

Bovine Tuberculosis Detection in Meat Products Based on Deep Learning Models

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Abstract: *Bovine tuberculosis (bTB)* is an infectious disease that threatens human health and possibly leads to death. It is known that tuberculosis can be transmitted to a healthy person through the air. However, it can also be transmitted through the consumption of animal products, such as meat and milk, which contain the bacteria that cause tuberculosis. Detecting tuberculosis in animal products is challenging and requires specialized expertise. There are many studies in which the detection of tuberculosis is performed using Deep Learning (DL) approaches. However, there is a lack of studies on the detection of *bTB* in animal products. In this study, we address this problem and propose a Convolutional Neural Network (CNN) DL approach for detecting *bTB* in meat products. We conducted experiments on a new dataset containing images of *bTB* infected and healthy meats. We evaluate the performance of different CNN architectures such as ResNet-50, DarkNet-53, MobileNet-v2, GoogleNet, and EfficientNet-b0 in detecting tuberculosis in meat products with respect to several metrics. We have been able to achieve validation accuracies of 100%, 99.67%, 100%, 98.04%, and 100%, for ResNet-50, DarkNet-53, MobileNet-v2, GoogleNet and EfficientNet-b0, respectively.

Keywords: deep learning; classification; bovine tuberculosis; meat products

Derin Öğrenme Modellerine Dayalı Et Ürünlerinde Sığır Tüberkülozu Tespiti

Özet: Sığır tüberkülozu (*bTB*), insan sağlığını tehdit eden ve ölümcül olabilen bulaşıcı bir hastalıktır. Tüberkülozun sağlıklı bir kişiye hava yoluyla bulaşabileceği bilinmektedir. Ancak, tüberküloz bu hastalığa neden olan bakterileri içeren et ve süt gibi hayvansal ürünlerin tüketimi yoluyla da bulaşabilir. Hayvansal ürünlerde tüberkülozu tespit etmek zordur ve özel uzmanlık gerektirir. Derin Öğrenme (DL) yaklaşımları kullanılarak tüberkülozun tespitine yönelik birçok çalışma bulunmaktadır. Bununla birlikte, hayvansal ürünlerde *bTB* tespiti üzerine yapılan çalışmalar oldukça sınırlıdır. Bu çalışmada, hayvansal ürünlerde *bTB* tespitini ele alıyoruz ve et ürünlerinde *bTB* tespiti için bir Evrişimli Sinir Ağı (ESN) yaklaşımı öneriyoruz. *bTB* ile enfekte ve sağlıklı etlerin görüntülerini içeren yeni bir veri kümesi üzerinde deneyler yürütülerek ResNet-50, DarkNet-53, MobileNet-v2, GoogleNet ve EfficientNet-b0 gibi farklı ESN mimarilerinin et ürünlerinde tüberküloz tespitindeki performansını çeşitli ölçütlere göre değerlendirilmiştir. ResNet-50, DarkNet-53, MobileNet-v2, GoogleNet ve EfficientNet-b0 için sırasıyla %100, %99.67, %100, %98.04 ve %100 doğruluğa ulaşılmıştır.

Anahtar Kelimeler: derin öğrenme, sınıflandırma, sığır tüberkülozu, et ürünleri

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1. Introduction

Tuberculosis is an infectious disease caused by *Mycobacterium tuberculosis* bacteria. According to the latest World Health Organization report (WHO), an estimated 10.6 million people worldwide were infected with tuberculosis in 2022. A total of 1.3 million people died from tuberculosis (including 167,000 people with Human Immunodeficiency Virus (HIV)). Tuberculosis is the 13th leading cause of death worldwide and the second leading infectious cause of death after COVID-19 (ahead of HIV and Acquired Immunodeficiency Syndrome (AIDS)) [1].

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Bovine tuberculosis, also known as *bTB*, is a persistently zoonotic disease that affects several livestock animals, primarily cattle but it also affects goats, dogs, pigs, buffalo, badgers, possums, deer and bison. Additionally, humans and, non-human primates [2, 3]. The causative agent of *bTB* in animals is *Mycobacterium bovis* (*M. bovis*), which is a member of the *Mycobacterium tuberculosis* complex (MTBC) [4]. Consuming products from infected animals- such as contaminated meat, contaminated and unpasteurized milk- can spread the *M. bovis* infection to humans. Although human-to-human transmission is very rare, it is transmitted through the air when a person with active tuberculosis coughs, sneezes or talks [5, 6]. Globally, there are more than 50 million infected cattle [7]. Although the disease's incidence varies by geography, some parts of Africa may have infection rates as high as 50%. In the US, Canada, and Europe, *bTB* is uncommon. Usually, outbreaks happen in places where wildlife populations are close to livestock numbers. The ailment is widespread in dairy cattle and is endemic to Central and South America [2]. Consequently, the detection of tuberculous in animal products is of great public health importance. However, detection of tuberculosis in animal products is difficult and time-consuming and requires expertise.

