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Microscopic identification of brazilian commercial wood species via machine-learning

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TECHNOLOGY OF FOREST PRODUCTS

ABSTRACT

Background: Multiple challenges are faced by industry and certification agencies when commercializing tropical species. Anatomical similarities of tropical hardwoods impair identification. Deep learning models can facilitate microscopic identification of wood by using sophisticated techniques such as deep convolutional networks (DCNN). Our objective was to microscopically identify 23 commercially available Brazilian wood species using a custom DCNN model.

Results: Photographs from microscopic slides of each wood species were processed, and the final data set contained 2,448 images. We applied stratified k-fold cross-validation technique during training to increase model's robustness and trustworthiness. Thus, the dataset was divided into approximately 80% training (1,958 images) and 20% validation (490 images) for each fold. A series of augmentations were performed only on training data to include variations in rotation, zoom, and perspective. Image augmentation was performed on-the-fly. The network consisted of convolutions, max pooling, global average pooling, and fully connected layers. We tested the performance of the DCNN against accuracy, precision, recall, and F1-score on the validation set for each fold.

Conclusion: The custom machine learned model accuracy was higher than 0.90. The model's worst performance was identified in distinguishing between Toona ciliata and Khaya ivorensis, which was due more to wood variability than to a machine learning deficiency. Future studies should focus on integration, verification/monitoring, and updating of current models for end user manipulation, trust, ethics, and security.

Keywords: convolutional neural networks (CNN); deep learning; tropical species; wood anatomy; wood identification.

HIGHLIGHTS

Novel, robust, and fast methods to accurately identify wood are needed.
Machine-learning can be applied to help anatomists' judgment in forensic wood identification.
The custom machine-learned model achieved accuracy higher than 0.90.
Sequential convolutional layers offered the best performance to identify Brazilian commercial wood species.

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INTRODUCTION

The Brazilian flora shows one of the most diverse collections of wood species in the world (Amaral et al. 1998). This carries deep consequences to local, national, and global markets due to the unique wood properties found in tropical species that are desirable and valued by multiple industries, namely high durability against decaying organisms; remarkable stiffness and strength; high density and hardness; acoustic properties, and adequate dimensional stability (Almeida et al. 2017; Longui et al. 2010). For this reason, tropical species are often illegally harvested or traded, resulting in major local, state, and international concerns such as fraud, misrepresentation, and misclassification (FMM). FMM can be intentional with the aim of deceiving the buyer and legal authorities, or unintentional due to a lack of knowledge about wood anatomical elements that are crucial to correct identification. Either way, FMM violates Brazilian and international laws, creates unbalanced environments, and economically affects Brazilian states and federal government (Grant and Chen, 2021).

To expand the level of wood identification, researchers across the globe have developed manuals, atlases, and identification keys for several species. A few examples are the Tropical Woods Series, developed by The School of Forestry at Yale University from 1925 through 1960, which described tropical species from Colombia, Venezuela, Guianas, and Brazil (Wilson 1960). In Brazil, the most extensive work in wood identification was made by the Brazilian Forest Service (LPF) and Florsheim et al. (2020). In Florsheim et al. (2020), more than 350 commercially available wood species were described in detail for in-creasing efficiency and assertiveness in the act of inspection. The dataset contains 10x magnified images of the cross section for identification. However, in some instances, identification of the species level is not feasible by only looking at macroscopic images or at 10x magnifying glass, thereby microscopic level is required.

Multiple approaches using machine learning have emerged in the last years to ameliorate the limitation of scalable wood identification as they rely on human expertise for forensic wood analysis. Most of the wood identification based on machine learning research is done through either feature extraction or computer vision approaches. Both techniques use either microscopic or macroscopic cross-sectional images of wood. In this context, de Andrade et al. (2020) developed intelligent systems able to classify 21 species of Brazilian flora using support vector machines (SVM). Results indicated that the best model achieved 97.7% accuracy. In other study, Souza et al. (2020) used local binary patterns (LBP) to extract information for discrimination of 46 Brazilian species using SVM, artificial neural networks and random forests. They reported F1-score of 97.67% when using SVM. However, the literature points out major drawbacks when using SVM. According to Han and Jiang (2014), SVM algorithm is prone to overfitting when the number of features is higher than number of samples, and can be time-consuming when training large datasets, as well as weak when finding boundary separations in large datasets (Cervantes et al., 2020). Similarly, LBP is not rotation invariant, and segmentation is determined based on pixel intensity codes (Vidya and Chandra, 2019).

