



INTEGRATING TRANSFER LEARNING IN CONVOLUTIONAL NEURAL NETWORKS FOR BRYOPHYTE CLASSIFICATION

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ABSTRACT

This study delves into the rich and varied realm of bryophytes, which are non-vascular plants that are essential to terrestrial ecosystems. Over millions of years, bryophytes—which include mosses, liverworts, and hornworts—have changed their surroundings by absorbing nutrients and water, releasing it gradually, and making room for new plant growth. The study explores the taxonomy of bryophytes, emphasizing the difficulties associated with manual classification because of the large number of species. The paper suggests using Convolutional Neural Networks (CNNs) for automated plant species classification to overcome these issues. Effective CNNs for bryophyte classification are DenseNet121, MobileNetV2, Xception, ResNet50, InceptionV3, and ResNet-152. The use of open-source datasets and the project's implementation utilizing Google Colab, the Keras platform, and a Tensor Flow backend are described in the methods section. Based on confusion matrices, loading times, and accuracy, the study evaluates the effectiveness of many CNN algorithms. Based on the results, MobileNetV2 is the best-performing model, with an average loading time of 31.30 seconds and 90.90% accuracy while ResNet50 has the lowest accuracy of 36.03% and the slowest model for the average loading time is Xception with 73.30 seconds. The accuracy and loading times of other models, such as ResNet152, and InceptionV3, differ. By automating the classification of bryophyte species, CNNs can be a useful tool for scientists and researchers, as this study concludes. The work advances knowledge about bryophytes and offers information on how machine learning might be used to classify them.

Keywords: bryophytes classification, deep learning, convolutional neural network, python.

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INTRODUCTION

People often see land plants growing in damp and shady areas. In humid climates or low-lying areas, bryophytes grow profusely, forming a deep, soft mat on forest floors and rocky surfaces, tree branches and twigs, and flower stem branches. Bryophytes grow in many terrestrial ecosystems where aquatic organisms live on land in the Viridiplantae family. However, between 510 and 630 million years ago, land plants evolved from green algae. Molecular phylogenetic studies have determined that bryophytes were the first divergent lineage of living land plants. They consider the movement of plants from aquatic environments to land. Bryophytes share many physical characteristics with land and water plants.

In this way, Bryophytes have a huge impact on our environment, living in sterile soils and taking nutrients and water, slowly releasing them into the ecosystem, and then creating space for new plants to grow. It is sometimes considered a taxonomic division consisting of three groups of land plants that are not related by blood. They are classified into liverworts, worms, and algae. Each of these classifications has a different role in the environment. Since there are about 11,000 species of algae, 7,000 species of liverworts, and 220 species of hornworts worldwide, identifying each classification is not easy. Because bryophytes are not flowering plants, they reproduce by spores rather than seeds [1].

Plant species taxonomy is critical to biodiversity protection and conservation. Manual classification takes time and money, and it necessitates the use of trained professionals, who are frequently in short supply. To address these challenges, a variety of machine learning techniques for automated plant species classification have been developed [2]. Also, it can be difficult to break down large amounts of data, especially if you are trying to identify the type of bryophyte you want to use in your research.

Convolutional neural networks (CNNs) have attracted attention for their powerful feature extraction and information mining. CNNs have been used in many applications such as object recognition, high-resolution images, word segmentation, etc. due to their powerful feature extraction and learning techniques [3]. Image classification using Convolutional Neural Networks (CNN) has revolutionized computer vision by automatically and accurately recognizing the content of images. CNN image classification algorithms have gained popularity due to their ability to automatically learn and extract complex features from raw image data.

Using the power of CNN diversity models will help many scientists and researchers to correctly classify bryophyte species without looking closely.

Big Data is a large, diverse sets of information that grow at ever-increasing rates. It often comes from



data mining and arrives in multiple formats [4]. It is used to make prediction systems by analyzing the collection of interconnected and interrelated data that affects the real world.