Deep learning (DL) systems have become an important tool in the diagnosis of many health problems due to their success and efficiency. There have been some studies using DL in the diagnosis of a variety of health problems such as EEG imagery, multiple sclerosis, breast cancer, brain cancer, hybrid detections of lung adenocarcinoma, stomach adenocarcinoma, and breast invasive carcinoma, epilepsy diagnosis, heart disease, Parkinson's disease and eye disease [8, 9].

There are many studies utilizing DL methods for tuberculosis detection in literature. El-Solh et al. used an artificial neural network using a general regression neural network. It is the first to predict active pulmonary tuberculosis with neural network and this study reported 0.923 ± 0.056 accuracy based on c-index [10]. Liu et al. aimed to enhance the classification accuracy of tuberculosis in X-ray images using a Convolutional Neural Network (CNN), focusing on unbalanced and less-category datasets. They explored various CNN architectures including transfer learning techniques and shuffle sampling with cross-validation. They achieved 85.68% classification accuracy [11]. Al-Timemy et al. developed a tuberculosis and COVID-19 detection method using pre-trained deep networks and machine learning classifiers, achieving 91.6% accuracy on 2186 X-ray images. The work is based on Central Processing Unit based approach and effective in low-resource settings [12]. Rahman et al. focused on detecting tuberculosis from chest X-ray images, using a combination of preprocessing, data augmentation, segmentation, and DL classification techniques. They utilized nine different deep CNN models for transfer learning on a dataset of 7000 X-ray images and conducted three experiments involving segmentation with U-Net models, classification using original and segmented lung images. Authors achieved 96.47% and 98.6% accuracy without segmentation and with segmentation, respectively [13]. Iqbal et al. developed the tuberculosis-U-Net and tuberculosis-DenseNet for segmenting human lung regions in chest X-ray images and for accurate classification of tuberculosis images, respectively. The tuberculosis-U-Net employs a Dilated Fusion Block and an Attention Block to adaptively adjust receptive fields and concentrate on regions of interest. tuberculosis-DenseNet utilizes five dual convolution blocks with varying filter sizes and a DenseNet-169 layer. They achieved 0.9510 accuracy in detecting various diseases, including tuberculosis [14]. Nafisah and Muhammad proposed a tuberculosis detection system from chest X-ray images using DL models. They used pre-trained CNN models such as ResNet, Xception, MobileNet, Inception and EfficientNet for feature extraction and compared their performance in tuberculosis detection on multiple public datasets. In this study, 98.7% average accuracy was obtained with EfficientNetB3 [15]. Momeny et al. proposed a new CNN model for classifying tuberculosis in microscopic images. Their method involved pre-processing with square rough entropy

thresholding and employing mixed pooling, batch normalization, Dropout, and parametric ReLU for enhanced CNN generalization. This approach significantly outperformed traditional classifiers, achieving a high accuracy rate of 93.4% in tuberculosis diagnosis [16].

In the field of tuberculosis detection in food products, there are some studies like Bezerra et al. and Sevilla et al [17, 18]. Bezerra et al. focused on detecting Mycobacterium including tuberculosis-causing bacteria, in raw milk from Brazilian dairy farms [17]. Sevilla et al. investigated the presence of mycobacteria, including tuberculosis-causing strains, in dairy and meat products using culture and DNA-based methods [18]. These studies utilize manual or semi-manual detection methods. Currently, there is a notable lack of research on automated systems for detecting tuberculosis in food products. However, despite various approaches using DL to detect tuberculosis, there is a research gap in the detection of tuberculosis in animal products. Using DL systems to detect tuberculosis in animal products presents several aims. These are:

- DL algorithms have potential to rapidly discriminate images of animal product infected with tuberculosis with high accuracy. This capability could significantly help prevent the transmission of tuberculosis by detecting contaminated meat before it reaches consumers.
- Reducing diagnostic errors in human assessments paves the way for DL algorithms to provide consistent and objective results with greater precision. This has the potential to reduce health problems caused by misdiagnosis and prevent associated complications.
- A DL system could continuously and remotely detect animal products infected with tuberculosis and quickly provide results, facilitating the resolution of related problems.

