Automated Diagnosis of Lymphoma with Digital Pathology Images Using Deep Learning

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UTHealth

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Human Neuron

CNN

Figure 2. A neural network is a computer system modeled on human brain

Introduction

Due to subtle differences in histologic findings between various types of lymphoma, initial microscopic assessment often presents a challenge to pathologists. Automated diagnosis applying machine learning algorithms to digital images would be helpful to assist pathologists in daily screening. Recent studies have shown promising results in using Deep Learning to detect malignancy in whole slide imaging, however they were limited to just predicting positive or negative findings for a specific neoplasm.

Objective

We attempted to use Deep Learning to build a lymphoma diagnostic model for four diagnostic categories.

Methods

Deep Learning using a convolutional neural network (CNN) algorithm was used to build a lymphoma diagnostic model for four diagnostic categories: (1) benign lymph node, (2) diffuse large B-cell lymphoma, (3) Burkitt lymphoma, and (4) small lymphocytic lymphoma. The coding language used for our algorithm was Python. We obtained digital whole-slide images of Hematoxylin and Eosin stained slides of 128 cases including 32 cases for each diagnostic category. Four sets of 5 representative images, 40 x 40 pixels in dimension, were taken for each case. A total of 2,560 images were obtained from which 1,856 were used for training, 464 for validation, and 240 for testing. For each test set of 5 images, the predicted diagnosis was combined from prediction of five images (majority voting).

Results

The test results showed diagnostic accuracy of 95% for image-by-image prediction and at 100% for set-by-set prediction.

Table 1. Accuracy in predicting diagnoses using one single image at a time

		Observed Diagnosis			
		BENIGN	DLBCL	BL	SLL
Predicted Diagnosis	BENIGN	56	0	0	4
	DLBCL	0	60	0	4
	BL	4	0	60	0
	SLL	0	0	0	52

Table 2. Accuracy in predicting diagnoses for sets of 5 images using majority voting

		Observed Diagnosis			
		BENIGN	DLBCL	BL	SLL
Predicted Diagnosis	BENIGN	12	0	0	0
	DLBCL	0	12	0	0
	BL	0	0	12	0
	SLL	0	0	0	12

Conclusion

Our study expanded on prior studies and included more tumor types achieving diagnostic accuracies nearing 100%. The inclusiveness and accuracy of our model provides pathologists a reliable and practical tool in their daily practice. This preliminary study provides proof of concept for incorporating automated lymphoma diagnostic screening into future pathology workflows to enhance productivity. Due to the generic nature of the CNN algorithm, the results from this study are readily extensible to histopathology images of other malignancies.

Figure 1. Processing pipeline of a convolutional neural network for the detection of visual categories in images