Big Data enables new, highly effective methods for organizing, carrying out, sharing, and evaluating research, revolutionizing the creation of knowledge both inside and outside of science. The last several decades have seen the development of new methods for gathering, storing, and analyzing data. This has led to the area of data science emerging, which combines statistical, mathematical, computational, and algorithmic techniques to extract insight from large data sets [5].

Big Data Analysis, using CNN, is applied to various fields such as speech recognition, image classification, and learning methods in language processing [6].

CONCEPTUAL LITERATURE

Transfer Learning

Machine learning models are often designed to perform in isolation and must be rebuilt when features and data change. However, previously learned machine learning knowledge is frequently transferable to similar jobs [7]. Instead of rebuilding the models, which often requires a significant amount of effort, transfer learning seeks to reuse the model and obtained knowledge, as well as substantially reduce model development time and increase model performance of isolated learning.

Architecture of TensorFlow

TensorFlow is designed to support and manage computational graphs with the latest ML models and source-level optimizations. TensorFlow supports programming language interfaces like C++, Python, etc. When building and compiling programs with the TensorFlow system, the language binding calls the TensorFlow library, which contains the main operating system. This allows developers to deliver complex computing on CPUs, GPUs, desktops, servers, or mobile devices [8].

This means that programmers can create a single program that can easily run on different devices. There are three main parts of the TensorFlow architecture: the first is data processing, which allows programmers to write code in many programming languages, and TensorFlow translates it into a set of hardware instructions for the CPU, GPU, Android, etc. The second is to build the pattern in layers. Since this is the last example to train and estimate the model, developers can use the Model Estimator with Keras. TensorFlow processors can support neural networks, logistic regression, and linear regression.

Bryophytes

They are non-vascular plants and they absorb nutrients and water from the air through their surface. Bryophytes thrive in damp environments but are also

found in diverse and extreme habitats. According to Noris Salazar Allen, Bryophytes can reveal information about how the first plants adapted in their quest for the terrestrial environment [9]. Having said that, all existing Bryophytes are newly evolved and a lot of the predecessors have disappeared.

Hornworts

Hornworts are spore-producing plants that do not bear flowers. The spores are usually produced in a tapering, needle- or horn-shaped capsule that forms from a flat, green sheet. They belong to the subclass Anthocerotidae, class Anthocerotopsida, order Anthocerotales. Their gametophytes are usually flattened and thallose structures are typically less than 2 cm. Their sporophyte, on the other hand, forms a tapered cylinder and is dependent on gametophyte for nutrients and water [10].



Figure-1. Hornwort.

Mosses

A moss is a type of plant that produces spores in the form of tiny capsules and lacks flowers. Like other Bryophytes, it shows an alternation of generation between gametophytes which consist of the reproductive organs, and sporophytes which produce the spores. The gametophytic generation constitutes the stemlike and leaflike structures while the sporophytic generation develops from the gametophyte that usually consists of a stalk or seta which terminates in the sporangium [11].



Figure-2. Moss.

Liverworts

The tiniest living plants are liverworts, which can have leafy filaments as small as 0.02 in (0.5 mm) in diameter, and plants as big as 8 in (20 cm) in diameter. Gametophytes develop straightforwardly from spores in the majority of the species of Liverworts. The two classifications of Liverworts are Thallose Liverworts which has a ribbon-like body and Leafy Liverworts which has a structure that resembles leaves and is most abundant in tropical and subtropical regions [12].



Figure-3. Liverwort.

DenseNet121

Densely Connected Convolutional Networks, or DenseNet for short, is a kind of Convolutional Neural Network (CNN) made by Gao Huang and his colleagues in 2016. This model allows each layer to obtain additional inputs from all the previous layers and passes its feature-maps to succeeding layers. Concatenation is used which means that all layers are connected in such a way that they would receive “collective” knowledge from previous layers thus this model has higher computational and memory efficiency. Being a deeper variant, it can learn more intricate patterns and representations from the data [13].

