, Tuned CNN, Hypercomplex Valued CNN

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1.INTRODUCTION

Leukemia is a major blood cancer characterized by defective and unrestrained leukocyte multiplication and growth. This anomaly impacts the blood and bone marrow and limits the blood's capacity to produce platelets and erythrocytes. The health care system is experiencing an increasing prevalence of acute lymphoblastic leukemia (ALL) each year, with the number of cases of ALL worldwide increasing from 49.1 thousand in 1990 to 64.2 thousand in 2017. Preliminary and rapid diagnosis of ALL contributes to starting the process of treatment and, as a result, patient survival. A conventional method for ALL diagnosis is the manual microscopic examination of the peripheral blood smear (PBS) by the diagnostic laboratory user. However, the sheer volume of PBS samples is a difficulty to laboratories and can result in incorrect diagnosis. ALL is prone to error due to the time-consuming nature of PBS surveys under the microscope, the need for highly experienced laboratory staff, and the fatigue daily experienced by them.Today, computer technologies such as artificial intelligence (AI) have received attention from researchers from different branches of science in diagnosing blood diseases, especially ALL. These technologies have produced astounding outcomes in ALL diagnosis and classification when used in the form of different algorithms.

In this research, convolutional neural network (CNN) is proposed for classifying microscopic blood cell images. To achieve better results, it is necessary to tune CNN hyperparameters which is an NP-hard optimization problem.In this paper, the Pytorch Gradient Calculation framework is adjusted for tuning some of the CNN hyperparameters. On the other hand, Hypercomplex- Valued CNN (HvCNN), based on Clifford algebra processing of HSV-encoded images is used to classify ALL. The HvCNN is known to have a much simpler architecture with significantly fewer parameters than real valued CNN. Hence performance of the two techniques are compared with traditional DL CNN and results are inferred.

2.LITERATURE SURVEY

Amit Negi et. al [1] proposed computer-aided diagnosis systems, including enhancement, augmentation, ensemble, feature extraction, and the usage of CNN-based methods. Two classes (Healthy/infected) are discretized. Classification models like VGG16, VGG19, XCEPTION, and Mobile-Net are used with an accuracy of 96% for vgg16, 94% for VGG19, 92% for XCEPTION, and 96% for Mobile-Net. It was concluded that Mobile-Net performed better than the other three models.All the models are utilized by using ensemble method with highest accuracy of 98 %.

Acharya V et al. [2] proposed a unique approach to segment the cytoplasm and nucleus of white blood cells. The several supervised classifiers are evaluated, and the one with the highest accuracy is used for the classification. A model is developed to extract the features and train the model. The outcome demonstrates how acute lymphoblastic leukaemia is divided into its three distinct types, namely ALL-L1, ALL-L2, and ALL-L3. The model can distinguish between a peripheral blood smear that is normal and one that is abnormal. Overall accuracy for the suggested methodology was 98.6 %.

Eva Tuba et. al [3] put forth a simple bare bones firework approach for fine-tuning a selection of CNN hyperparameters and on a common benchmark dataset for the detection of acute lymphoblastic leukaemia, the proposed technique was evaluated. It was compared to CNN without hyperparameter tuning and the optimised SVM method, and it outperformed the other two techniques in terms of accuracy.

Guilherme Vieira et al.[4] combined real-valued convolutional networks with eight hypercomplex-valued convolutional neural networks (HvCNNs) to perform the classification of ALL. The outcomes demonstrated that HvCNNs outperform the real-valued model, displaying superior accuracy with a significantly fewer number of parameters.

Jesse C. Sealand et. al [5] proposed a study that utilised four machine learning gradient-boosting algorithms and five tree- based models to find patterns in ALL patients who experience relapses and use those patterns to predict relapses in advance. Marcos Eduardo Valle et al. [6] extended the bipolar RCNNs to handle hypercomplex-valued input. The stability of the novel hypercomplex-valued RCNNs employing synchronous and asynchronous update modes is then addressed after the mathematical foundation for a large class of hypercomplex-valued RCNNs is presented. The computational tests validate the potential use of hypercomplex-valued RCNNs as associative memories aimed at the storage and retrieval of grayscale images.

