Computer-Aided Diagnosis using Class-Weighted Deep Neural Network



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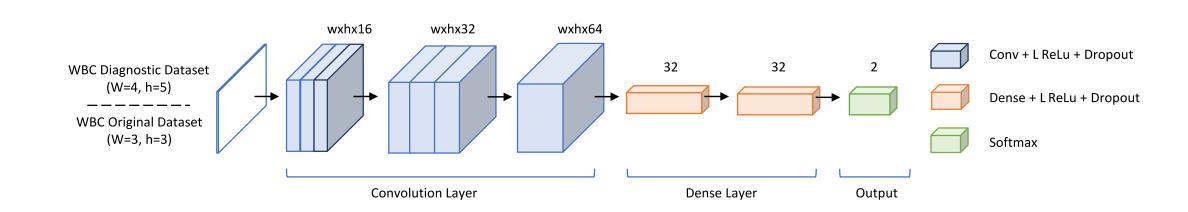


Abstract

Computer-aided diagnosis has become a major focal point of Artificial Intelligence. Interpreting medical images is often time-consuming and requires significant human expertise. Hence, there is an increasing demand to use machine learning techniques to correctly classify different medical images captured by mammography, CT scans, and MRI among others. This paper presents a deep learning method for computer-aided differential diagnosis of benign and malignant breast cancer tumors by avoiding potential errors caused by poor feature selection as well as class imbalances in the dataset. We design, develop and test an end-toend convolutional neural network architecture for two different breast cancer datasets of fine needle aspiration biopsy samples, and show that our network outperforms the state of the art. Furthermore, we have introduced a loss coefficient which can be adjusted to fine-tune the performance of our network. The proposed method can be used to support oncologists in the detection of breast cancer with high confidence.

Proposed Method

We propose a CADx system based on a deep CNN to classify malignant and benign breast tumors, outperforming the state of the art. We propose a class-weighted loss function for our model which provides the ability to tune an additional hyper-parameter with the goal of removing the diagnostic bias caused by data imbalance. Furthermore, our model performs with a very low standard deviation compared to previous studies, which implies a consistent and reliable diagnosis.



Our Proposed architecture is illustrated in the figure above. After reshaping the WBC Diagnostic data to a 5×6×1 matrix, and WBC Original data to a 3×3×1 matrix, we use 7 layers of convolution and 2 layers of fully connected layers followed by a Sigmoid-based classifier.

Model Training

To tackle the challenge of class imbalance, we used a custom class-weighted loss function to train our model, defined below:

Loss =
$$-\sum_{i=1}^{N} [\lambda y_i \log P(y_i|I_i) + (1-\lambda)(1-y_i) \log(1-P(y_i|I_i))]$$