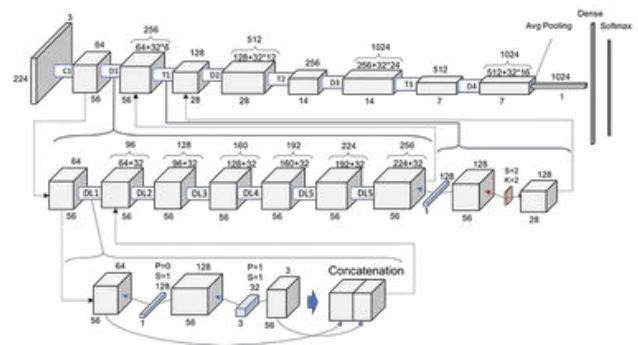


Figure-4. Diagram of DenseNet121.

MobileNetV2

Unlike traditional residual models, which use expanded representations in the input, the MobileNetV2 architecture is based on an inverted residual structure, where the input and output of the residual block are thin bottleneck layers. In the intermediate expansion layer, MobileNetV2 filters features using lightweight depthwise convolutions [14]. They are based on a simplified architecture that can create lightweight deep neural networks with minimal latency for mobile and embedded devices using depthwise separable convolutions. It was introduced by Google in 2017 based on TensorFlow [15].

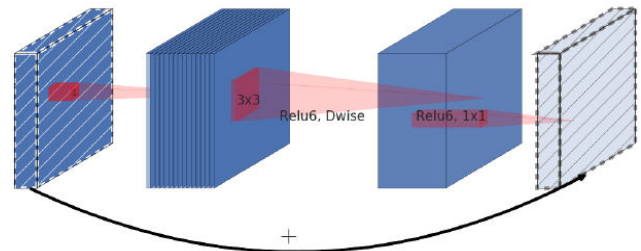


Figure-5. Diagram of MobileNetV2.

Xception

Stands for “Extreme Inception”, this model’s architecture is a linear stack of depthwise separable convolutions with residual connections. As a model that utilizes depthwise separable convolutions, it can look at channel and spatial correlations independently in successive steps [16]. This model was made by Francois Chollet, who works at Google and is also the creator of Keras, and its name was taken from Christopher Nolan’s movie “Inception” which focuses on embedded dream state [17].

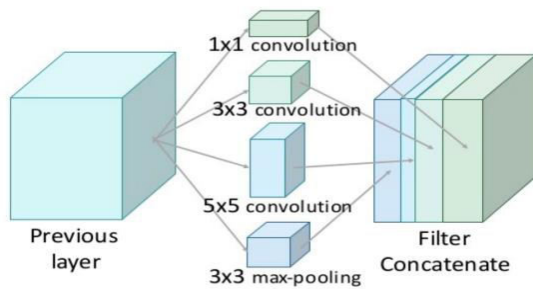


Figure-6. Diagram of Xception.

ResNet50

ResNet models paved the way to increase the number of convolutional layers in a CNN without encountering the vanishing gradient problem using the idea of shortcut connections [18]. Meaning, the shortcut connection skips some layers thereby converting a regular network into a residual one. This model was introduced in the paper “Deep Residual Learning for Image Recognition by Kaiming He, Xiangyu Zhang, Shaoqing Ren, and Jian Sun in 2015 [19].

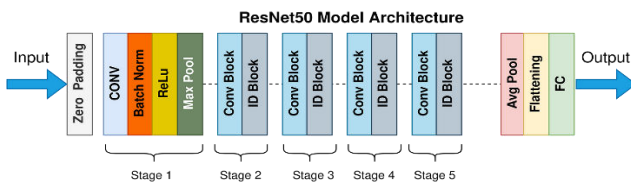


Figure-7. Diagram of ResNet50.