Mustafa Ghaderzadeh et al. [8] utilised a model based on deep convolutional neural networks to distinguish ALL instances from hematogone cases and then identify ALL subtypes. Ten well-known CNN architectures (EfficientNet, MobileNetV3, VGG-19, Xception, InceptionV3, ResNet50V2, VGG-16, NASNetLarge, InceptionResNetV2, and DenseNet201) were used for feature extraction of various data classes after colour thresholding-based segmentation in the HSV colour space by designing a two-channel network. Based on DenseNet201, a model was created and put forth that performed the best.

Pradeep Kumar Das et. Al [9] used a deep CNN-based framework for efficient detection and classification of ALL and used a method in which a novel probability based weight factor is suggested, which has a significant role in efficiently hybridizing MobilenetV2 and ResNet18 while preserving the benefits of both approaches.

Sarmad Shafique et al [10] employed deep convolutional neural networks for the automated detection of acute lymphoblastic leukaemia and the classification of its subtypes into 4 classes, namely L1, L2, L3, and Normal.Pre-trained AlexNet had been used, which was then adjusted for the dataset.The pretrained network's last layers were swapped out for new layers that categorised the input images into one of four groups.

Sarmad Shafique et al. [11] analysed microscopic blood picture data and devised an automated method to identify acute lymphoblastic leukaemia. White blood cells, red blood cells, and platelets were separated out of the image's various cell types first. After that, white blood cells and lymphocytes were divided.These lymphocytes' shape and colour properties were then retrieved, and the SVM classifier was used to classify the cells into normal and blast categories.

Srikanth Tammina [12] classified images using one of the pre-trained models, VGG-16 with Deep Convolutional Neural Network. In order to transfer low-level characteristics, such as edges, corners, and rotation, and learn new level features related to the goal problem, which is to categorise the images, the pretrained VGG-16 model is utilised as leverage.

Subhash Rajpurohit et al. [13] proposed a few automated systems for detection of Acute Lymphoblastic Leukemia (ALL) which entails extracting features from blood images using MATLAB and employing different classifiers to get results. The proposed system is further improving the classification accuracy. It uses openCV and skimage for image processing to extract relevant features from blood image and not just sheer number of features and further classification is carried out using various classifiers: CNN, FNN, SVM and KNN of which CNN gives the highest accuracy of 98.33%. The accuracies obtained by other classifiers: FNN, SVM, and KNN are 95.40%, 91.40% and 93.30% respectively.

Vinay Ayyappan et. al [14] developed a set of ML classifiers, including convolutional neural networks, to discern healthy B cells from lymphoblasts and classify stages of B cell acute lymphoblastic leukemia. The average dry mass and volume of normal B cells are lower than those of cancerous cells and these morphologic parameters increase further alongside disease progression. The relaxed training requirements of a ML approach are conducive to the classification of cell type, with minimal space, training time, and memory requirements.

Zhencun Jiang et al. [15] introduced the ViT-CNN ensemble model to aid in the diagnosis of acute lymphoblastic leukaemia by identifying cancer cells images and normal cells images. The vision transformer and convolutional neural network (CNN) models are combined to create the ViT-CNN ensemble model.The findings demonstrated that the model suggested in this article was more accurate than other models and had a balanced capacity for classification.

Zhou Min et al. [16] proposed an end-to-end leukaemia detection system was by integrating new deep learning algorithms and utilising raw photos without any pre-processing. By identifying and excluding uncountable and smashed cells, then classifying and counting the remaining cells to arrive at a diagnosis, the algorithm cleverly mimicked the workflow of a haematologist. The accuracy, precision, and F1 score of CNN's classification of WBCs were 82.93%, 86.07%, and 82.02%, respectively. Additionally, the performance in identifying acute lymphoid leukaemia was 89% accurate, 86% sensitive, and 95% specific.

