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CNN-Based Classification of Melanoma Cells Using Biospeckle Images

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Early detection and monitoring of drug impact on cancerous cells are essential for treatment and livelihood. Traditional methods of drug impact detection are often labor-intensive and time-consuming. Although several algorithms have shown their utility in detecting activity inside the cell using biospeckles images. To incorporate automated monitoring and classification, convolutional neural networks (CNNs) are getting attention for analyzing biospeckles. In this paper we deployed CNN architectures: AlexNet, MobileNet, and VGG16 on biospeckle image dataset. A comprehensive dataset of biospeckles images of melanoma cells, categorized into cells with drug-induced and without drug, was used for the model implementation and evaluation. Images were preprocessed and augmented for model generalization. Each model was trained individually. Their performance is compared against the custom dataset generated by data augmentation.

Keywords: Biospeckle, AlexNet, CNN, melanoma

INTRODUCTION

When a laser irradiates a surface, the backscattered rays produce a granular structure having temporal fluctuations with phase shifts. This pattern is known as biospeckle or dynamic speckle [1]. This method is non-destructive and non-contact approach. It is used in different domains like cell imaging [1], fruit and crop quality assessment [2], biomedical [3], and many more. Biospeckle laser techniques (BSL) are used to monitor physiological and biological activities. This method depicts an activity map of a living or physical sample based on analyzing biospeckles patterns.

When sample is illuminated by a laser beam, biospeckle pattern is produced by stationary and moving scatterers of the sample. There are intensity fluctuations in the patterns received via backscattered beams. These variations in intensity measured by several biospeckle descriptors which characterize the process or activity. The extraction of meaningful information carried by biospeckle patterns requires different algorithms. Spatial contrast, speckle time evolution, and time history of the speckle pattern (THSP) are a few biospeckle signal descriptors. The computation of spatial contrast was done by the speckle pattern of a single-exposure image [3]. Speckle time evolution can be analyzed using the co-occurrence matrix (COM). This is obtained from the THSP. THSP is a matrix in which pixels are arranged in horizontal lines that indicate the evolution of biospeckle concerning time [4].

Numerical indexing and visual analysis were used in the literature for analyzing biospeckle images. Visual techniques include subtraction average, Fujii's method, structural function, Generalized difference, and many more. Spatial-temporal speckle correlation techniques can evaluate activity evolution. Temporal changes are calculated by correlation analysis of speckle patterns and the correlation coefficient is a function of the movement speed of moving sample scatters [5]. Researchers reported analysis in statistical, frequency domain, and time domain [6]. advancements in machine learning (ML) domain analysis of biospeckle become automated [7]. Including emerging

technologies artificial intelligence for data /signal analysis, automates the analysis process and reduces the computational time.

Recent advancements in deep learning have impacted various domains, signal and image processing, plant disease detection, and drug monitoring systems. Convolutional neural networks (CNNs) are explored and implemented for this purpose. CNNs are used for image classification tasks and can automatically learn and extract features from raw image data. Deep learning models were recently used to analyze biospeckles images for seed disease and viability detection [8]. Aegun et al CNN architectures used for the for medical image analysis on three different datasets: skin lesion images, retina images, and brain tumor [9]. CNNs enables learning of highly representative, data-driven, layered hierarchical image features using sufficient training data [10]. Several CNN-based models have been proposed like LeNet, AlexNet etc. LeNet focus on increasing the network depths. AlexNet support designing of more flexible structures. VGG- Net, GoogLeNet, ResNet, and SPP-Net are some more CNN architecture with increased computational power and performance. Author proposed deep learning-based system is for spatio-temporal analysis alongwith classification of biospeckle data for different experimental parameters [8]. This model is capable of learning and extracting spatial and temporal features form the biospeckle images of healthy and diseased seeds efficiently. The author reported DL models are capable of accurate classification the biospeckle data. In continuation, we attempt to classify the melanoma cancerous cell with and without drug using Various CNN architectures. The primary objective of this study is to deploy DL models AlexNet, Mobile Net, and VGG16 to improve the automated monitoring and classification of melanoma cells using biospeckle images. diseases. Specific objectives include:

- To preprocess and augment a comprehensive dataset of biospeckle images of melanoma cells, both drugs induced and without drug.
- To train AlexNet, MobileNet, and VGG16 models individually and optimize their performance.

