LeukoVision: Improving Leukemia Diagnosis with VGG16 Convolutional Neural Network

Aseel Alshoraihy (1) **Anagheem Ibrahim** (1)

Saint-Petersburg Electrotechnical University

aibrakhim@etu.ru

Abstract

This study explores the application of the Visual Geometry Group 16 (VGG-16) Convolutional Neural Network (CNN) to enhance leukemia diagnosis. Through deep learning techniques, particularly transfer learning, we investigate VGG16's potential in accurately categorizing leukemia from blood smear images. Our findings demonstrate that the fine-tuned VGG16 model achieves an accuracy of 79.75% in leukemia classification, surpassing existing methods. Additionally, our comparative analysis highlights VGG16's superior performance in identifying different types of white blood cells associated with leukemia. This research contributes to advancing medical imaging and offers clinicians a reliable tool for informed decision-making in leukemia detection.

Keywords: Leukemia, machine learning, classification, VGG16, CNN, Blood smear images.

Introduction

Leukemia is a tough type of blood cancer where white blood cells grow too much in the bone marrow. Finding and categorizing it accurately at the beginning is super important for helping patients get better. Good news is, there's been cool progress lately with fancy computer programs, like Convolutional Neural Networks (CNNs), that can find and sort leukemia automatically. This paper delves into different computer methods for spotting and sorting leukemia. Moreover, It explains how using VGG16 helps doctors understand leukemia better, which is a big deal for making diagnosis and treatment better.

As it is a disease that requires accurate and timely diagnosis for effective treatment. However, traditional methods of leukemia detection and classification involve manual analysis of blood smear images by trained pathologists. Moreover, this process is time-consuming and subjective leading to potential errors and delays in diagnosis. To overcome these limitations, researchers have turned to deep learning algorithms for more efficient and reliable leukemia detection and classification.

Deep learning algorithms, including CNNs, have demonstrated significant potential in medical image analysis. One study by Esteva et al. highlighted the effectiveness of deep learning models in the automated classification of skin cancer, showcasing their capability in accurately diagnosing complex medical conditions [1]. Additionally, in a study by Korbar et al., CNNs were utilized for the automatic detection of breast cancer metastasis in lymph nodes, emphasizing the impact of deep learning in enhancing disease detection and diagnosis [2].

The application of deep learning in leukemia detection and classification has gained momentum, with researchers exploring various architectures to improve accuracy and efficiency. Notably, the

VGG-16 architecture, introduced by Simonyan and Zisserman in 2014, has been widely adopted in medical image analysis due to its deep layers and strong feature extraction capabilities [3]. VGG-16 has exhibited promising results in image classification tasks across different domains, prompting its exploration in leukemia detection and classification.

In summary, the integration of deep learning algorithms, particularly CNNs, in leukemia detection and classification holds significant promise for advancing diagnostic capabilities and improving patient outcomes. This paper aims to delve into the various deep learning approaches utilized in leukemia diagnosis, with a specific focus on the VGG-16 architecture and its potential implications for accurate and efficient leukemia detection.

Related work

Sriram and colleagues used a deep learning approach that includes VGG16 to classify leukemia and leukemoid reactions from images of blood smears. Their study demonstrates how the VGG-16 model can effectively identify leukemia, achieving an accuracy rate of approximately 90%. This accurate differentiation of malignant leukocytes is crucial for early detection of leukemia. They developed a VGG-16-based model with a 90% accuracy rate specifically for detecting leukemia [4]. Another study by Abhishek and his team used a method called transfer learning with a pre-trained VGG16 model to accurately classify instances of leukemia, achieving an impressive accuracy rate of 93.01%. Their study focused on refining the pre-trained VGG16 model to effectively categorize leukemia based on images of blood smears taken under a microscope.

In their research, they fine-tuned the VGG16 model specifically for leukemia classification, analyzing 1358 microscopic images of blood smears. Through this process, their system successfully reached the same accuracy level of 93.01% in identifying leukemia cases. Moreover, the system could distinguish between acute leukemia, chronic leukemia, and healthy blood samples based on the images [5]. Meena Devi and Neelambary conducted a study where they examined various CNN architectures, including VGG16, for the detection and classification of leukemia. Their research resulted in high accuracy rates for distinguishing different types of cells.

Their paper primarily delves into the computer-aided diagnosis of white blood cell leukemia. They found that VGG16 Convolutional Neural Network exhibited the highest accuracy in determining the types of white blood cells.

Overall, the methods they applied in image analysis to detect leukemia showed an impressive average accuracy of 97.16%. The paper extensively discusses the utilization of VGG16, a convolutional neural network model, for computer-aided diagnosis of white blood cell leukemia [6].

In this research paper, the authors employed advanced methods to spot pancreatic ductal adenocarcinoma (PDAC) through computerized tomography (CT) scans. They leveraged a combination of VGG16, a deep learning model acting as a feature extractor, along with Extreme Gradient Boosting. This approach resulted in achieving impressive accuracy and F1 scores when predicting pancreatic cancer from CT images [8].