The advancement of artificial intelligence is the core of enhanced performance for all industries to implement industry 4.0. Computer vision methods have risen since the breakthrough in machine learning, more specifically deep learning, with the work of (Krizhevsky et al., 2012) using convolutional neural networks to identify 1,000 different classes. Since then, CNNs have been applied in several domains namely, precision agriculture, information content security, data monitoring, and surveillance (Rahnemoonfar and Sheppard, 2017; Christiansen et al., 2016; Muhammad et al., 2018; Moy de Vitry et al., 2019). More recently, CNNs have been implemented in wood identification based on anatomical features. For example, Hafemann et al. (2014) identified microscopic images from Martins et al. (2013) dataset using CNNs with two convolutional and maxpooling layers, followed by fully connected layers. The method reached 97.32% of accuracy. However, it is not clear how the validation set was defined. Similarly, in research developed by Garcia-Pedrero (2020), a convolutional neural network model was developed to microscopically segment xylem vessels of Nothofagus pumilio. The method achieved 90% of pixel accuracy. Furthermore, deep learning has the potential to revolutionize and expand the wood anatomy field, promote a sustainable environment, and ensure economic growth.

Machine learning is rapidly growing into the wood identification field (Hafemann et al. 2014; Tang et al. 2017, 2018; De Geus et al. 2021) as the number of professionals capable of performing identification is declining (Lens et al. 2020). Furthermore, this new technology has the potential to alleviate current constraints in the wood identification body. To that end, our hypothesis is that convolutional neural networks can identify a wide range of microscopic Brazilian wood species accurately, reliably, and quickly. The overall goal of this research was to expand the use of artificial intelligence and machine learning, in microscopic wood anatomy for the Brazilian market. To that end, our objective was to develop a custom deep convolutional neural network (DCNN) to accurately identify 23 commercially available species. For training and validation of the DCNN model, we used a limited dataset from microscopic slides of the cross-section, and to increase robustness and trustworthiness, we performed data augmentation and cross-validation.

MATERIAL AND METHODS

Dataset acquisition

The species were donated from other Brazilian to build a research and development program in wood anatomy. Identification of each species was carried out by an expert with many years of training in microscopic identification of Brazilian flora, which ensures rigidity in the process for high accuracy and robustness of the machine learning model. Some species were chosen based on their potential to be commercialized in the Brazilian market by legal means.

Before image acquisition microscopic slides were produced for each species. First, wood species with size of 2 cm × 2 cm × 3 cm (radial × tangential × longitudinal) were softened through boiling in deionized water. Thereafter, 20 μm permanent histological microscopic were obtained by using a commodity microtome. The veneer was dehydrated by a series of alcohol concentration, and thereafter colored using safranine (Yeung et al. 2015). Finally, the cross-sectional images were obtained from the veneers using a 50× micro-scope (Zeiss Axion Scope). The resulting images were then saved in JPEG format with a resolution of 2584 pixels × 1936 pixels. Table 1 describes the 23 species used in this work and the number of images per species and in Figure 1 the anatomical images.

Image pre-processing and training set-up

Deep learning models require a large number of images for accurate training and validation (Krizhevsky et al, 2012). To that end, the images were divided into eight non-overlapping 646 pixels x 486 pixels (width x height) sub-patches of grayscale depth to enlarge the initial dataset. The final dataset contained 2,448 images, and it was composed of imbalanced classes with minimal and maximum images varying from 80 to 192 respectively.