Result

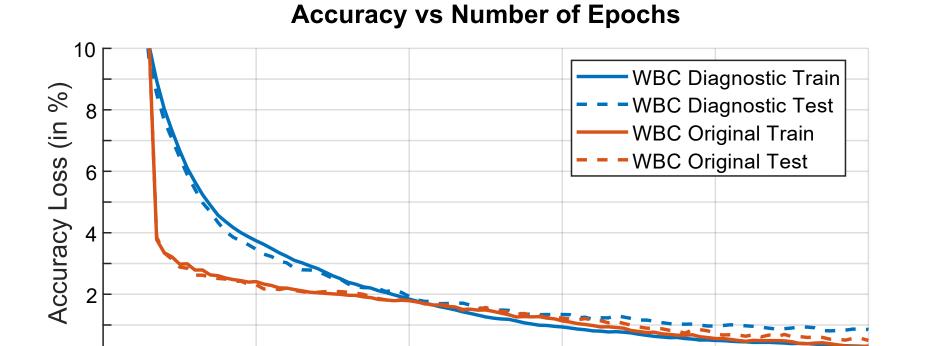


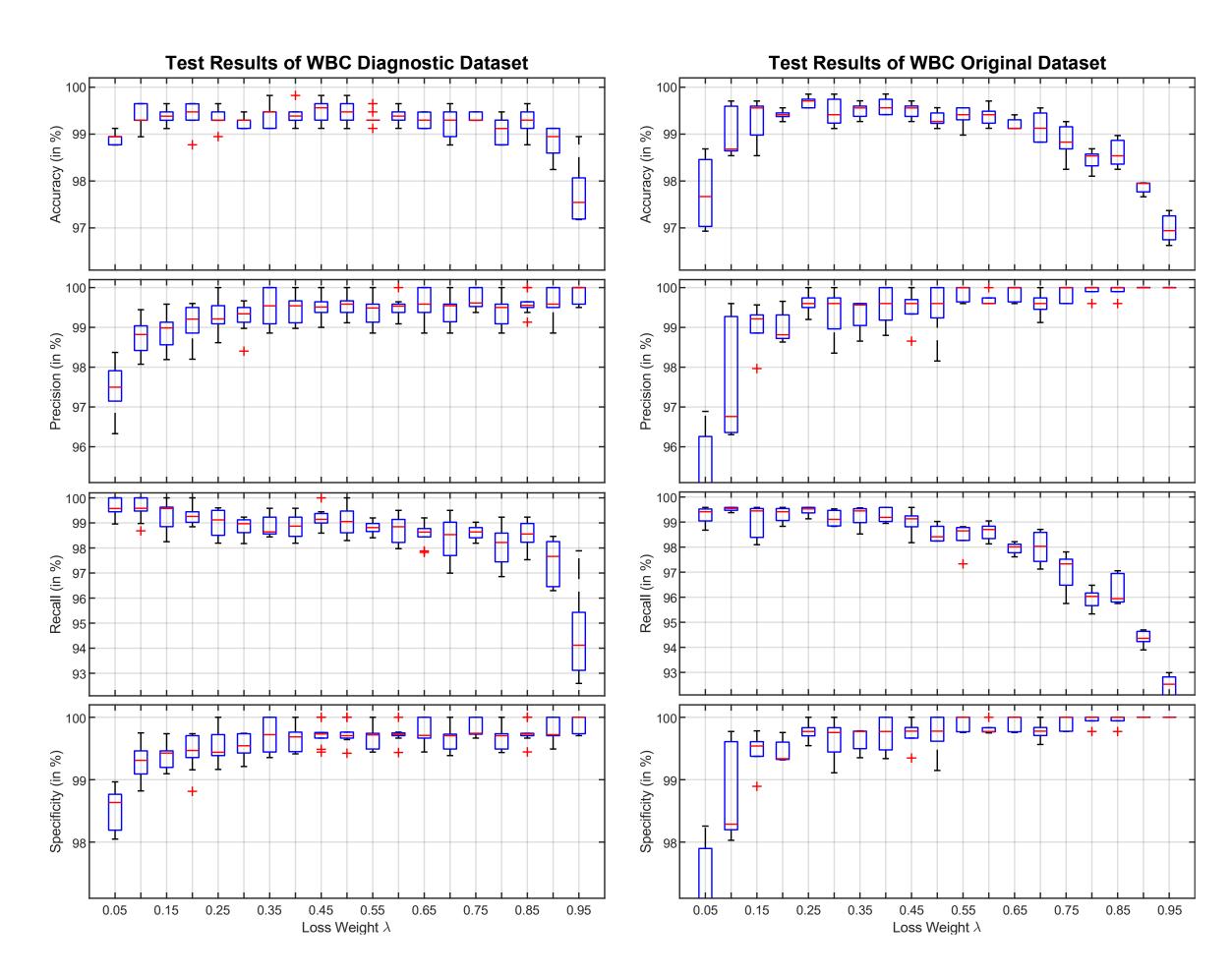
TABLE I
PERFORMANCE COMPARISON OF OUR METHOD VS. OTHER STUDIES ON THE WBC DIAGNOSTIC DATASET.

Proposed by	Algorithm	Accuracy
Ref. [12]	GP evolved ANN	98.0%
Ref. [10]	Random Forest	94.7%
	Random Forest (PCA)	95.3%
Ref. [13]	Probabilistic Neural Network	96.2%
Ref. [8]	Neural Network (Softmax)	92.40%
	Neural Network (ReLu)	90.64%
Ref. [3]	Grated Recurrent Unit - SVM	93.75%
	Linear Regression	96.09%
	Multi Layer Perceptron	99.04%
	Softmax Regression	97.65%
	Support Vector Machine	96.09%
Ref. [11]	DTC - Principal Component Analysis	96.2%
Our Method	CNN with Modifiable Loss Function	99.52%

TABLE II
PERFORMANCE COMPARISON OF OUR METHOD VS. OTHER STUDIES ON THE WBC ORIGINAL DATASET.

Proposed by	Algorithm	Accuracy
Ref. [4]	Multilayer Perceptron	96.85%
	Support Vector Machine	94.99%
Ref. [14]	Random Forest	97.0%
Ref. [11]	DTC - Symmetric Attribute Selection	94.72%
Our Method	DNN with Modifiable Loss Function	99.68%

Analysis



Accuracy, precision, recall, and specificity of WBC Diagnostic and Original datasets are plotted for different λ values. We also illustrate that our model performs with low standard deviation for different values of λ using 10-fold cross validations.

Conclusion

In order to obtain a reliable computer-aided diagnosis system, we proposed an end-to-end regularized deep convolutional neural network for automated classification of breast tumors. Issues such as data imbalance often result in a diagnosis bias in machine learning methods. Our proposed solution is capable of addressing these challenges, outperforming the state of the art and achieving a classification accuracy of 99.52% and 99.68% for the WBC Diagnostic and Original datasets respectively. The advantages of our proposed architecture are its low error rate, lack of need for feature selection or dimensionality reduction, and the ability to adjust the performance for higher accuracy, precision, recall, or specificity values, where needed.