3.Dataset Description

The images of the dataset under consideration were prepared in the bone marrow laboratory of Taleqani Hospital (Tehran, Iran). This dataset [7] consisted of 3256 PBS images from 89 patients suspected of ALL, whose blood samples were prepared and stained by skillful laboratory staff. This dataset is divided into two classes of benign and malignant. The former comprises hematogones and the latter is the ALL group with three subtypes of malignant lymphoblasts: Early Pre-B, Pre-B, and Pro-B ALL. All the images were taken by using a Zeiss camera in a microscope with a 100x magnification and saved as JPG files. A specialist using the flow cytometry tool made the definitive determination of the types and subtypes of these cells. After color thresholding-based segmentation in the HSV color space segmented images are also provided.

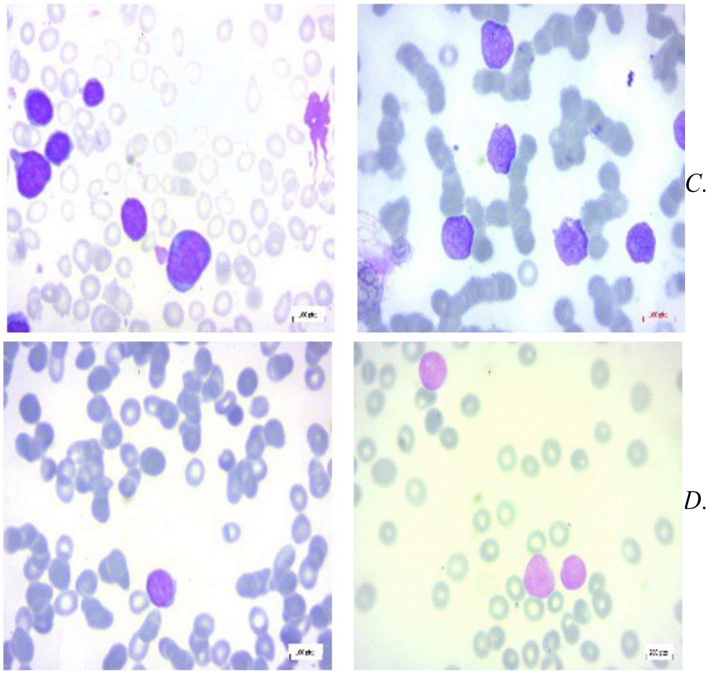


Figure 1: Subtypes of Acute Lymphoblastic Leukemia

A. *Architecture*

B. 4. Proposed System

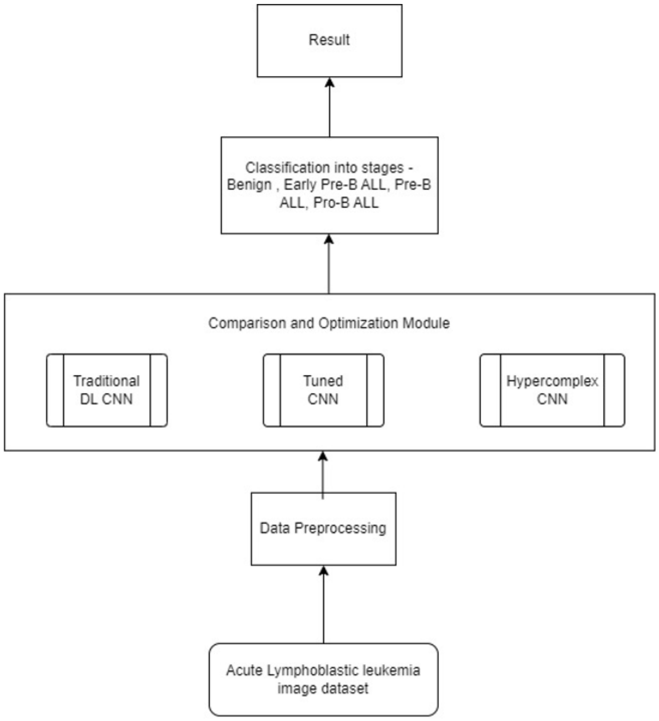


Figure 2: The architectural model of the system

C. *Traditional Deep Learning CNN Model*

Convolutional, pooling, and fully connected layers constitute the layers that make up the conventional deep learning Convolutional Neural Network (CNN) model. Learning hierarchical representations of the blood smear images is the aim of these layers. This model uses transfer learning using vgg16 and bottlenck features are obtained to classify the images into the stages.