In order to control or avoid any possible model's overfitting and account for an unbalanced dataset, we leveraged the stratified k-fold cross-validation technique. In this procedure, the final dataset was randomly split into 5 (k=5) folds of mutually exclusive and shuffled subsets (training and validation) of proportional size. In other words, the dataset was divided into 80% training (1,958 images) and approximately 20% validation (490 images) for each fold. It is important to note that any given image appears only in the train or validation set, but never on both at the same time. In addition to cross-validation method, to overcome the highly variable nature of the target wood dataset, a series of augmentations were performed only on training data to account for variation in rotation, zoom and perspective. Image augmentation was per-formed on-the-fly. The images were firstly resized to 299 pixels x 299 pixels in size and randomly augmented for each epoch of training. The images were also randomly rotated (90°). Random perspective shifting in the range of (0, 0.15) was applied to simulate a variation in viewing distance. Finally, the images were randomly and vertically flipped. Without these techniques the custom network is drastically overfitted by memorizing the training dataset.

Table 1. The 23 wood species used for classification.

ID	Family	Common name in Brazil	Species	images
Aca	Fabaceae	Acácia	*Acacia mangium* Wild	5
Ang	Fabaceae	Angico	*Hymenolobrium petraecem*	5
Anp	Fabaceae	Angelim pedra	*Hymenolobium petraeum*	5
Anv	Fabaceae	Angelim vermelho	*Dinizia excelsa* Ducke	5
Cav	Fabaceae	Caviúna	*Dalbergia nigra*	5
Ced	Meliaceae	Cedro	*Cedrela* sp.	6
Cer	Fabaceae	Cerejeira	*Amburana cearensis*	5
Gar	Fabaceae	Garapa	*Apuleia leiocarpa* (Vogel) J. F. Macbr.	6
Gon	Anacardiaceae	Goncalo alves	*Astronium* sp.	5
Jac	Moraceae	Jaca	*Artocarpus heterophyllus* Lam.	6
Jeq	Lecythidaceae	Jequitiba	*Cariniana legalis* (Mart.) Kuntze	6
Kha	Meliaceae	Mogno africano	*Khaya ivorensis* A. Chev.	6
Kir	Paulowniaceae	Kiri	*Paulownia tomentosa* (Thunb.) Steud	10
Lou	Lauraceae	Louro canela	*Nectandra rubra* (Mez) C. K. Allen	12
Mar	Simaroubaceae	Marupa	*Simarouba amara* Aubl.	5
Mui	Anacardiaceae	Muiracatiara	*Astronium lecointei*	5
Pam	Rutaceae	Pau marfim	*Balfourodendron riedelianum* (Engl.)	11
Rox	Fabaceae	Roxinho	*Peltogyne angustiflora* Ducke	8
Swi	Meliaceae	Mogno brasileiro	*Swietenia macrophylla* King	11
Tau	Lecythidaceae	Tauari	*Couratari* spp.	10
Tec	Lamiaceae	Teca	*Tectona grandis* L. F	5
Too	Meliaceae	Cedro australiano	*Toona ciliata* M. Roem	6
Vin	Fabaceae	Vinhático	*Plathymenia foliosa* Benth.	5