In this study, automated and accurate classification of *bTB* from meat images with DL models is proposed. Collected images are pre-processed including resizing, color imbalance correction, and noise reduction as per the requirement of utilized algorithms. This work also presents the flip and rotation methods to expand the *bTB* infected and healthy meat images. Finally, five pre-trained DL models namely, ResNet-50, DarkNet-53, MobileNet-v2, GoogleNet, and EfficientNet-b0 are utilized. To the best of our knowledge, the study is the first DL approach to detect tuberculosis in animal products.

2. Materials and Methods

In this paper, a deep learning-based algorithms namely ResNet-50, DarkNet-53, MobileNet-v2, GoogleNet, and EfficientNet-b0 to detect *bTB* infected subjects using meat images. The architecture of the proposed methodology is shown in Figure 1.

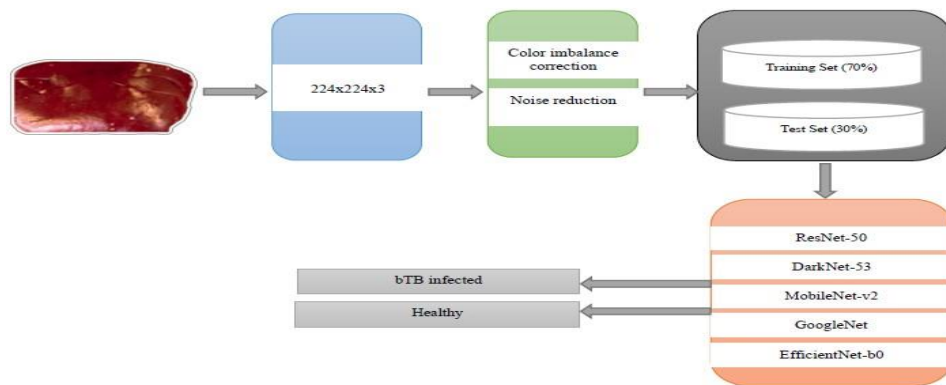


Figure 1. Architecture of the proposed methodology

2.1. Data Preparation

The dataset consists of bovine meat images classified into two categories: *bTB* infected and healthy. This section explains data acquisition and preprocessing steps. Figure 2 is shown example of bovine meat with tuberculous and healthy.



Figure 2. Healthy (left) and *bTB* infected (right) image samples of bovine meat

2.1.1. Data Collection

First, we collected images of bovine meat with *bTB* infected and healthy. The dataset was created from scratch and contains a total of 379 images, of which 324 are of healthy meat and 55 are of *bTB* infected meat. Healthy meat samples were obtained from food and animal-related websites using various keywords such as healthy beef, red meat, healthy meat, animal product, clean red meat, and special plugins. *bTB* infected samples were collected from anti-tuberculosis foundations as well as from medical literature and veterinary health publications. The selection of these images was based on compliance with a certain quality standard. Images containing noise, distortion, or inappropriate perspective were eliminated.

2.1.2. Data Augmentation

The effectiveness of CNN depends on the quality and balance of the training data. Unbalanced data distribution of classes can affect the learning capabilities of the CNN method. To address this issue, our methodology employs a number of data augmentation and balancing techniques: brightness adjustment, image symmetry, zooming techniques and random rotation.

By duplicating images from the less represented class, we obtained a balanced dataset in which both classes were equally represented. As a result, our final dataset consisted of 1000 images in each class, totaling 2000 images. With this approach, the model can learn to effectively identify features in both classes without biasing one against the other. Finally, all images were resized to 224x224 pixel sizes to comply with the transfer learning methodology requirements. For experiment analysis, the dataset is divided into two subsets: 70% for training and 30% for validation. Figure 3 is shown example of data augmentation techniques.

Original Image	low brightness	x-symmetry low brightness	x-symmetry low brightness zoom out	x-symmetry and Zoom in	Angle Change

Figure 3. Example of Augmentation Techniques

2.2. State-of-the-art CNN Models

CNN models are employed for identifying tuberculosis in images of bovine images. The models include ResNet-50, DarkNet-53, MobileNet-v2, GoogleNet, and EfficientNet-b0. These models are selected based on their success in different problems [19]. These models are extensively utilized and achieve high accuracy in a variety of image classification tasks. Model selection was based on minimizing parameters while maximizing accuracy. Therefore, the objective was to classify bovine images with high accuracy using a minimal model size. Table 1 shows the input size and depth for each model's input image. This information will be useful for understanding the distinct characteristics of these models and assessing their suitability for specific classification tasks.

