

IMPLEMENTATION OF ABBASI ET AL'S PAPER: "LMBiS-NET: A LIGHTWEIGHT MULTIPATH BIDI- RECTIONAL SKIP CONNECTION BASED CNN FOR RETINAL BLOOD VESSEL SEGMENTATION"

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1 INTRODUCTION

The goal of this project is to implement the LMBiS-Net model that is presented in "LMBiS-Net: A Lightweight Multipath Bidirectional Skip Connection based CNN for Retinal Blood Vessel Segmentation." (1) In addition to implementing LMBiS-Net, we decided to apply the model to a different dataset that is not used in the paper. The dataset we chose was FIVES, a Fundus image dataset for AI-based vessel segmentation. The authors of Abbasi et al. did not make their implementation of LMBiS-Net publicly available, and thus we worked on creating our own implementation of LMBiS-Net from scratch to see if we were able to replicate the results achieved by Abbasi et al. To further test the robustness of our model, we further tested on the FIVES dataset to confirm that our model can be used with other datasets beyond just CHASE_DB1 and STARE.

1.1 IMPORTANCE

It's not uncommon for researchers to purposely choose datasets where their models perform particularly well. Applying the model to a new dataset will add more credibility to the generalizability of LMBiS-Net. LMBiS-Net's primary benefit is that it provides an accurate retinal blood vessel segmentation model that is more computationally efficient compared to current state-of-the-art models. This CNN model is applied to retinal imaging. The LMBiS-Net research paper claims that retinal blood vessel segmentation is beneficial for early detection and treatment of retinal diseases. This model can significantly reduce the amount of time ophthalmologists spend manually identifying retinal vessels. Additionally, the model can reduce human error in that task. Retinal diseases are a major cause of visual impairment and blindness (12). Studies show that 5%-20% of the global population ages 40+ have retinal disorders (12). Examining retinal vessels can provide important information regarding the underlying medical conditions leading to retinal diseases.

1.2 PROJECT CONTRIBUTIONS

Our team created the first publicly available implementation of LMBiS-Net along with code to augment retinal images to increase the size of training datasets. Our findings add credibility to the original paper's claims that LMBiS-Net is a computationally efficient and accurate state-of-the-art retinal blood vessel segmentation model.

2 RELATED WORK

Image segmentation is a well established research area in the medical field. Staal et al. (11) had early on introduced a method to automate the segmentation of blood vessels in 2004. Their method used a neural network (NN) classifier and sequential forward feature selection. Recently, there have been many new models based on the U-Net model. U-Net is a CNN specifically developed for biomedical image segmentation that excels at being precise and efficient (15). In 2018, Yan et al. (14) published their work on blood vessel segmentation model that targets the different problems associated with segmenting thick and thin vessels. Wang et al. (13) created a multi-decoder model

that classified image features as ‘Easy’ or ‘Hard’ and then processed those feature types separately with subdecoders .

In 2022, Zhang et al. (16) presented Bridge-Net, which used U-Net as its base model. When processing vascular features, Bridge-Net uses large-scale patches to add contextual information to small-scale patches .

All of the previously mentioned work suffers from the same problem: computational complexity caused by the multipath structure to segment thick and thin blood vessels. Additionally, these models can struggle with segmenting thin vessels because some of the vessel features are lost during the successive convolution and pooling operations. LMBiS-Net addresses both of those issues. This model uses few model parameters compared to the existing body of knowledge, which addresses the issue of high computational complexity. To reduce the spatial information loss of thin blood vessels, LMBiS-Net only uses two max-pooling layers.

In 2015, Olaf Ronneberger et al. (10) first introduced U-Net, a type of convolutional neural network (CNN), with the specific intention to use it for biomedical image segmentation. The U-Net architecture has a contracting path to capture context and a symmetric expanding path for precise localization, providing a U-shaped structure. The use of data augmentation and data segmentation allows for superior performance on limited amounts of images .

Du et al. (3) expands on this by providing a comprehensive overview of medical image segmentation using U-Net. Their review focuses on the application of U-Net in various medical imaging systems like CT, MRI, ultrasound, OCT, PET, and X-ray. It discusses the advantages of U-Net in accurately segmenting target features, efficiently processing medical images, and aiding in precise medical diagnoses. This overview illustrates various ways in which U-Net can be enhanced to fit specific use cases within the medical field.

Both of these papers contributed to LMBiS-Net, given its utilization of these aspects of the U-Net design. LMBiS-Net, however, also introduces modifications such as multipath feature extraction blocks and bidirectional skip connections, which enhance its performance. LMBiS-Net is optimized for segmentation of retinal blood vessels and designed to be lightweight with a lower number of parameters, making it more efficient, especially in terms of computational resources and training time.