InceptionV3

InceptionV3 is a deep learning based on CNN that is employed as an image recognition model. This model uses factorized convolutions to reduce the computational complexity while maintaining representational power thus giving this model a better accuracy and less computational costs [20]. This was introduced by Szegedy *et al.* in their paper “Going Deeper with Convolutions” in 2014 [21].

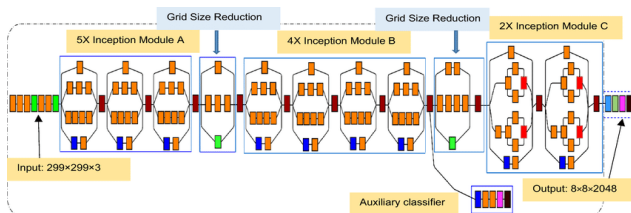


Figure-8. Diagram of InceptionV3.

ResNET-152

The proposed coding network is a modified ResNet-152 network, where the first two blocks are determined, and the weights of the last block are learned using the transfer learning method. The above coder can reduce the computational complexity of the proposed model and take advantage of features and components.

The researchers proposed a multidimensional feature extraction (MFE) feature block that combines the Pyramid Pooling Architecture (PPA) with several convolutional heuristic layers that exploit the high-level features of the coding network to extract features at different scales. Using PPA in the MFE block preserves the maximum value in all composite regions, maintains contextual relationships between pixels in complex video frames, and can handle various challenging situations. The proposed decoding network consists of cross-conversion layers that predict the score map by learning the map from image space to image space. The developer of this model is the same as the developer of ResNet50.

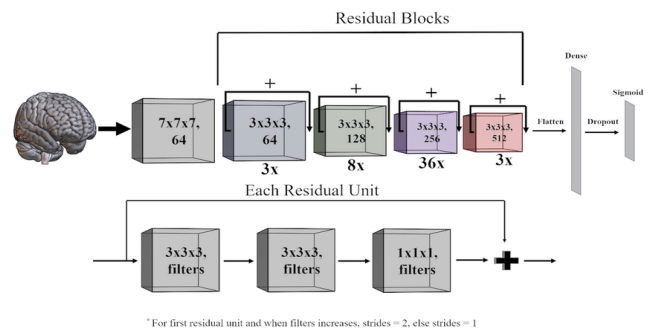


Figure-9. Diagram of ResNet152.

METHODOLOGY

Data Sets

The images needed for the development of the project are collected from the www.britishbryologicalsociety photo atlas specifically in www.britishbryologicalsociety.org.uk and from different research institutes and organization sites. Figure 1 shows a sample of images of bryophytes classified as Hepaticopsida (Liverworts), Anthocerotopsida (Hornworts), and Bryopsida (Mosses).



Figure-10. Sample images of dataset.



The datasets come from a collection of open-source biological research institutes and other free-text biological websites and are manually imported. The

dataset is composed of 3 categories of bryophytes and each image is in a .jpeg extension. There is a total of 2 83 images and the breakdown is shown in Table-1.

Table-1. Dataset.

Bryophytes	Number of Images	Train Data	Test Data	Validation Data
Hepaticopsida (Liverworts)	465	393	72	72
Anthocerotopsida (Hornworts)	391	319	72	72
Bryopsida (Mosses)	479	404	75	75
Total	1335	1116	219	219

The dataset is divided to 80% for training and 20% for testing. The validation data is collected from either the train data or the test data. As shown in Table-1, train data composed of 1,116 images while the validation data composed of 219 images.

Experiment

The program will be implemented using Google Collab which allows anybody to write and execute arbitrary Python code through the browser. Keras platform will be used with the TensorFlow backend in coding the system. This system can classify different classes of bryophytes specifically: Hepaticopsida (Liverworts), Anthocerotopsida (Hornworts), and Bryopsida (Mosses). This will be done by using the transfer of learning of convolutional Neural Networks such as Desnet121, MobileNetV2, Xception, Resnet50, InceptionV3, and ResNET-152.

the model without its top layers as they will be replaced with custom layers for the specific classification task. The weights of the pre-trained layers are frozen to prevent them from being updated during training. The global average pooling layer and two dense layers are added to the model for classification. The model is compiled with the Adam optimizer. After completing the foundation of the codes, the training and validation data are loaded using 'flow_from_directory' with a specified target size and batch size. Each model is trained using the fit method with the training and validation generators. The trained model was saved and will be used to determine the accuracy test of the specific model.