Table 1. CNN model parameters

CNN model	Input size	Depth
ResNet-50	224x224	50
DarkNet-53	224x224	53
MobileNet-v2	224x224	51
GoogleNet	224x224	22
EfficientNet-b0	224x224	82

ResNet-50, a variant of the ResNet architecture, consists of 50 layers, including convolution layers, fully connected layers, and batch normalization layers [20]. ResNet-50 provides a balance between computational efficiency and accuracy in performance. The architecture used in this study is given in Figure 4.

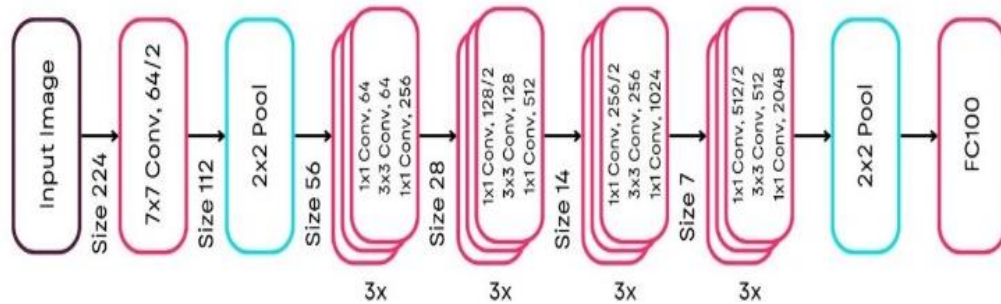


Figure 4. The proposed ResNet-50 architecture (FC: Fully Connected, 2x2 Pool: Pooling Layer)

DarkNet is a DL framework used in image processing and is the basis for the YOLO (You Only Look Once) object detection system [21]. DarkNet-53 is an advanced architecture, its role as the backbone of the YOLOv3 object detection system. This version significantly expands the architecture with 53 layers. It incorporates residual connections, enhancing its learning capability and improving accuracy in object detection tasks. The proposed DarkNet-53 architecture given in Figure 5.

	TYPE	FILTERS	SIZE	OUTPUT
1x	Convolutional	32	3x3	256x256
	Convolutional	64	3x3/2	128x128
	Convolutional	32	1x1	128x128
	Convolutional	64	3x3	
2x	Residual			128x128
	Convolutional	128	3x3/2	
	Convolutional	64	1x1	64x64
	Convolutional	128	3x3	
8x	Residual			64x64
	Convolutional	256	3x3/2	
	Convolutional	128	1x1	32x32
	Convolutional	256	3x3	
8x	Residual			32x32
	Convolutional	512	3x3/2	
	Convolutional	256	1x1	16x16
	Convolutional	512	3x3	
4x	Residual			16x16
	Convolutional	1024	3x3/2	
	Convolutional	512	1x1	8x8
	Convolutional	1024	3x3	
	Residual			8x8
	Avgpool		Global	
	Connected		1000	
	Softmax			

Figure 5. The proposed DarkNet-53 architecture (Avgpool: Average Pooling Layer)

MobileNet-v2 incorporates an inverted residual structure, where residual connections exist between bottleneck layers [22]. MobileNet-v2 includes the fully convolution layer with 32 filters, followed by 19 residual bottleneck layers. MobileNet-v2 is pivotal for enhancing information and gradient flow within the network, leading to improved efficiency and performance. MobileNet-v2 stands out for in various tasks adaptable to different model sizes. Figure 6 show the architecture we used in this study.

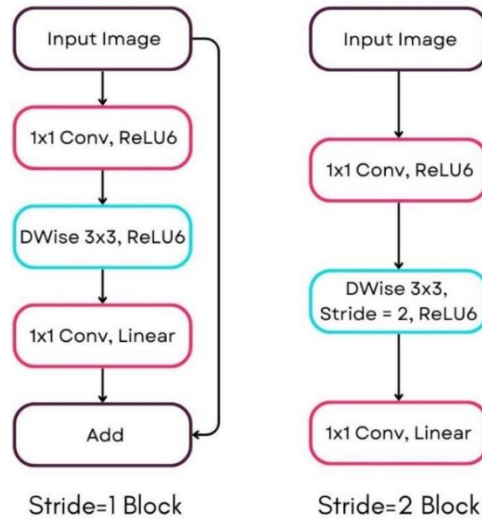


Figure 6. The proposed MobileNet-v2 architecture (DWise: depthwise separable convolution)

GoogleNet, also known as Inception v1, is a deep convolutional neural network architecture introduced by researchers at Google [23]. One of its defining features is the inception module, a novel component that reduced the number of parameters in the network, addressing concerns of computational efficiency and overfitting. This module applies multiple filter sizes within the same layer of the network, allowing it to capture information at various scales. GoogleNet comprises 22 layers. The GoogleNet architecture used in the study is given in Figure 7.