Li et al. (9) presents a new model, named DEF-Net, that designed to segment retinal vessels automatically, which consists of a dual-encoder unit and a decoder unit. Fused with recurrent network and convolution network, a dual-encoder unit is proposed, which builds a convolutional network branch to extract detailed features and a recurrent network branch to accumulate contextual features, and it could obtain richer features compared to the single convolution network structure. Furthermore, to exploit the useful information at multiple scales, a multi-scale fusion block used for facilitating feature fusion efficiency is designed. Extensive experiments have been undertaken to demonstrate the segmentation performance of our proposed DEF-Net.

Fraz et al. (5) presents a new supervised technique for segmenting blood vessels in retinal photographs that uses both bagged and boosted decision trees and implements a feature vector based on the orientation analysis of gradient vector field, morphological transformation, line strength measures, and Gabor filter responses. The feature vector encodes information to handle the healthy as well as the pathological retinal image. The method is evaluated on various databases, among them the DRIVE and STARE, and a new retinal vessel reference dataset consisting of retinal images from multi-ethnic children called CHASE_DB1.

FCNs have emerged as a common choice for semantic segmentation in this context, with the M3FCN proposal, a variant incorporating a multiscale input block, as described by the authors of Jiang et al. (7). They proposed an automatic retinal vessel segmentation framework using deep fully convolutional neural networks (FCN), which integrate novel methods of data preprocessing, data augmentation, and full convolutional neural networks. It is an end-to-end framework that automatically and efficiently performs retinal vessel segmentation. The framework was evaluated on three publicly available standard datasets: DRIVE, STARE, and CHASE_DB1 datasets, like Fraz et al. Their experimental results show that their proposed framework achieves very high vessel segmentation performance in all benchmarks (7). Deshmukh and Roy (2) proposed vessel vector-based phase portrait analysis (VVPPA) and a hybrid between VVPPA and a clustering method proposed earlier

for automatic optic disk (OD) detection called the vessel transform (VT). The algorithms are based primarily on the location and direction of retinal blood vessels and work equally well on fine and poor quality images. We test the proposed combination against state-of-the-art OD detection methods. The results show that the proposed algorithms outperform the benchmark methods, especially on poor quality images. Furthermore, the HM can supplement practically any segmentation model as long as it offers multiple OD candidates. In order to prove this claim, we test the efficiency of the HM in detecting retinal abnormalities in a real clinical setting.

Fathi and Naghsh-Nilchi's (4) work presented a new multi-scale vessel enhancement method based on complex continuous wavelet transform (CCWT). They optimized CCWT's parameters to represent line structures in all directions and separate them from simple edges. An efficient circular structure operator is employed on the centerline of vessels to estimate their diameters. The performance of the proposed method is measured on the publicly available DRIVE and STARE databases, like Fraz et al., and compared with several state-of-the-art methods.

Despite the fact that all of these papers proposed new and potentially preferable methods, we stuck with LMBiS-Net due to reliability and consistency. Our results depend on furthering the techniques used in Abbasi et al. (1). Furthermore, the methods used in the other papers were tested, but only on certain datasets or in certain situations. This does not guarantee their reliability in the cases we are using LMBiS-Net for. LMBiS-Net has been tested over a variety of datasets and situations, and thus is fairly well established. Thus, we know that it will not act as a confounding variable that may affect our results and conclusions.

3 PROJECT SCOPE/STRUCTURE

3.1 LMBiS-NET ARCHITECTURE

Figure 1 shows the model architecture used for implementation. Convolution layers and ReLU activation functions are utilized to extract features from the input data. To stabilize training and expedite optimization convergence, a batch normalization layer is applied. Following batch normalization, max pooling is used to condense the feature maps' spatial dimensions while retaining crucial feature details.

The multipath feature extraction block combines 1×1 , 3×3 , and 5×5 convolution blocks, each followed by ReLU activation and batch normalization. The outputs from these blocks are summed to generate a comprehensive feature map, representing the encoder stage's output. The bottleneck layer is crucial for training the model efficiently, acting as a vital link between the encoder and decoder sections.

In the decoder stage, transpose convolution layers are employed for up-sampling, effectively enlarging the feature maps' spatial dimensions. This operation reverses the standard convolution process. Finally, a softmax layer in the last decoder stage normalizes the output, presenting the model's output in a probabilistic format.

Dice pixel classification gauges the overlap between the predicted and actual images, commonly used in segmentation tasks to assess their similarity. Skip connections, an impactful architectural element in neural networks, empower the training of deep models. The proposed LMBiS-Net incorporates bidirectional skip connections linking its encoding and decoding layers, merging low-level and high-level feature data using forward skip connections. Additionally, reverse skip connections are employed to map the decoded features back to the encoder.