The formation of the confusion matrix is plotted to assess the performance of the classification model. By setting up the confusion matrix, the first is to evaluate the model on the validation set. Next, that is to generate and plot the confusion matrix. The confusion matrix is computed using the true and predicted labels. With the help of 'seaborn' and 'matplotlib,' the confusion matrix will be plotted automatically.

In order to determine the accuracy of each model. At first, the saved model has been save to that file. After that, evaluating the model on the test set is necessary. The method to assess the model's performance on the test set. The test set is processed in batches, and the number of steps is determined. Finally, the test loss, and test accuracy will be determined.

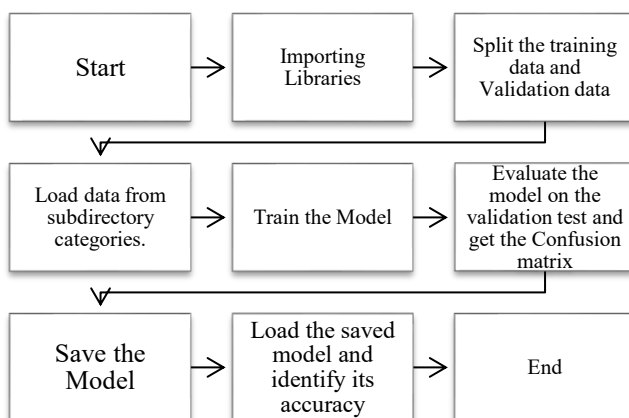


Figure-11. Program flowchart of the Python Code.

The program starts with organizing imports such as numpy, Keras, tensorflow, and matplotlib. Then, split the training and testing data by configuring the dataset into specific directories (training, testing, and validation). After that, define each constant specifically: Image size, Batch Size, Epochs, and the number of classes. Next is to load

RESULTS

To compare and validate the effectiveness of each pre-trained convolutional neural network in the classification of bryophytes, the following criteria were used: confusion matrix, loading time, model accuracy and model loss.

Confusion Matrices

Figure 12-17 depicts the confusion matrices of various models over the three classes of the classification of bryophytes. The row denotes a predicted class, whereas the column represents the actual class. This demonstrates



the misclassification similarities among the various convolutional neural networks.

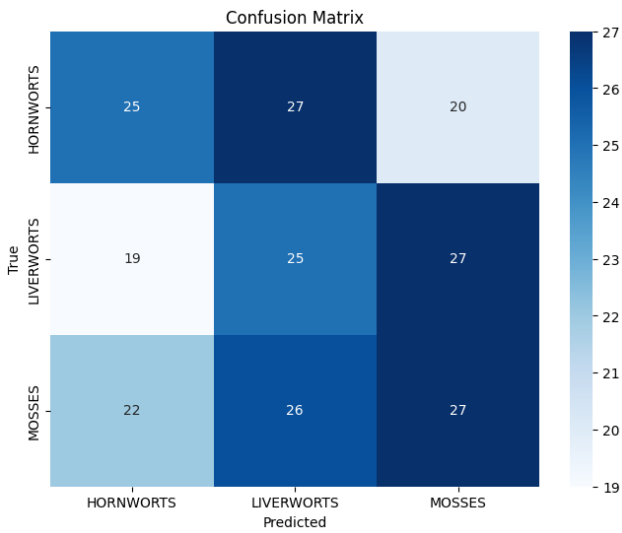


Figure-12. Confusion matrix of MobileNetV2.