2. Theory

The proposed work involves collection of biosepckle signal/ image, image processing methods, and convolution neural network (CNN) models for analysis and classification. A "Biosepckle laser on cloud "a platform for gathering raw data from biospeckle laser applications is available by means of cloud storing [11]. It provides public access to a database of BSL raw images. For research purpose, we have downloaded the BSL images of melanoma cells with and without drug [12] from the cloud. Further to increase the dataset, a data augmentation technique is used.

Data augmentation has been used to achieve optimum performance gains for deep learning (DL) based applications. This results in increased accuracy, stability, and reduced overfitting for deep-learning-based electroencephalography [13]. We have used an image data generator for the data augmentation task. Within the Google Colab environment, this approach generates many images from a single input image. The Image Data Generator, a critical component of TensorFlow's Keras interface, is used for this. The Image Data Generator is configured for data augmentation. This component provides the basic set of augmentation options, such as rotation, height/width modifications, shear, zoom, and flip.

CNN is Artificial Neural Networks (ANN) having ability to discover and interpret patterns. This ability is very useful for image analysis and classification. CNN architecture consists of different layers having specific functions. The input layer is the first layer and it stores raw data. The second layer "convolutional layer" is responsible for calculating the output by performing a dot product between the image patch and filters. This layer is followed by an activation function and pooling layer. Pooling layer reduces the computation costs. After the pooling layer computation, its outputs passed to the last layer [14].

In recent years, researchers have been using CNN-based models for the diagnosis of various diseases, brain cancer, Parkinson's disease, heart disease, COVID-19, breast cancer, etc. Extract of unique features is very important for the diagnosis and analysis using CNN. We proposed biosepckle features extraction for melanoma skin cancer cells. There is a pre-trained network LeNet-5, AlexNet, Inception Net ResNet, VGG-16 Net, and DenseNet to to train a new dataset. Pre trained models have been for the classification of images in medical domains. AlexNet, GoogleNet, and ResNet are Network architecture of CNN model. The deep features are extracted from CNN model [15]. AlexNet is basic deep learning model and enable learning of higher dimensional features. It consists of several layer such as convolutional layer, rectified linear unit (ReLU), pooling layer and the last one is fully connected layer. ReLU used to accelerate the learning and to prevent the overfitting. The GoogLeNet network resolve overfitting, gradient disappearance, and gradient explosion issues. For a single network of Google Net, multiple convolutions or pooling operations are required. Additionally, it can extract more features with the same amount of work and use computing resources more effectively.

The training set's accuracy declines as the network gets deeper, although deep residual networks (ResNet) can fix this issue. To address the issue of degradation in deep networks, ResNet incorporates a residual block. ResNet involves two types of mapping: identity mapping and residual mapping and Yu et al compared different, Convolutional neural networks for the medical domain. Author reviewed common CNN models, AlexNet, GoogleNet, ResNet, R-CNN, and FCNN [16].

3. PROPOSED METHOD

The proposed method is based on three convolutional neural networks (CNN): AlexNet, MobileNet, and VGG16. Our work involves preprocessing and augmentation of a comprehensive dataset of biospeckle images of melanoma cells, both drug-induced and without drug. It also includes training of AlexNet, MobileNet, and VGG16 models individually and optimize their performance for classification purpose. The methodology involves data collection and preprocessing, individual model training, ensemble integration, and performance evaluation. Figure 1 illustrate the methodology adopted for proposed work.