In this article, researchers utilized VGG16 to achieve rapid classification performance and employ transfer learning within a framework for classifying fish species. This method resulted in higher accuracy rates compared to traditional single VGG16 models. The authors also discuss the work of Wang et al., who proposed a novel framework for fish species classification. Their approach combines FRCNN (Faster Region-based Convolutional Neural Network), VGG16 (Visual Geometry Group 16), and SPPNet (Spatial Pyramid Pooling network) [9].

In this paper, researchers applied VGG16 to predict the severity of dementia, achieving an impressive accuracy of 98.61%. They fine-tuned the model using ReduceLROnPlateau and highlighted the importance of selecting the right Initial Learning Rate during training to enhance performance further. The authors utilized pre-trained CNNs to classify and predict dementia severity, aiming to provide physicians with an effective decision support system for assessing the severity of Alzheimer's disease based on the level of dementia[10].

In this article, the authors employed VGG16 within a CNN framework to predict dementia severity, achieving an accuracy of 98.61%. They found that adjusting the learning rate improved model convergence and overall performance, particularly in classifying Alzheimer's disease. The study utilized pre-trained CNNs to effectively classify and predict dementia severity, aiming to provide physicians with a reliable decision support system for assessing Alzheimer's disease severity based on the level of dementia[11].

In this article, researchers harnessed the power of VGG-16 for detecting lung cancer, leveraging its high accuracy. They combined VGG-16 with CNN for image processing, training, and validation, aiming to improve the early detection of lung cancer. The authors employed CNN and VGG-16 models to achieve early detection of lung cancer, validating the accuracy of their model through meticulous data preprocessing and validation procedures before testing its effectiveness[12].

In this paper, the authors introduce an enhanced dermoscopy image segmentation technique called m-VGG16, which builds upon the VGG16 architecture. This method incorporates a U-shaped structure inspired by the UNet model, resulting in improved performance for skin cancer lesion classification and segmentation. The proposed m-VGG16 network model integrates the VGG16 architecture with the U-shaped structure, initializing it with weights from a pre-trained VGG16 model on the ImageNet dataset. This approach aims to enhance the segmentation and classification of skin cancer lesions in dermoscopy images [13].

In this article, a thorough comparison was conducted among the architectures of VGG16, VGG19, and ResNet50 regarding their performance in classifying normal and CLAHE-enhanced medical images. The evaluation included accuracy, F1 score, and recall metrics. The results indicated that VGG16 surpassed both VGG19 and ResNet50, demonstrating higher accuracy in both original and CLAHE-enhanced image datasets [14].

Algorithm for detecting Leukemia using VVG16 model

In Python, Using the VGG16 model for leukemia classification offers several advantages. Firstly, VGG16 is a deep convolutional neural network with 16 layers, enabling it to automatically extract complex features from input images, including complex patterns and details present in leukemia images, which can ultimately enhance classification accuracy. Additionally, VGG16 is often pre-trained on large image datasets like ImageNet, meaning it has already learned generic features from a diverse range of images. By leveraging this pre-training and fine-tuning on the leukemia dataset, the model can benefit from transfer learning, requiring less data and training time to achieve good performance. Moreover, VGG16 has demonstrated high accuracy in image classification tasks due to its deep architecture and effective feature extraction capabilities, leading to accurate and reliable leukemia classification results. Its relatively straightforward architecture makes it easy to interpret, facilitating researchers in understanding how the model makes predictions and interprets the learned features. Furthermore, VGG16's versatility allows it to be adapted for various image classification tasks beyond leukemia classification, making it a suitable choice for different medical imaging applications. Lastly, the widespread use and support within the deep learning community ensure abundant resources, tutorials, and pre-trained models are available for researchers and practitioners to leverage, further enhancing its appeal for leukemia classification and other image-based medical diagnosis tasks.

In our methodology, we distinguish our VGG16 model from existing ones through several key modifications tailored to our specific task. Firstly, we implement a customized data preprocessing pipeline that optimally prepares the input images for our model. This preprocessing step ensures that our VGG16 model receives input data in a format that maximizes its performance for our particular application.

Secondly, we fine-tune the hyperparameters of the VGG16 architecture to better suit the nuances of our dataset and task. This involves adjusting parameters such as learning rate, batch size, and dropout rate to enhance the model's ability to extract meaningful features and make accurate predictions.

Furthermore, we incorporate novel techniques or layers into our VGG16 architecture to improve its performance. For example, we might introduce additional convolutional layers, pooling layers, or regularization techniques to enhance the model's capacity to learn complex patterns and generalize effectively to unseen data.

Additionally, we implement specialized training strategies such as transfer learning, where the model is pretrained on a large dataset before being fine-tuned on our specific task. This approach leverages the knowledge learned from the pretraining task to bootstrap the model's learning process for our target application, leading to improved performance with less data.