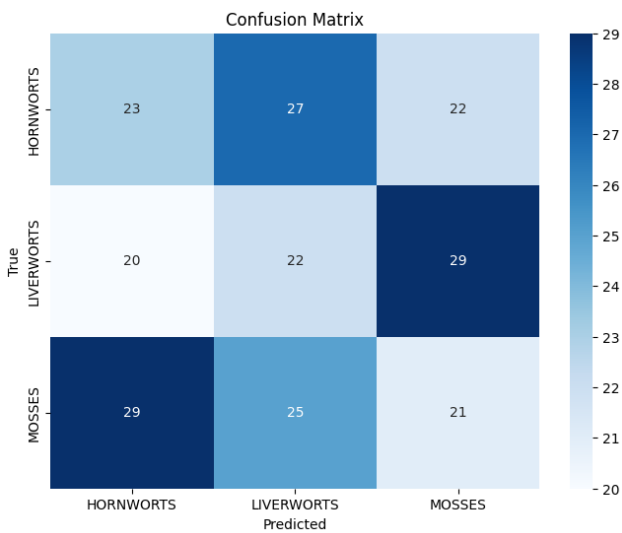


Figure-13. Confusion matrix of Xception.

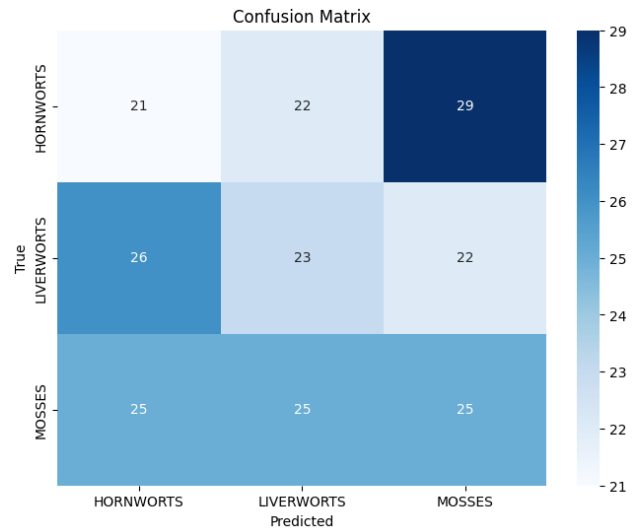


Figure-14. Confusion matrix of ResNet152.

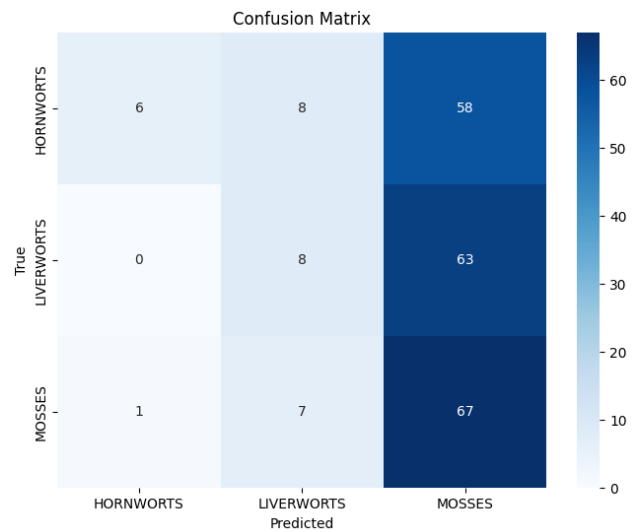


Figure-15. Confusion matrix of ResNet50.