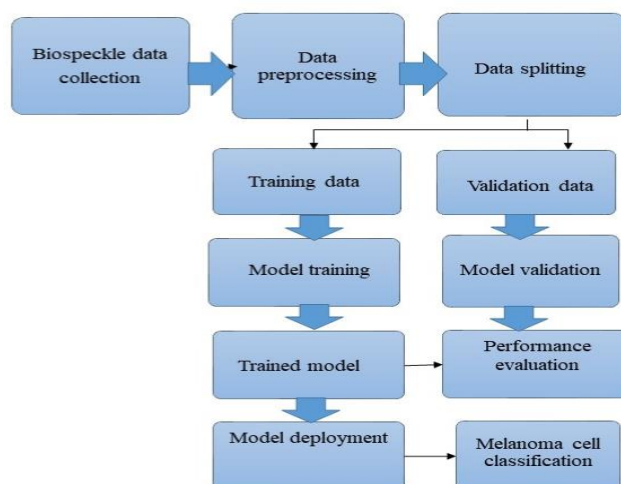


Figure 1. Process of data augmentation for biospeckle images

• **Data Collection:** A dataset of melanoma cell images is collected from public repositories biospeckle laser on cloud. In Figure 2, the sample biospeckle images of melanoma cells with and without drug is presented.

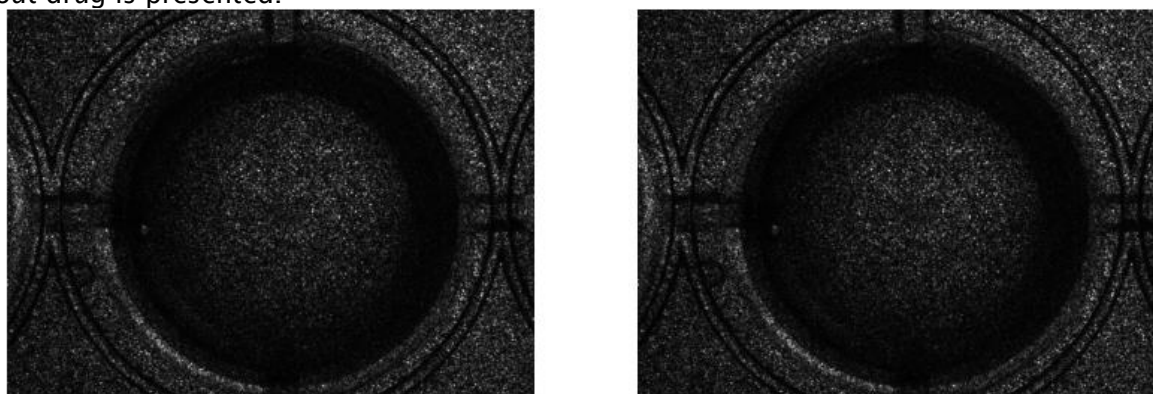


Figure 2. Input Images

• **Preprocessing:** Images are resized to a uniform dimension to meet the input requirement of the CNN models. Data augmentation techniques rotation, flipping, scaling, and cropping are performed to increase the variability of the dataset and improve model generalization. The custom data set is created for the deep learning model training. Ostu thresholding is used for the preprocessing of all the images.

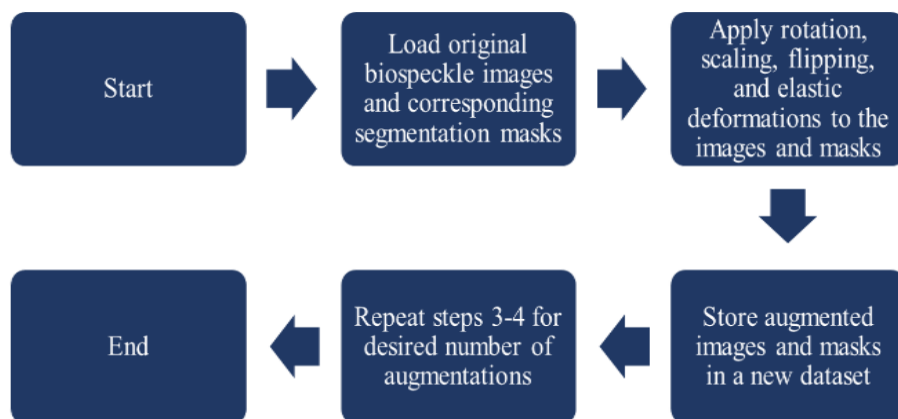


Figure 2. Process of data augmentation for biospeckle images

· Deployment of Model: Custom data set is split into training, validation and test data set. Three models were used for the training DL models: AlexNet, MobileNet, and VGG16. AlexNet consists of five convolutional layers and three fully connected layers. It is known for its relatively simple architecture and efficiency in processing images. MobileNet is a deep network with 28 layers, including deep convolution layer, 1×1 -point convolution layer, batch normalization, ReLU, average collecting layer, and softmax. VGG16 model has a deep architecture with 16 layers, characterized by small receptive fields and a uniform architecture, contributing to its high performance in image recognition tasks. Model deployment involves model training on the training dataset and after training model is deployed and validated against validation data.