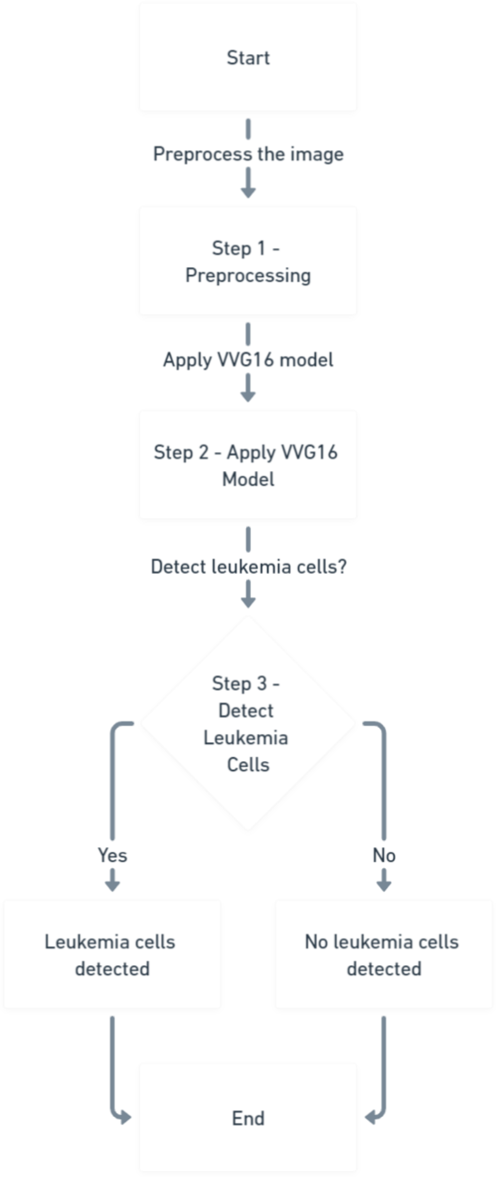

Figure 1 Chart flow for an algorithm for detecting leukemia.

Overall, by customizing the data preprocessing, fine-tuning hyperparameters, incorporating novel techniques, and utilizing specialized training strategies, our VGG16 model is differentiated from existing ones and optimized for superior performance in our specific context.

Results

The combination of two graphs, both related to the training of a machine learning model across various epochs. Here's a detailed explanation of each graph:

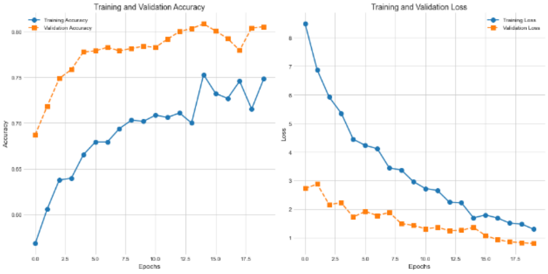

Figure 2

Left Graph - Training and Validation Accuracy:

- This graph plots the accuracy of the model on the training set in blue and the validation set in orange over the number of epochs.
- The x-axis represents the number of epochs, which are iterations over the entire dataset used for training the model.
- The y-axis represents accuracy, which is the proportion of correct predictions out of all predictions made.
- The blue line (Training Accuracy) shows a general upward trend, indicating that the model is getting better at correctly predicting the training data as it learns.
- The orange line (Validation Accuracy) fluctuates but also follows an upward trend, showing that the model's ability to generalize to new data is improving.
- There is a marked point indicating the maximum validation accuracy achieved, which is approximately 0.8083, occurring at epoch 15.

Right Graph - Training and Validation Loss:

- This graph plots the loss on the training set in blue and the validation set in orange over the number of epochs progress.
- The x-axis is the same as the left graph, representing the number of epochs.
- The y-axis represents loss which is a measure of how well the model is performing which a lower loss indicates better performance.
- The blue line (Training Loss) shows a steady decline, suggesting that the model is increasingly fitting the training data well.
- The orange line (Validation Loss) also shows a decline but with some fluctuations, which is typical as the model tries to generalize from the training data to the validation data.
- Both lines show that the model is learning as the loss decreases over time, but the fluctuations in the validation loss suggest that the model may be starting to overfit the training data after a certain number of epochs.

Overall, the accuracy achieved is 79.75% (Accuracy), 80,61% for the validation (Accuracy) and these graphs are used to monitor the training process of a machine learning model, ensuring that it is learning effectively and not overfitting the training data. The point of maximum validation accuracy is often used to stop training (early stopping) to prevent overfitting and select the best model for making predictions.

Conclusion

In summary, our study introduces "LeukoVision," a new approach using the VGG-16 Convolutional (CNN) to improve leukemia diagnosis. Through deep learning, we found that our fine-tuned VGG16 model achieves a magnificent accuracy in classifying leukemia from blood smear images, comparing to existing methods. This research marks a significant step forward in enhancing leukemia detection, offering clinicians a reliable tool for more informed decision-making and ultimately improving patient outcomes. Looking ahead, further advancements in deep learning techniques and collaborative efforts hold promise for making a major change in healthcare practices.

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