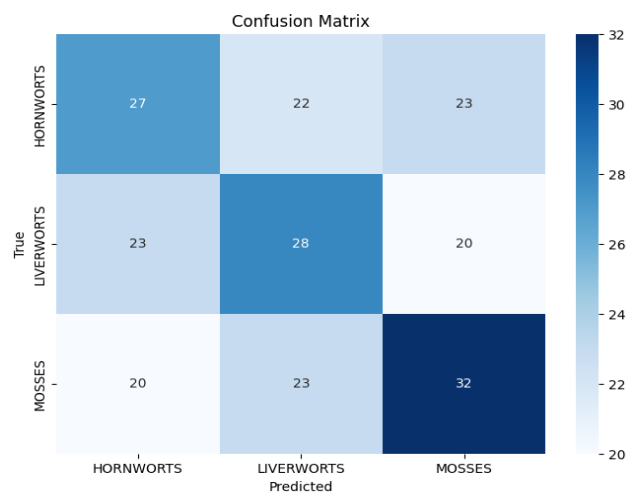


Figure-16. Confusion matrix of DesNet121.

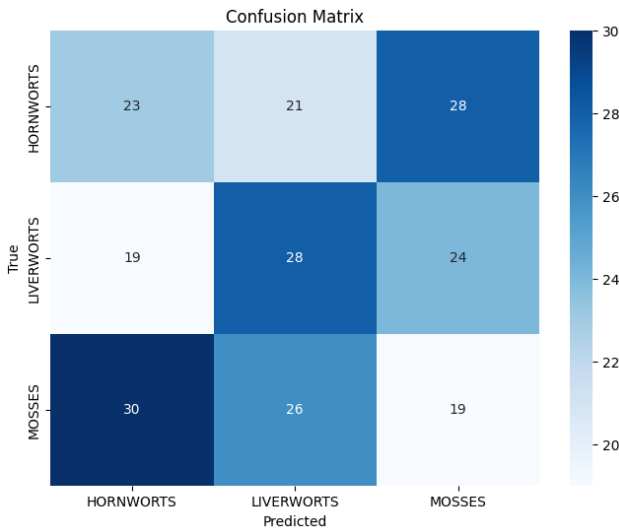


Figure-17. Confusion matrix of InceptionV3.

Model Accuracy and Model Loss

Figure 18-23 depicts the model accuracy and model loss of various models over the three classes of the classification of bryophytes. The accuracy metric is used to quantify the algorithm's performance in an understandable way. The accuracy of a model is often assessed after the model parameters and calculated as a percentage.



Figure-18. Model accuracy and model loss of MobileNetV2.

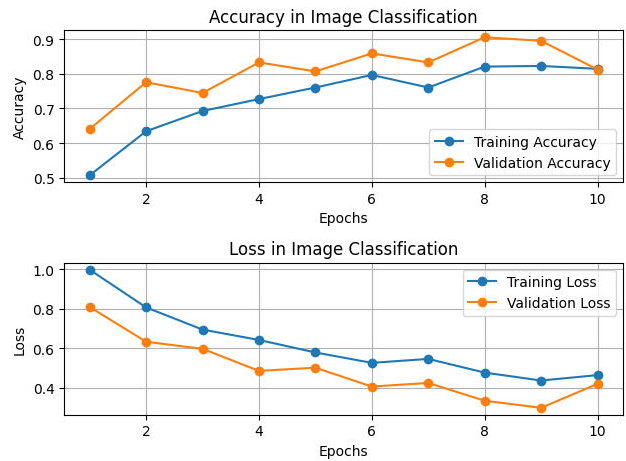


Figure-19. Model accuracy and model loss of Xception.

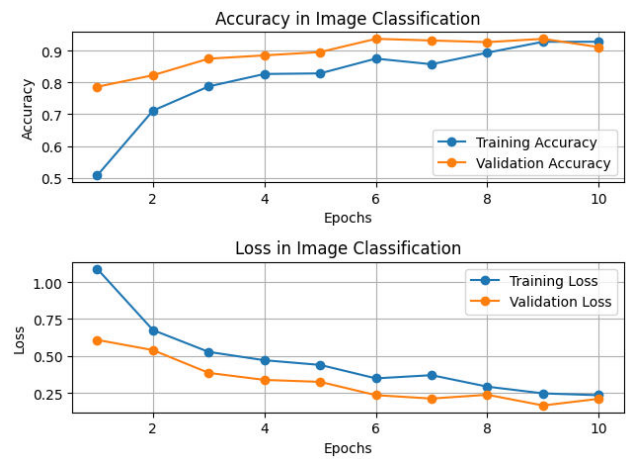


Figure-20. Model accuracy and model loss of ResNet152V2.