3.2 SOFTWARE DESIGN

We implemented LMBiS-Net using Tensorflow on Google Colab. The implementation is divided into several sections: Dataset Preparation, Model Architecture, Model Training, and Model Evaluation. In Dataset Preparation, the retinal image datasets are loaded. Data augmented is used to increase the size of the datasets to match the sizes used in the original paper. The Model Architecture details all the layers of the LMBiS-Net. This CNN is composed of three encoder layers, a bottleneck layer, and three decoder layers. Our implementation uses a combination of self-built functions and functions from the tensorflow.keras library. The Model Training section simply takes

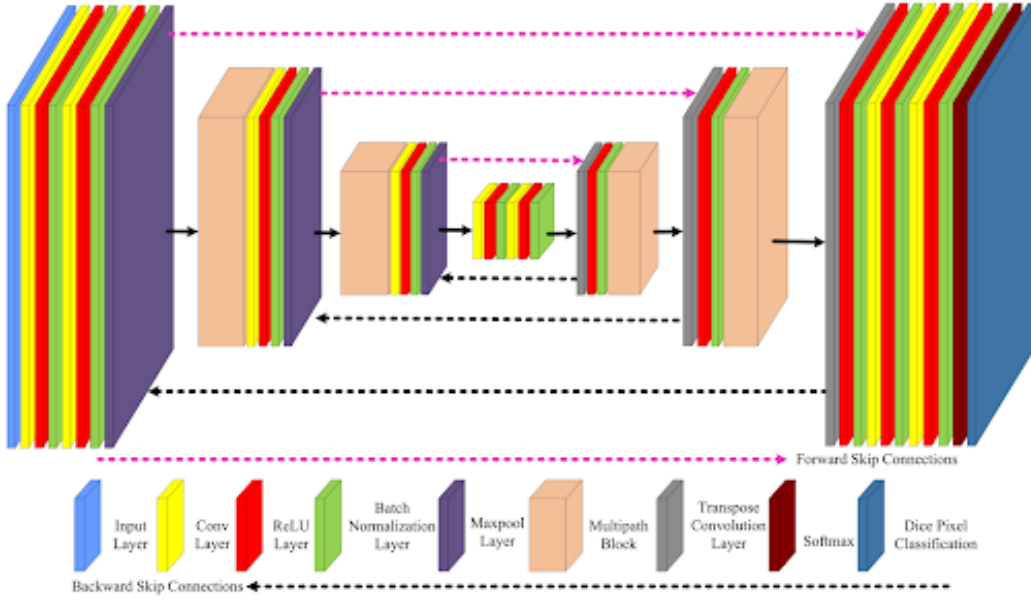


Figure 1: Block Diagram of LMBiS-Net (1)

the compiled model from the Model Architecture section and trains it for a specified number of iterations. The Model Evaluation displays the evaluation metrics (See Section Below) after feeding the test dataset to the trained model. All this code is packaged into an easy-to-use file where our implementation of LMBiS-Net can be executed by simply running all cells in the Google Colab.

4 METHODOLOGY AND DATA DESCRIPTION

Our first goal was implementing LMBiS-Net from scratch, and then using our LMBiS-Net on the Chase_DB1 (5) and STARE(6) datasets that were used in Abbasi et al. After this, we chose to further test our implementation on the FIVES (8) dataset. Although each dataset had different image resolution, each image was resized to 512x512 pixels before model training. Data augmentation techniques were used to increase the training images. Augmentation techniques used include random rotation, random cropping, random brightness, random contrast, and random flipping.

Chase_DB1 is a dataset commonly used in retinal blood vessel segmentation. It contains 28 color retina images collected from the left and right eyes of 14 children, and the images were annotated by two human experts independently.

STARE, or Structured Analysis of the Retina, is another well known dataset when it comes to blood vessel segmentation. It consists of 20 color fundus images, with two sets of annotations for each image.

The last dataset we chose to implement, and one that was not explored by Abbasi et al. was the FIVES dataset. FIVES consists of 800 multi-disease color fundus images. Annotations were crowd-sourced and are available for every image in the dataset.

4.1 ATTEMPTED IDEAS

We opted to retain LMBiS-Net rather than exploring alternative methods or models for several reasons. Most notably, the original paper by Abbasi et al. employed LMBiS-Net, thus influencing our decision to maintain consistency. We reconstructed the model from the ground up and applied it to both the CHASE and STARE datasets, enabling a direct comparison of results. This approach allowed us to assess the extent of dissimilarity, if any, between our implementation and the model used by Abbasi et al. Choosing a different model could introduce confounding variables, making it

challenging to attribute changes in results to the correctness of our implementation rather than the choice of model.