D. *Tuned CNN Model*

Tuned CNNs are CNN models that have several hyperparameters adjusted specifically for a given task or dataset. Hyper- parameters are configurations that the user selects rather than learning through training. A pre-trained VGG-16 model serves as the transfer learning model. When the transfer learning model is loaded, the initial classifier layers are swapped out for new ones for the improved model, and the model weights are locked to prevent further training. During training, only the weights of the newest neural network layers are modified. In order to facilitate the exploration, the model parameters are defined as a set. Finally, after fine-tuning the hyperparameters, the pictures are classified into one of the four stages using the CNN model with the best hyperparameter values.

E. *Hypercomplex-valued CNN Model*

Eight hypercomplex-valued convolutional neural networks (HvCNNs) are used for the categorization. Hv-CNNs can be used to analyze the images to classify ALL. Hypercomplex numbers provide a natural representation of orientation and rotation information, which can be useful for analyzing the structural and geometric features of blood cells in images. The input image would be represented as a hypercomplex-valued data tensor, and the convolutional layer performs convolution operations on the input data using hypercomplex-valued filters. The features extracted by the convolutional layer is then processed by fully connected layers, which will make the final classification decisions based on the learned features. The hypercomplex-valued model has a layer layout of convolutional layers followed by a max pooling layer with kernels, where each channel of the hypercomplex-valued corresponds to four real-valued feature channels, so that it uses much fewer filters per convolution layer. A quaternion numerical network constructed using quaternion algebra is used. Quaternions are the four-dimensional extension of complex numbers.

A[-1, -1], A[-1, +1], A[+1, -1], and A[+1, +1]

B[-1, -1], B[-1, +1], B[+1, -1], B[+1, +1]

There are a total of eight 4-dimensional hypercomplex algebras. They are all associative, four anti-commutative and the rest commutative.

	$\boldsymbol{i}$	$\boldsymbol{j}$	$\boldsymbol{k}$
$\boldsymbol{i}$	s_{11}	$s_{12}\boldsymbol{k}$	$s_{13}\boldsymbol{j}$
$\boldsymbol{j}$	$s_{21}\boldsymbol{k}$	s_{22}	$s_{23}\boldsymbol{i}$
$\boldsymbol{k}$	$s_{31}\boldsymbol{j}$	$s_{32}\boldsymbol{i}$	s_{33}