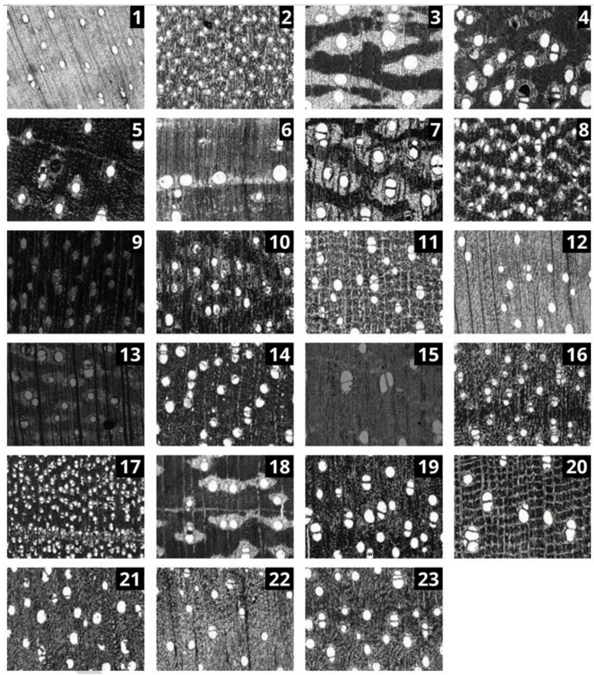

Figure 1. The 23 wood species used for classification (1: Aca; 2: Ang; 3: Anp; 4: Anv; 5: Cav; 6: Ced; 7: Cer; 8: Gar; 9: Gon; 10: Jac; 11: Jeq; 12: Kha; 13: Kir; 14: Lou; 15: Mar; 16: Mui; 17: Pam; 18: Rox; 19: Swi; 20: Tau; 21: Tec; 22: Too; 23: Vin).

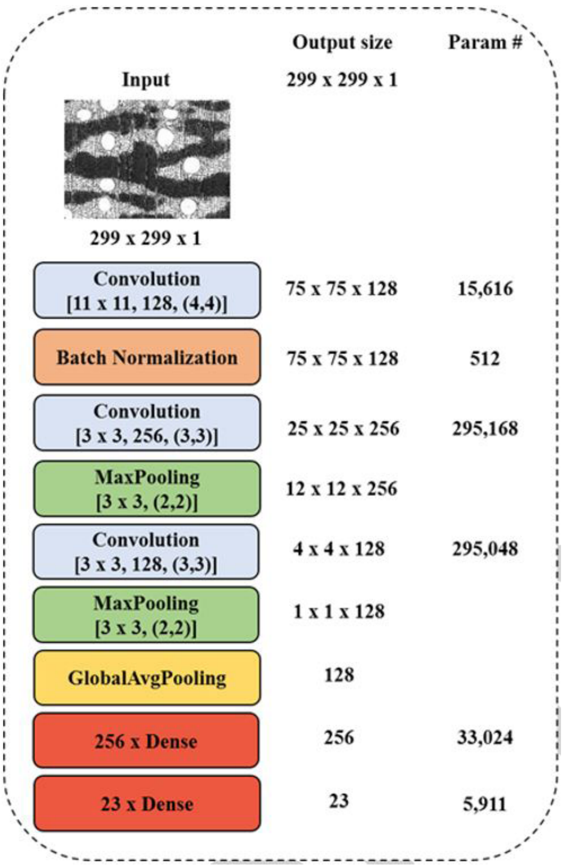

Figure 2. Network architecture. For convolution and max pooling layers [kernel size, filters, and strides] and [pool size, and strides], respectively.

In this study, a custom convolutional neural network model was developed to classify microscopic images of 23 wood species. The CNN model was inspired by Krizhevsky et al. (2012) with the use of convolutions, max pooling, batch normalization, and fully connected layers. The overall architecture is displayed in Figure 2.

The network took as input 299 x 299 grayscale images and outputted a vector for each image with one entry for each class (species). The network had one 11 x 11 convolutional layer, followed by a batch normalization layer. This was mapped into a 3 x 3 convolutional layer that increased the number of filters from 128 to 256. The reason for working with large receptive fields was to capture complex wood structures, such as vessels, parenchyma, and rays. This convolutional layer was followed by a 2 x 2 max pooling layer that decreased the image size by half. Next, a second 3 x 3 convolutional layer with reduced number of filters from 256 to 128 was applied followed by a 3 x 3 max pooling layer that also decreased the image size by half. Next, the network was composed of a global average pooling layer that calculated the average output of each feature map from the previous layer to reduce data complexity and prepare the model for final classification. Finally, the network had two fully connected layers, which produced a vector of size 256, and 23 which corresponded to the class probabilities (species). The entry with the highest value determined the predicted class of the species. In total, the network was constituted of 645,015 trainable parameters. The weights of the network were randomly initialized with glorot uniform. After each convolutional, batch normalization, max pooling, and fully connected layers, the rectified linear unit (ReLU) activation function that introduces non-linearity decision boundaries in the network was used. The ReLU function was defined as:

f(x)=x, if x>0
0, otherwise

The categorical cross function was iteratively minimized by training the CNN with the Adaptive Moment Estimator (Adam) optimizer, leveraging the stochastic descent and backpropagation algorithms. The learning rate was initially set to 10-2, and then progressively decreased by an exponential rate adapted from Szegedy et al. (2015). The training step was stopped when the training loss stalled for 25 epochs. We monitored training loss to certify model's convergence. The CNN model was run on Nvidia GPU with a batch size of 64 using Python 3.6, Tensorflow 1.14, and Keras 2.3.1. Training lasted for, on average, 298 epochs. It used Keras Model_checkpoint callback to evaluate model's performance after training, which saved the model when validation loss reached a minimum value. In this work, we trained the architecture from scratch. Average accuracy, precision, F1-score, and recall were then calculated on the validation set to evaluate the performance of the CNN, which correspond to Equations 1-4, respectively. The metrics were based on Sokolova and Lapalme (2009).

$$\text{Accuracy} = \frac{(\text{True Positives} + \text{True Negatives})}{(\text{Total Number of Samples})} \quad (1)$$

$$\text{Precision}=\frac{\text{(True Positives)}}{\text{(True Positives+False Positives)}} \quad (2)$$

$$\text{Recall}=\frac{\text{(True Positives)}}{\text{(True Positives+False Negatives)}} \quad (3)$$

$$\text{F1 score}=\frac{(\text{Precision}\times\text{Recall})}{(\text{Precision}+\text{Recall})} \quad (4)$$

Where: True Positives: Number of correctly recognized class examples. True Negatives: Number of correctly recognized examples that do not belong to the class. False Positives: Number of incorrectly assigned examples to the class. False Negative: Number of not recognized examples as class examples.

RESULTS

Figure 3 shows the loss and accuracy for each fold and epoch during training. For all folds the model reaches validation accuracy above 0.9.

Table 2 documents averaged model's performance against several metrics across all five cross-validated folds. The overall adjusted accuracy was 92.4% with several species reaching F1-score, which is the harmonic mean between precision and recall, near or higher than 95%.

Another method used to assess performance of machine learning models is confusion matrix. Figure 4 shows the averaged confusion matrix for the five-fold cross-validation method. As noted, several species reached remarkable accuracy such as, Ang, Anp, Gar, Gon, Kir, Mar, Pam, Rox, and Tau with more than 95% accuracy, which exceeds the performance of any field trained and wood anatomy expert.

DISCUSSION

The yellow and orange curves represent validation and training losses, respectively (Figure 3). Training loss supports the idea that the model was capable of fully learn all patterns of the training set, which in all cases converged in learning (loss app. 0 and accuracy app. 1). Validation loss is an index of how robust a model is during training when predicting "unseen images". Some fluctuations are normal as the model learns all features of each species. It is observed that validation loss decreased as training loss also decreased, which did not indicate overfitting. Blue and gray curves represent training and validation accuracies. They carry minimal performance results as high validation accuracy by itself does not indicate a model's prediction capacity on truly unseen data. To that end, the average lower validation loss during training was 0.2233.

It is crucial to break down the performance by species to fully understand where improvements need to be made (Table 2) In this case, data collection, network architecture, and hyperparameters should be altered to