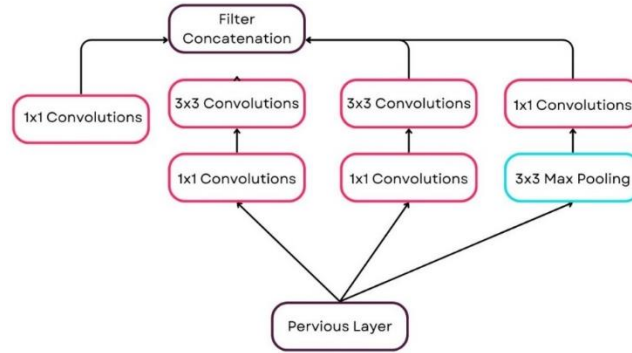


Figure 7. The proposed DarkNet-53 architecture (Avgpool: Average Pooling Layer)

EfficientNet is a series of convolutional neural network models designed with efficiency in mind, both in terms of computational resources and model accuracy [24]. EfficientNet models are based on a scaled-up version of a baseline network. This scaling up is done systematically using a novel compound scaling method. This method involves simultaneously scaling the depth, width, and resolution of the network based on a set of fixed scaling coefficients, ensuring that the network enlarges uniformly at all dimensions. One of the advantages of EfficientNet is that it provides a family of models (b0-b7) that offers a range of complexities, allowing users to choose a model that best fits their computational constraints and accuracy requirements. The proposed architecture is given in Figure 8.

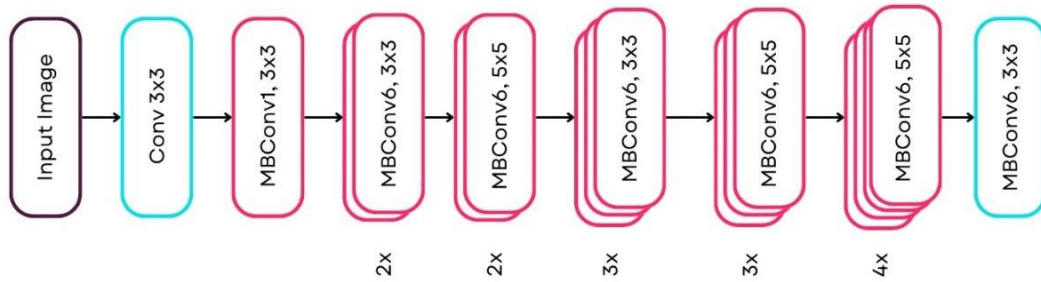


Figure 8. The proposed EfficientNet-b0 architecture (MBCCConv: MobileNetV2 Inverted Residual Bottleneck Convolution)

3. Experimental Study

3.1. Implementation Details and Evaluation Metrics

Experiments were conducted using the Matlab R2022b. The study was performed on a system equipped with 16 GB DDR4 RAM, an Intel Core i7 12700H processor, and an Nvidia GeForce RTX 3070 graphics card. The Deep Network Designer tool within Matlab was employed to facilitate model training through transfer learning methods.

In this study, the effectiveness of the DL models namely ResNet-50, DarkNet-53, MobileNet-v2, GoogleNet, and EfficientNet-b0 is evaluated using F1-score and accuracy which are calculated based on the following definitions:

- True Positive (TP): This term refers to the number of instances where meat products infected with tuberculosis are accurately identified as tuberculosis.

- False Positive (FP): This denotes the occurrences where animal products that are in fact healthy are incorrectly classified as tuberculosis.
- False Negative (FN): This term describes the situations where animal products that actually have tuberculosis are incorrectly identified as healthy.
- True Negative (TN): This is indicative of the situations where healthy animal products are correctly identified as not being infected.