Notes for Fig. 1:
-The convolutional layers (C) perform 'feature extraction' consecutively from the image patch to higher level features.
-The max pooling layers (S) reduce image size by subsampling
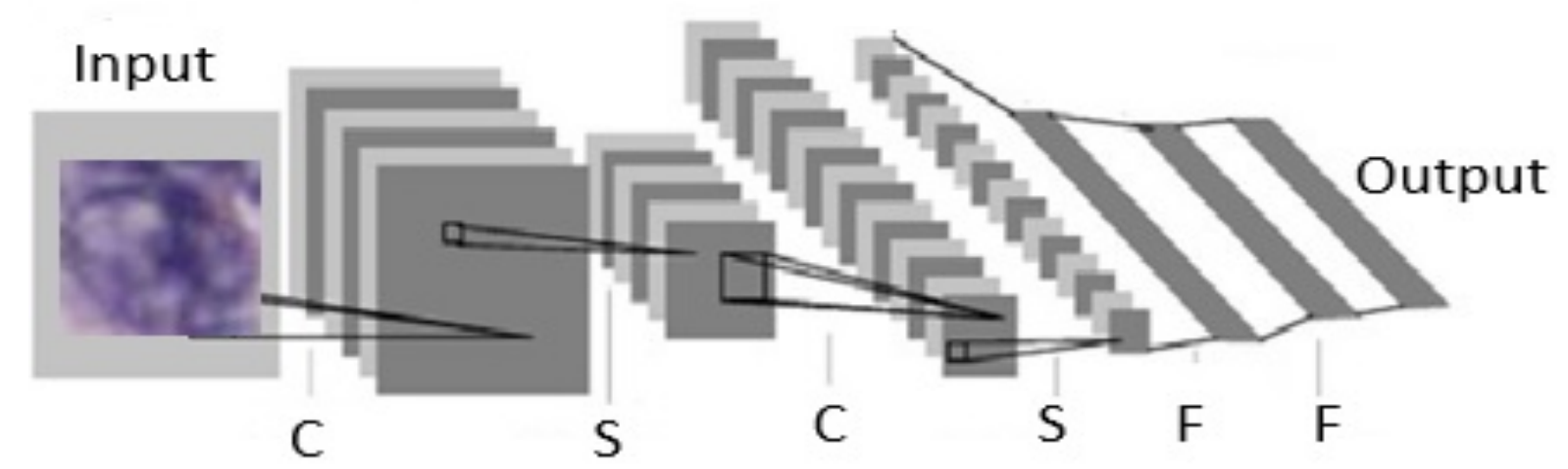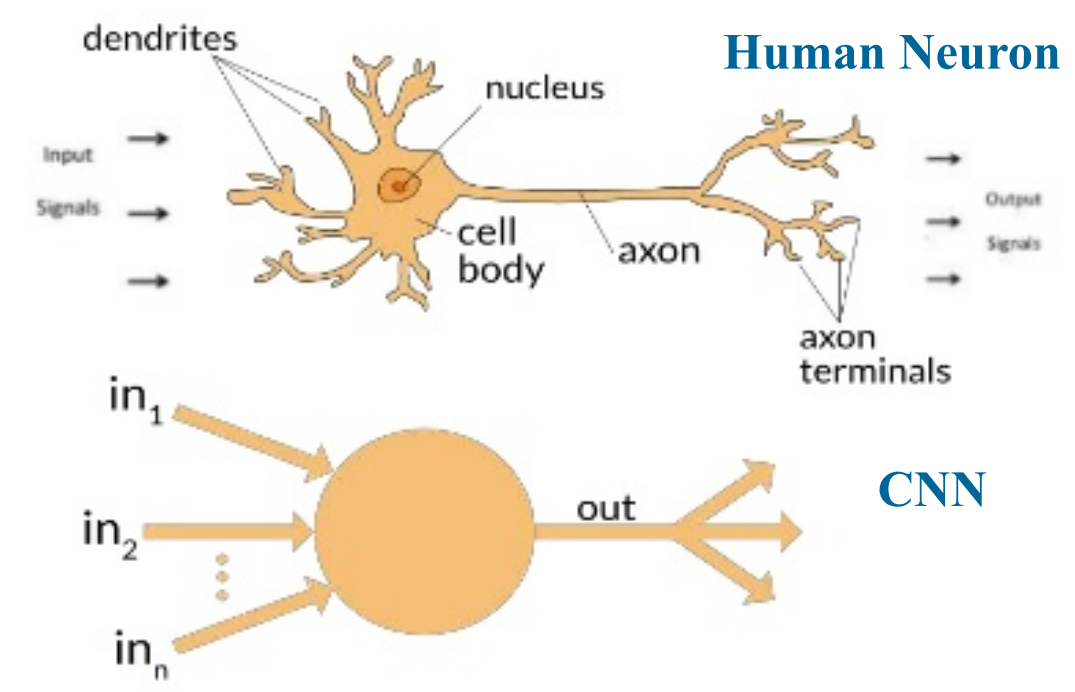-The last fully-connected layers (F) provide prediction based on the given features.

References

Shaimaa Al-Janabi, Andre Huisman & Paul J Van Diest. Digital pathology: current status and future perspectives. Histopathology 2012, 61, 1–9.