4. RESULT

The proposed method was simulated on Google Colab using keras library. All the programming is done in python. This framework provides all functionalities needed for the model deployment. Table 1 indicates the parameters used for the reported work.

Table 1. Parameters

Parameter	Value
Dataset	Collected from “biospeckle laser on cloud” [1,2]
Split Ratio	70% /15%/ 15% (Train/Test/Validation)
Pre-trained Model	AlexNet, MobileNet, and VGG16
Learning Rate	0.001
Optimization Algorithm	Adam
Batch Size	32
Number of Epochs	10
Loss Function	Categorical cross-entropy

Table 2 provides a numerical value of the accuracy of CNN architecture in identifying the biospeckle image of melanoma cells with drug-induced at a specific concentration. Across all architecture, MobileNet has the best training and validation accuracy as compared to AlexNet, and VGG Architecture.

Table 2. Training and validation accuracy

CNN Architecture	Training Accuracy	Validation accuracy
AlexNet	85.3	83
VGG	91.3	81.9
MobileNet	93.8	90

Figure 3 illustrates the comparative chart for training and validation loss and accuracy. MobileNet is giving highest accuracy for biospeckle image dataset.

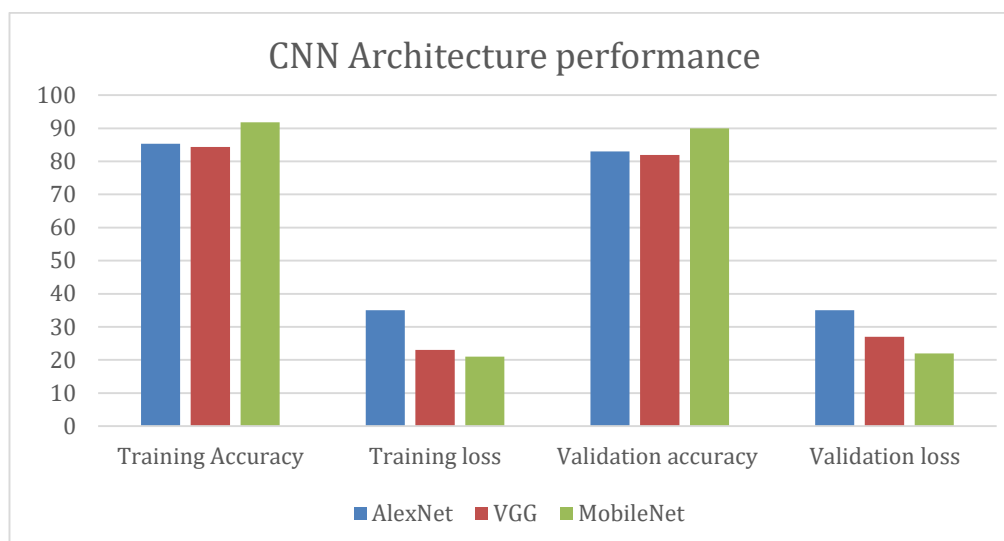


Figure 3. CNN architecture performance on melanoma biospeckle dataset

5. CONCLUSION

To incorporate automated monitoring and classification, convolutional neural networks (CNNs) are deployed to analyze biospeckles images of melanoma cells. Three CNN architectures: AlexNet, MobileNet, and VGG16 were implemented for the classification task. A comprehensive dataset of biospeckles images of melanoma cells, categorized into cells with drug-induced and without drug, using CNN. Also, the preprocessing and augmentation improve model generalization. The contributions of this research are: The development of a comprehensive and well-augmented dataset of biospeckle images from the available dataset and analyzing the performance of AlexNet, MobileNet, VGG16 models on this dataset.

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