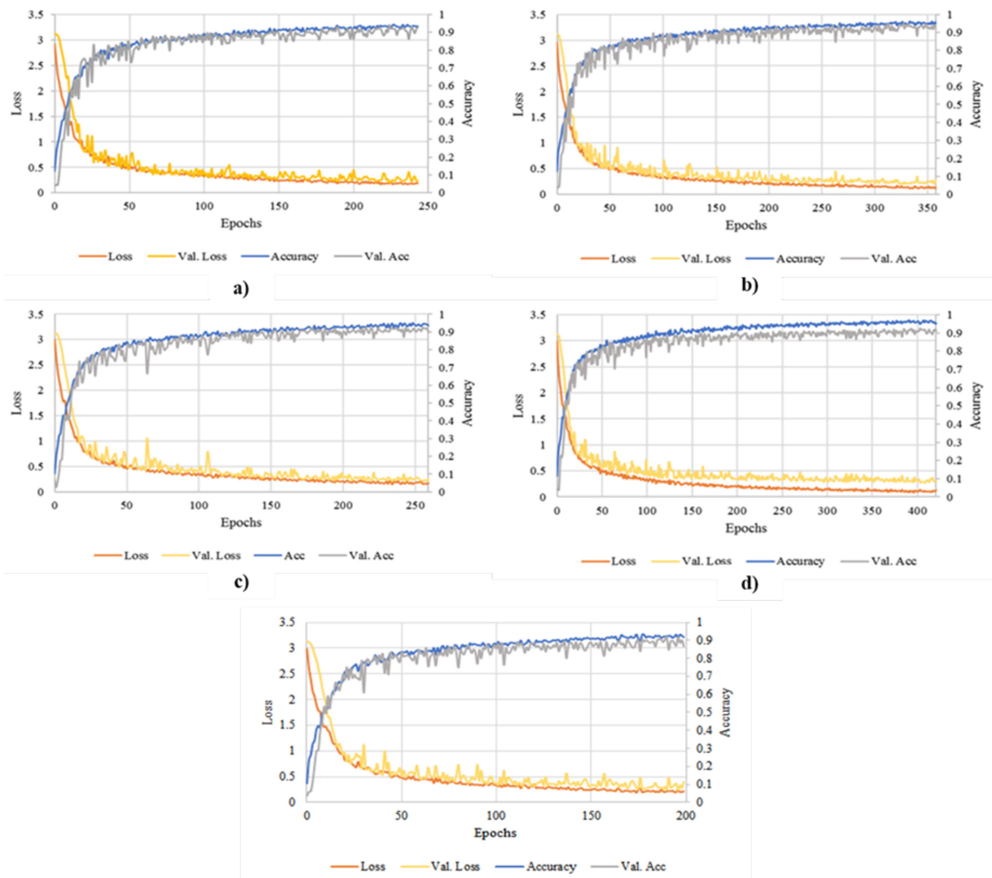

Figure 3. Training and validation losses and accuracies for fold 1 (a) through fold 5 (e).

obtain a better model performance. To that end, the F1-score of seven species, namely Ced, Jac, Kha, Swi, Tec, Too and Vin was below 90%. Similar results were found by Lens et al. (2020) using combination of both SVM and LBP to identify microscopic images of wood species (89.3% of accuracy). In our case, it may be explained by the lack of unique images, even though heavy data augmentation was performed.

Misclassifications were prevalent for Ced, Kha, Tec and Lou. with 0.21, 0.19, 0.21, and 0.14, respectively. The model confuses approximately 6% of Ced with Kha and Too, and 4% with Tec. Similarly, 16% of Kha is confused with Too and 9% with Tec. Lastly, another 5% of Tec images are confused with Vin. Similarly, Ravindran et al. (2018) found that a custom convolutional neural network model also showed poor performance in classifying images of Khaya, which was misclassified with *Carapa guianensis*. By reviewing the particular case of Kha and Too (Figure 5), although Too is a semi-ring-porous species and Kha is a diffuse-porous, this difference was not evidence from our dataset. Both species have solitary and radial multiples pores that are large to very large in size as well as scanty, vasicentric and marginal parenchyma. Maruyama et al. (2018) also reported misclassification while identifying microscopic images of hardwood charcoal. Species that had similar attributes were assigned to the wrong category.

Table 2. Averaged performance of the custom convolutional neural network.