Table 1: The multiplication table of the eight algebras

I. RESULTS

A. *Traditional Deep Learning CNN*

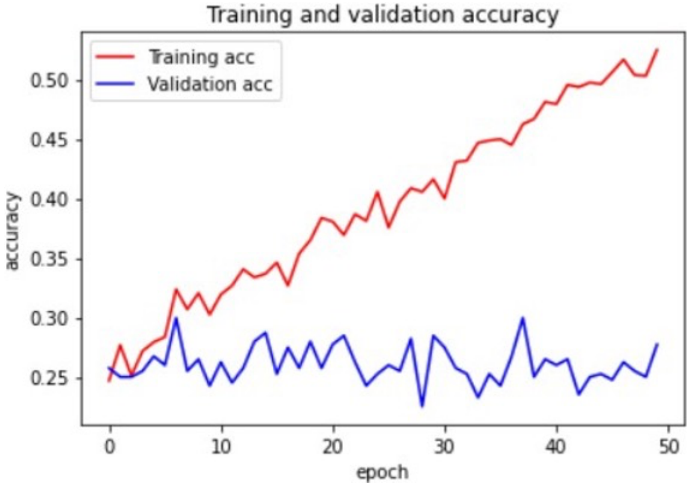


Figure 6: Graph depicting training and validation accuracy

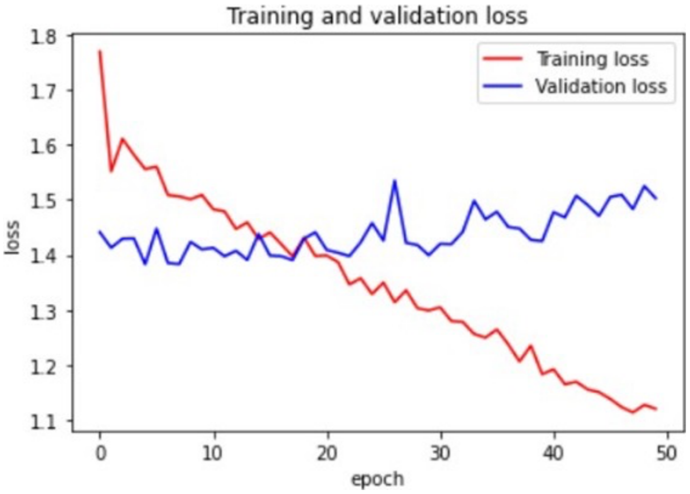
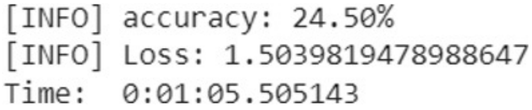


Figure 7: Graph depicting training and validation loss



```
[INFO] accuracy: 24.50%
[INFO] Loss: 1.5039819478988647
Time:  0:01:05.505143
```

Figure 8: Results for the traditional CNN model

MRI images slides at different angles are repetitive and distorted.Accuracy and performance of the model can be considerably increased with improved preprocessing techniques and hyperparameters. At present an accuracy of 24.5% is achieved.

B. *Tuned CNN Model*

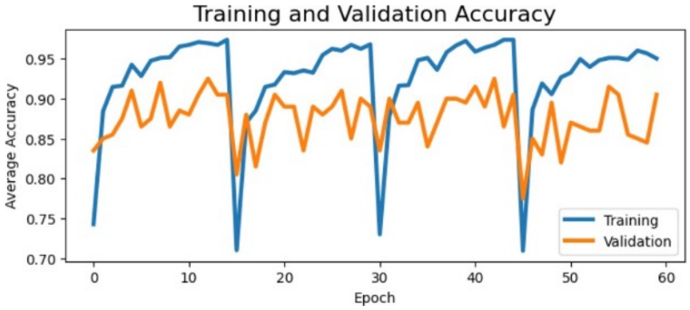
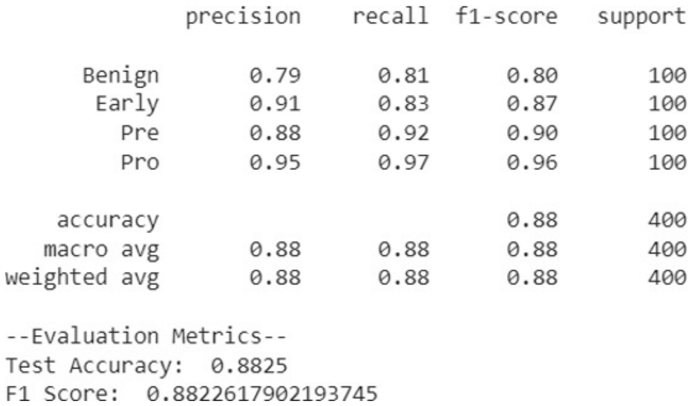


Figure 9: Graph depicting training and validation accuracy



```
             precision    recall  f1-score   support

      Benign       0.79      0.81      0.80       100
       Early       0.91      0.83      0.87       100
         Pre       0.88      0.92      0.90       100
         Pro       0.95      0.97      0.96       100

    accuracy                           0.88       400
   macro avg       0.88      0.88      0.88       400
weighted avg       0.88      0.88      0.88       400

--Evaluation Metrics--
Test Accuracy:  0.8825
F1 Score:  0.8822617902193745
```

Figure 10: Graph depicting training and validation losses

Figure 11: Classification report for the tuned CNN model

Tuning of cnn proved to be efficient. Increased number of epochs and different hyperparameter values will possibly increase the accuracy to great extent. Higher computation power is desirable. At present an accuracy of 88 % is obtained for the best hyperparameter set of droupout rate = 0.4, learning rate = 0.001, batch size = 25 and hidden units = 256.