5 RESULTS

5.1 EVALUATION METRICS

Sensitivity(S_e), Specificity(S_p), Accuracy(A_{cc}), F1-Score, and Area Under the Curve (AUC) were the metrics used in the original paper to evaluate the performance of the LMBiS-Net. The LMBiS-Net model is essentially a binary classification of every pixel in the image 1 indicates a blood vessel, 0 indicates not a blood vessel. The Formulas:

[T_P = true positive, T_N = true negative, F_P = false positive, F_N = false negative]

$$S_e = \frac{T_P}{T_P + F_N} \quad S_p = \frac{T_N}{T_N + F_P}$$

$$A_{cc} = \frac{T_P + T_N}{T_P + T_N + F_P + F_N}$$

$$F_1 - Score = \frac{2 \times T_P}{(2 \times T_P) + F_P + F_N}$$

$$AUC = 1 - \frac{1}{2} \left(\frac{F_P}{F_P + T_N} + \frac{F_N}{F_N + T_P} \right) \quad IoU = \frac{T_P}{T_P + F_P + F_N}$$

5.2 ANALYSIS OF RESULTS

Dataset	AUC	IoU	Specificity	Dice Coef.
CHASE _ DB1	0.8688	0.6562	0.9493	0.7931
STARE	0.6835	0.4300	0.9870	0.6100
FIVES	0.8321	0.7030	0.9959	0.8147

Table 1: Results Achieved with Our Team’s Implementation of LMBiS-Net

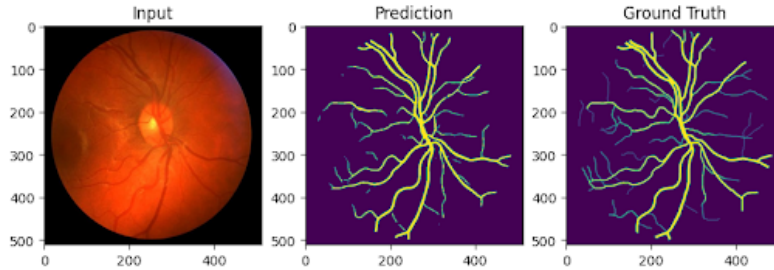


Figure 2: Retinal Blood Vessel Segmentation Example from CHASE_{DB1}

Table 1 shows the results that we achieved by using our LMBiS-Net model implementation on the CHASE_DB1, STARE, and FIVES datasets. We were successful in implementing a LMBiS-Net model from scratch. As Fig. 2 shows, there are very minor differences between our predictions and the ground truth from Abbasi et al. Thus, we were able to replicate the original results achieved with the CHASE_DB1 and STARE datasets to a close degree.

Since FIVES was not used in Abbasi et al., we have no results to compare our results towards. The main idea behind including this dataset was confirming that our implementation would extend to

previously unused datasets. Our results confirm that our implementation did indeed work on FIVES and we were able to extract results. The only comparisons we can draw are between the results achieved with FIVES and the results achieved with the other two datasets. As Table 1 shows, we achieve a high specificity with the FIVES dataset, and data in similar ranges for the other categories. This confirms that our model is well-suited to work with many datasets.

6 CONCLUSION / FUTURE WORK

Our team has developed the first publicly available implementation of LMBiS-Net, complete with code for enhancing retinal images to expand training datasets. Our research corroborates the assertions made in the original paper, Abbasi et al., affirming that LMBiS-Net stands as a computationally efficient and accurate state-of-the-art model for retinal blood vessel segmentation.

The limitations of our implementation were brought on by a multitude of factors. The hyperparameters that Abbasi et al. used for their implementation were not specified in the paper, so we had to decide the weight of these parameters at our own discretion. Given more time, we could have better fine tuned these parameters to produce better results for all of our evaluation metrics. Another large limitation to our implementation was the lack of computational capabilities and processing power when working within Google Colab. Although we benefited greatly from the ease of working dynamically together on building this model due to Colab, we had to compromise on performance somewhat, which may have affected the result.

To improve our project, we could compare against papers with results beyond Abbasi et al. Doing so would further cement our results and the validity and accuracy of our LMBiS-Net model. Furthermore, we can also compare our results with studies that used different datasets than ours, and possibly even papers that used their models on the FIVES dataset. This would support our results if correct, or potentially point out any flaws in our implementation if not. Extending our implementation to more datasets and conditions would only add to the credibility of LMBiS-Net, which itself is already considered an accurate and reliable model. In addition, we could work off our limitations and work on fine-tuning parameters for better results and using a more suitable coding environment without the limitations of Colab. Although such issues did not harm our work significantly, they did make our tasks more complicated and time-consuming, and making changes on these areas would only streamline our work and contribute to accuracy and efficiency.

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