Precision is the proportion of animal products identified as having tuberculosis that are actually infected. It is calculated as the ratio of TP to the sum of TP and FP. Precision is formulated based on the equation below.

$$Precision = \frac{TP}{TP + FP} \quad (1)$$

Recall is the proportion of animal foods that are actually diseased with tuberculosis and are correctly identified as such. It is computed as the ratio of TP to the sum of TP and FN. Recall is formulated as given the following equation.

$$Recall = \frac{TP}{TP + FN} \quad (2)$$

F1-score is the harmonic mean of precision and recall, providing a balance between them. F1-score is formulated in equation below.

$$F1 - score = \frac{2 \times Precision \times Recall}{Precision + Recall} \quad (3)$$

Accuracy is the overall correctness of the model, defined as the ratio of the sum of TP and TN to the total number of cases. Accuracy is formulated the following equation.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (4)$$

3.2. Experimental Results

A collected bovine meat dataset with tuberculous infected and healthy images is utilized to evaluate the performance of the proposed models. Adam, RmsProp and Sgdm algorithms were used as optimizers. The Adam optimizer is a well-known method that uses previous gradients to adjust learning rates adaptively through gradient-based momentum [25]. RMSProp is among the most widely used stochastic optimization algorithms in deep learning applications. SGDM is a traditional momentum method that is frequently utilized in machine learning due to its excellent convergence accuracy. For the DL models to be properly trained, 3 epochs with a batch size of 133 and a validation frequency of 15 are selected. The experiment is conducted with the same setup for all models. Table 2 provides a summary of the experimental results obtained results on the use of CNNs for the diagnosis of tuberculosis.

Table 2. Performance metrics obtained from confusion matrices

Model	Optimizer	Accuracy (%)	F1-score (%)
ResNet-50	RmsProp	97.0	96.99
	Adam	97.17	97.1
	Sgdm	100.0	100.0
DarkNet-53	RmsProp	75.33	79.84
	Adam	96.0	95.83
	Sgdm	99.67	99.67
MobileNet-v2	RmsProp	98.0	98.04
	Adam	100.0	100.0
	Sgdm	99.83	99.83
GoogleNet	RmsProp	95.0	94.74
	Adam	97.67	97.71
	Sgdm	98.0	98.04
EfficientNet-b0	RmsProp	100.0	100.0
	Adam	99.5	99.5
	Sgdm	100.0	100.0

In the scenario where Sgdm is used as the optimizer, ResNet-50 achieves perfect classification accuracy, correctly identifying all 300 tuberculosis samples and all 300 healthy samples, resulting in no FN (healthy samples incorrectly identified as tuberculosis infected) or FP (tuberculosis infected samples incorrectly identified as healthy) as shown in Figure 9. Conversely, with the RmsProp and Adam optimizers, the number of FN (animal products that actually have tuberculosis are incorrectly identified as healthy) is high.

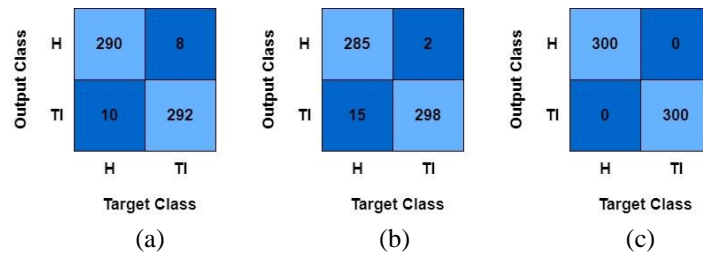


Figure 9. ResNet-50 with (a) RmsProp (b) Adam and (c) Sgdm (H: Healthy, TI: Tuberculosis Infected)

DarkNet-53 with the RMSprop optimizer, DarkNet-53 has the highest count of missed tuberculosis cases, with 141 TN (healthy animal products are correctly identified as not being infected), but it only misclassifies 7 healthy image as tuberculosis, resulting in 7 FN (animal products that actually have tuberculosis are incorrectly identified as healthy). The highest number of FN (animal products that actually have tuberculosis are incorrectly identified as healthy) samples are obtained with the Adam optimizer. The results are shown in Figure 10.

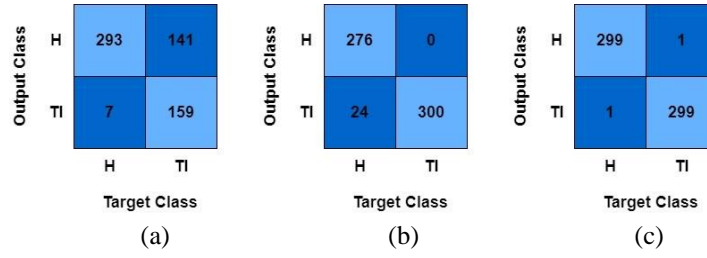


Figure 10. DarkNet-53 with (a) RmsProp (b) Adam and (c) Sgdm (H: Healthy, TI: Tuberculosis Infected)

MobileNet-v2 with Adam achieves perfect classification accuracy, correctly identifying all 300 tuberculosis samples and all 300 healthy samples, resulting in no FN (healthy samples incorrectly identified as tuberculosis infected) or FP (tuberculosis infected samples incorrectly identified as healthy) as shown in Figure 11. However, with RmsProp and Sgdm optimizers, the number of FN (healthy samples incorrectly identified as tuberculosis infected) samples are calculated as 0.