Species ID	Precision	Recall	F1 Score
Aca	0.978	0.914	0.942
Ang	0.976	0.964	0.97
Anp	0.966	0.964	0.962
Anv	0.928	0.902	0.912
Cav	0.976	0.952	0.962
Ced	0.93	0.79	0.844
Cer	0.938	0.926	0.93
Gar	0.922	0.97	0.944
Gon	0.988	0.964	0.976
Jac	0.816	0.906	0.856
Jeq	0.97	0.968	0.966
Kha	0.802	0.812	0.802
Kir	1	1	1
Lou	0.966	0.866	0.912
Mar	0.988	0.988	0.988
Mui	0.916	0.888	0.9
Pam	0.994	0.988	0.994
Rox	0.908	0.968	0.936
Swi	0.904	0.88	0.89
Tau	0.988	0.976	0.978
Tec	0.808	0.788	0.79
Too	0.762	0.918	0.818
Vin	0.86	0.928	0.892

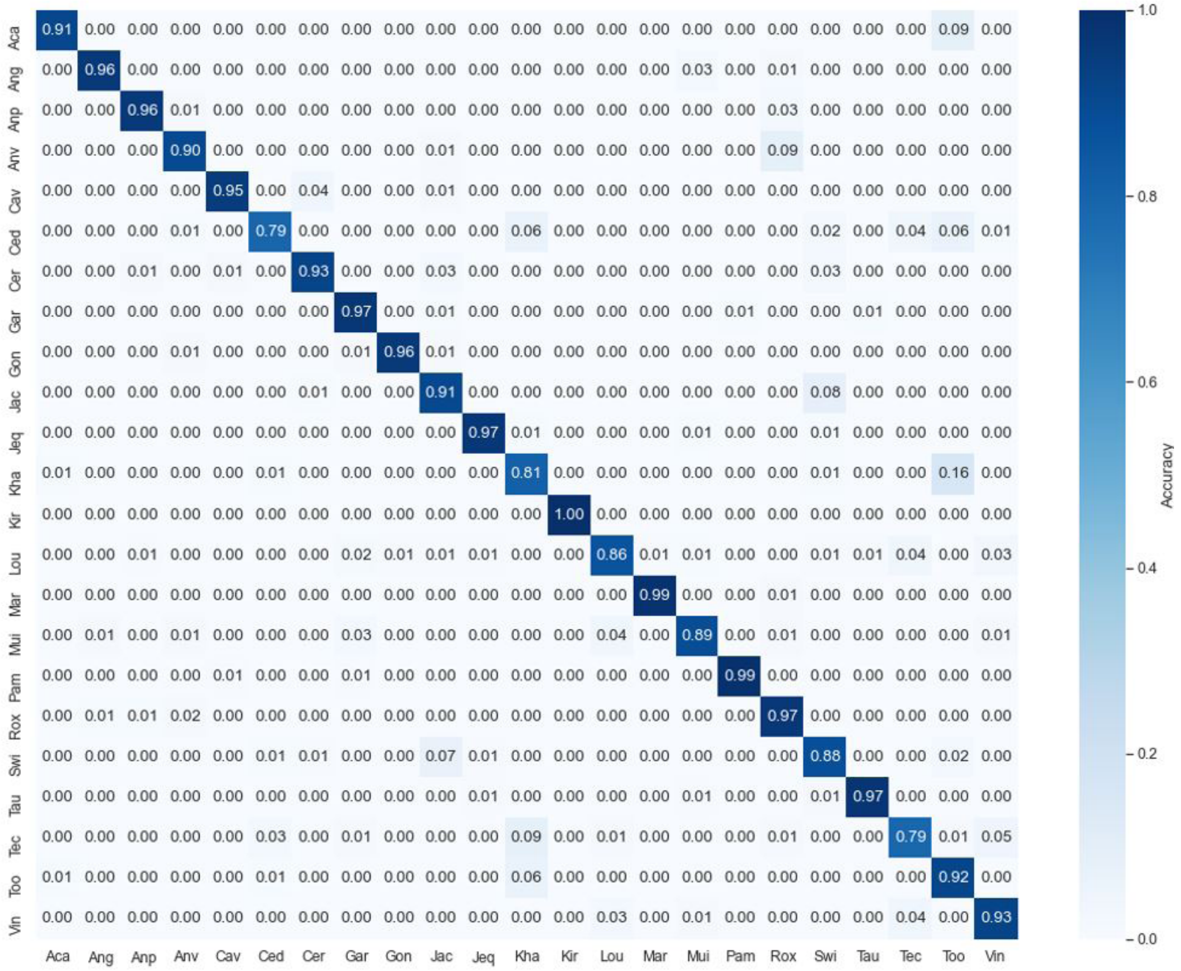

Figure 4. Averaged confusion matrix for five folds cross-validation.