C. Hypercomplex Valued CNN

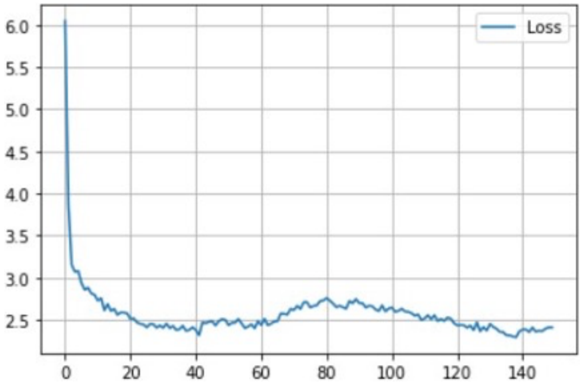


Figure 12: Graph depicting model loss

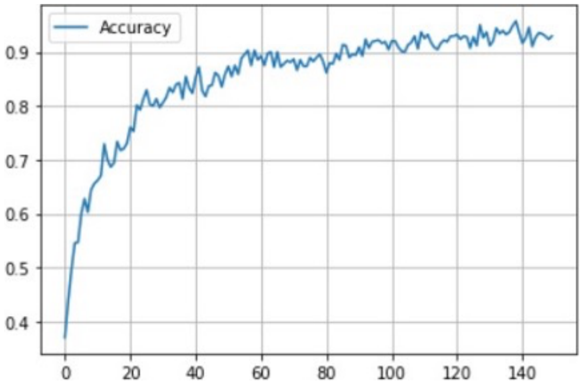


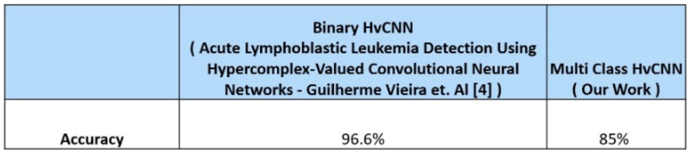
Figure 13: Graph depicting model accuracy

```
              precision    recall  f1-score   support

      Benign       0.93      0.75      0.83        36
       Early       0.79      0.87      0.83        30
         Pre       0.87      0.84      0.85        31
         Pro       0.82      1.00      0.90        23

    accuracy                           0.85       120
   macro avg       0.85      0.86      0.85       120
weighted avg       0.86      0.85      0.85       120
```

Figure 14: Classification report for the HvCNN model

HvCNN provided an accuracy of 85% , from this we infer that the tuned CNN gives a higher accuracy rate than the HvCNN.

D. Comparing Results with Previous Work



	Binary HvCNN (Acute Lymphoblastic Leukemia Detection Using Hypercomplex-Valued Convolutional Neural Networks - Guilherme Vieira et. Al [4])	Multi Class HvCNN (Our Work)
Accuracy	96.6%	85%

Figure 15: Comparing the results of two works

Acute Lymphoblastic Leukemia Detection Using Hypercomplex-Valued Convolutional Neural Networks - Guilherme Vieira et. Al [4] used the co-quaternion HvCNN to classify the dataset as lymphoblasts or healthy cells and achieved an accuracy of 96.6% for the same. Our work has extended the co-quaternion HvCNN to classify the dataset into Benign, Early Pre-B, Pre-B and Pro-B categories and achieved an accuracy of 85% for the same.

CONLUSION

In this work , we have explored various CNN models to classify Acute Lymphoblastic Leukemia into it's stages based on peripheral blood smear images. The traditional deep learning CNN model achieved an accuracy of 24.5 % , the tuned CNN model achieved an accuracy of 88 % and the hypercomplex-valued cnn achieved an accuracy of 85 %.We find that the tuned CNN is the best optimized model to classify ALL into it's stages. To conclude, we have discussed, in this report, the detailed solution design for classifying Acute Lymphoblastic Leukemia into it's stages using state-of-the-art CNN algorithm, the hyperparameter tuned CNN. We also compared the performance of Hyperparameter Tuned CNN with HvCNN.

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