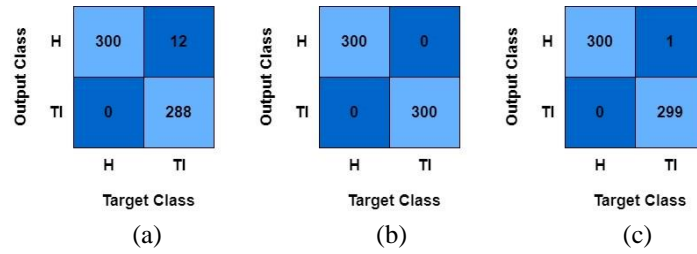


Figure 11. MobileNet-v2 with (a) RmsProp (b) Adam and (c) Sgdm (H: Healthy, TI: Tuberculosis Infected)

GoogleNet gives the worst performance with the RmsProp optimizer so that 30 FN (healthy samples incorrectly identified as tuberculosis infected) samples are reported as shown in Figure 12.

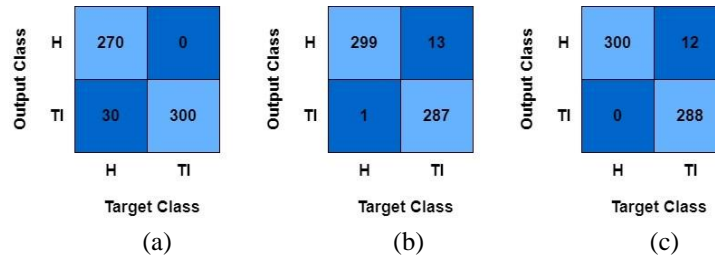


Figure 12. GoogleNet with (a) RmsProp (b) Adam and (c) Sgdm (H: Healthy, TI: Tuberculosis Infected)

EfficientNet-b0 model correctly classifies all samples for the two optimizers namely RmsProp and Adam given with Figure 13.

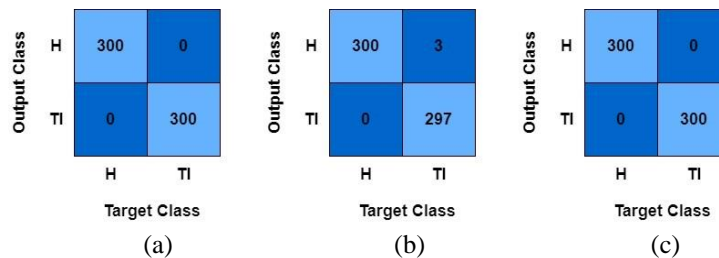


Figure 13. EfficientNet-b0 with (a) RmsProp (b) Adam and (c) Sgdm (H: Healthy, TI: Tuberculosis Infected)

Our findings are showcased through loss graphs depicting the top-performing deep learning models which consist of ResNet-50 with sgdm, DarkNet-53 with sgdm, MobileNet-v2 with adam, GoogleNet with sgdm and EfficientNet-b0 with sgdm in Figure 14 only for 1 epoch and 116 iterations. These findings illustrate the overall performance of applied algorithms. The training and validation errors decrease as the number of iterations increases. To sum up, the simulation results indicate that the loss-rate estimates derived from the algorithms are sufficiently precise for practical applications.