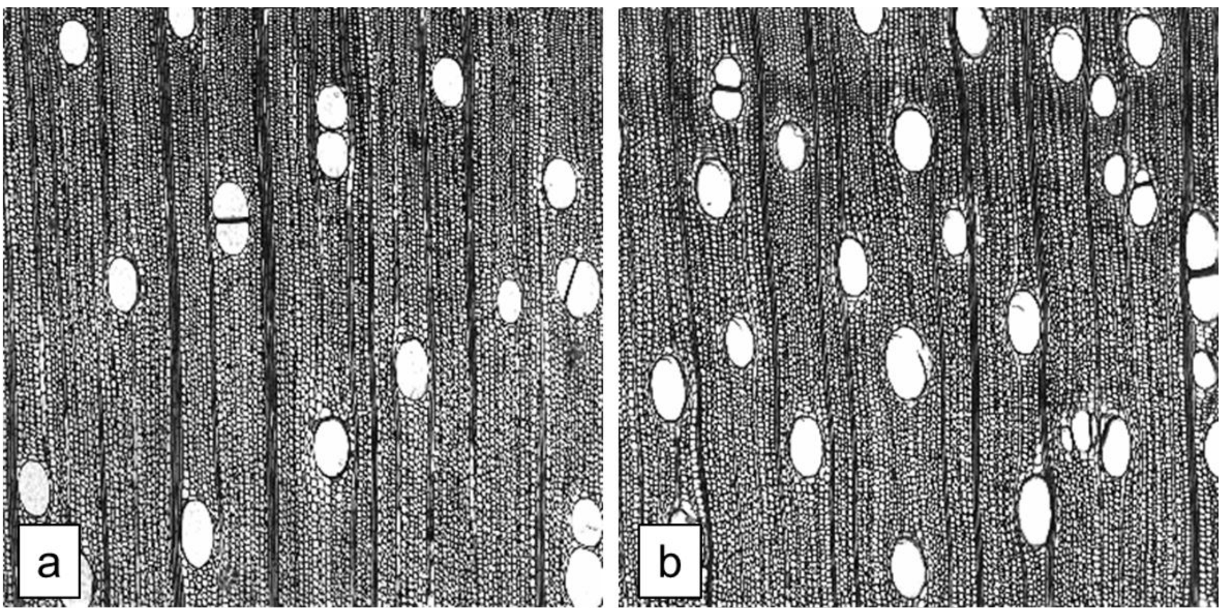

Figure 5. Example of images highlighting model's misclassification classes between Too (a) and Kah (b).

CONCLUSIONS

A custom convolutional neural network was constructed for distinguishing images of commercially available species either introduced or native from Brazil. The machine learned custom model accuracy was considered excellent (>0.90). In fact, in some instances the F1-score reached 0.99, which surpasses any human identification. The poor model's performance in distinguishing between Toona ciliata and Khaya ivorensis was more due to wood variability than a machine-learning problem.

Machine learned algorithms are becoming more frequent in wood science, which greatly offers rapid and robust analysis. In the context of this research, a trained deep learning model can significantly increase forensic wood identification and law enforcement and assist agencies economically as well as risk minimization. However, the wood science community still faces machine-learning deployment challenges even with modern timber identification performance. Therefore, future studies should focus on integration, verification/ monitoring and updating of current models for end user's manipulation, trust, ethics and security.

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AUTHORSHIP CONTRIBUTION

Project Idea: DJVL, JCM
Funding: DJVL, JCM
Database: JCM, LBM
Processing: DJVL, GSB, RFO
Analysis: DJVL, GSB, RFO
Writing: DJVL, JCM, LBM, GSB, RFO
Review: DJVL, JCM, LBM, GSB, RFO
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