Figure-21. Model accuracy and model loss of ResNet50.

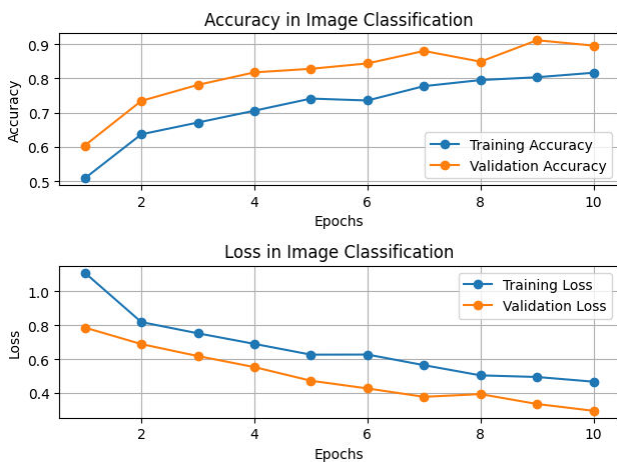


Figure-22. Model accuracy and model loss of DensNet121.

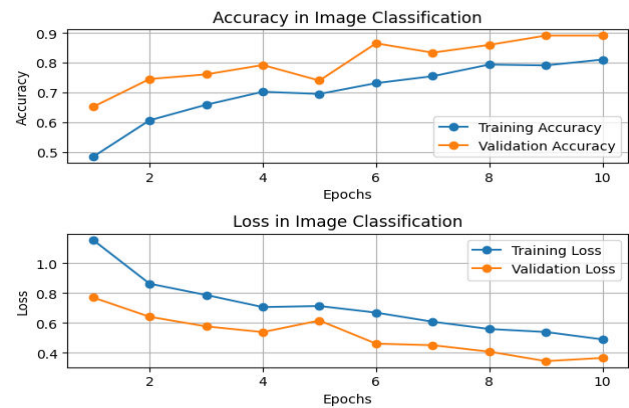


Figure-23. Model accuracy and model loss of InceptionV3.

Loading Time, Weight Size and Accuracy

The highest performing model is MobileNetV2 with an accuracy of 90.90%, with a weight size of 9.87MB, and with a loading time of 31.3 seconds. ResNet50 had the lowest accuracy of 36.03% while also having the highest validation loss which peaked at more than 100%.

Table-2. Evaluation of each model by its accuracy and loading time.

Model	Weight size	Loading time (seconds)	Accuracy (Percent)
MobileNetV2	9.87MB	31.3	90.90
Xception	81.58MB	73.3	87.22
ResNet152V2	224.52MB	38.4	90.81
ResNet50	91.98MB	37.8	36.03
DensNet121	27.85MB	36.4	89.43
InceptionV3	85.17MB	83.8	84.10

CONCLUSIONS

This study is used to classify different images of Bryophytes by recognizing every pixel of the images in the data set to provide which would be very hard if we relied on our perception and the recognition of our naked eyes alone.

As seen from the results from the six pre-trains CNN models utilized for this study, MobileNetV2 is the best performing one with an accuracy of 90.90% while at the same time, also having the fastest average loading time per epoch of 31.30 seconds and weight size of 9.87MB. On the other hand, ResNet50 had the lowest accuracy of 36.03% while also having the highest validation loss which peaked at more than 100%. The slowest model for average loading time is Xception with 73.30 seconds.

More research is needed to gather more accurate data when using pre-trained Convolutional Neural Networks (CNN) for classifying Bryophytes. The proposed method would help generate more datasets that

are collected by experts of the field to better utilize the CNN’s powerful ability to analyze and classify big data.

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