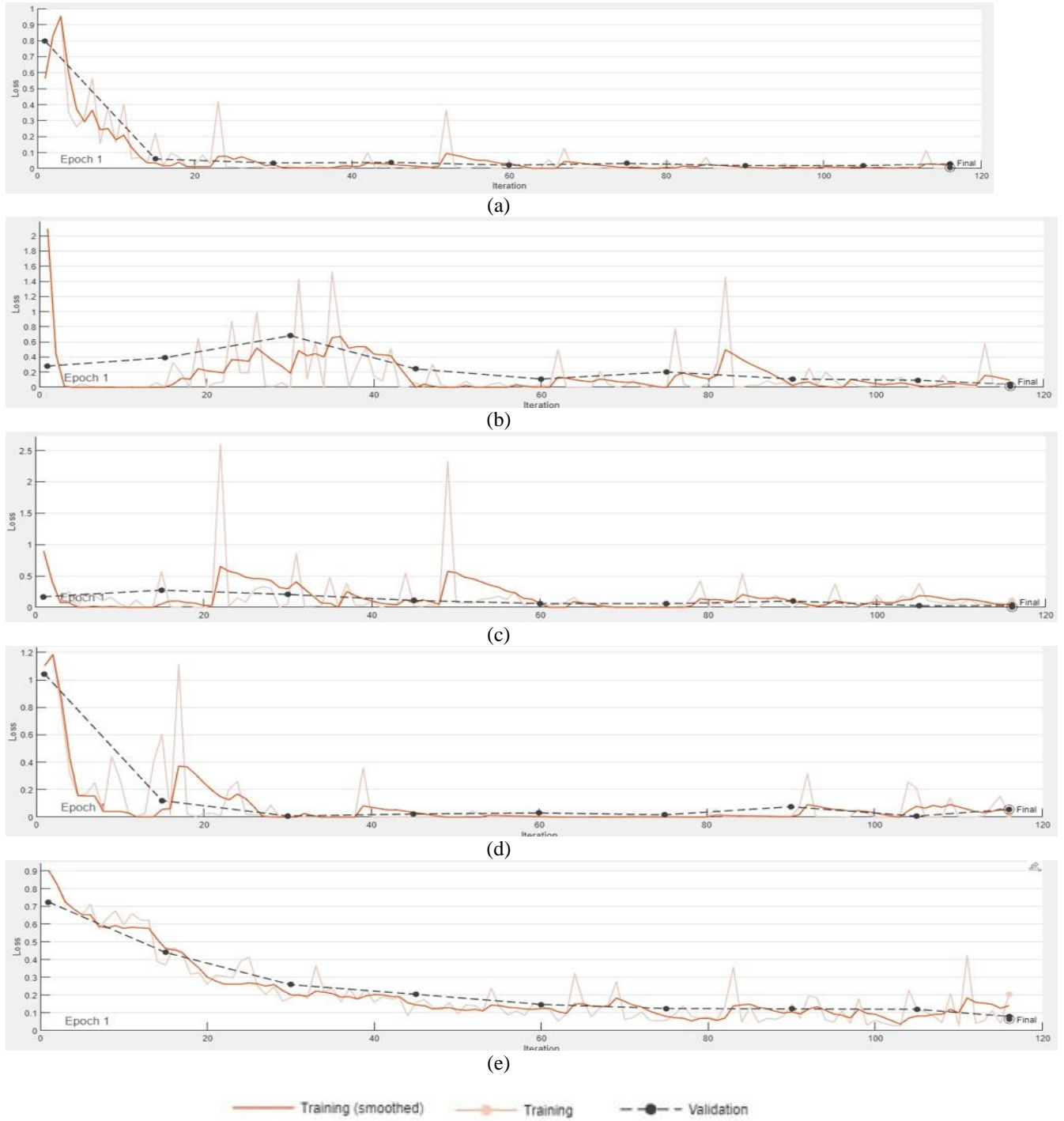


Figure 14. Loss graphs for (a) ResNet-50 (sgdm) (b) DarkNet-53 (sgdm) (c) MobileNet-v2 (adam) (d) GoogleNet

4. Conclusions

To effectively classify bovine meat dataset as tuberculous infected and healthy this research provides a systematic and comprehensive use of DL models. This image dataset is analyzed using, ResNet-50, DarkNet-53, MobileNet-v2, GoogleNet, and EfficientNet-b0 with RmsProp, Adam and Sgdm optimizers to classify and identify the *bTB*. Performance parameters are computed to measure the superiority of the DL models. The classification results indicated that the ResNet-50, DarkNet-53 and GoogleNet with Sgdm optimizer, MobileNet-v2 with Adam optimizer and EfficientNet-b0 with RmsProp and Sgdm optimizers, are obtained the highest classification accuracy in the classification of bovine meat images into healthy and tuberculous infected classes. Based on these findings, our comprehensive evaluation demonstrates that the introduced DL models showcase promising performance in tuberculous detection.

In summary, the main contributions of this study are as follows:

- The dataset is unique, comprising images of both tuberculosis-infected and healthy meat products from different sources.
- A comparative analysis of different CNN models (ResNet-50, DarkNet-53, MobileNet-v2, GoogleNet and EfficientNet-b0) in the context of *bTB* detection is important to determine how effectively these models can solve this problem.

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