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Disease detection in rice leaves using transfer learning techniques

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Abstract. Recent development in deep learning techniques have had a massive impact in the field of agricultural disease detection. The negative impact of pest and bacterial diseases to rice plants are well known, and for regions where rice is staple, this issue carries a lot of weight. This work proposes a high accuracy, transfer learned model that can provide a mobile solution for farmers and agricultural organizations to detect rice leaf diseases at hand. This study also utilizes a generative adversarial network to balance the number of disease samples. We compare our model to other transfer learning architectures as well. The presented model tested on a GAN augmented dataset, achieves an average cross validation accuracy of 98.79% outperforming paradigm classification architectures. The model is also compared on 3 different datasets, without the GAN augmentation, establishing benchmark performance of 98.38% average accuracy.

1. Introduction

Rice is one of the most cultivated crops in the world, in over a hundred countries. As per reports by interest groups, rice consists of a total harvested area of approximately 158 million hectares, producing more than 700 million tons annually (470 million tons of milled rice) [1]. As of 2018, Asia represents 90.2% of global production. The Americas and Africa take up 5% and 4.2% respectively [2].

With rice being such a valuable commodity, a common problem that widespread cultivators face is infestation of rice leaf diseases. Early detection of these diseases allows cultivators to consult experts and treat their crops better, before the infection reaches an irreversible state. Taking into consideration the large range of possible diseases, it becomes a difficult task for cultivators to individually identify these cases, especially for large fields. Artificial intelligence aided systems could provide solutions for the fast and reliable detection of these diseases. While there exist, significant artificial intelligence based solutions in areas like crop, pest and diseases management, soil irrigation and storage monitoring [3], there is still large potential and scope for further developments in these sectors.

Focusing on disease detection and control, this paper proposes a high accuracy, automated rice leaf disease classification model based on a customized transfer learned architecture. This study looks to address the various research gaps and improvements in the field of rice leaf disease diagnosis.

2. Related works

For the niche of automated rice leaf disease detection using deep learning techniques, the number of publications is lower, compared to that of general plant diseases. This section illustrates the various methods and studies that authors have conducted in regards to this field from the period of January, 2016- October, 2020.



Recent studies have, in a notable majority, utilized the transfer learning technique for training classification models. In a study by Ghosal et al., a customized VGG-16 based architecture was used for rice leaf disease classification [4]. In a similar strategy, Shrivastava et al. utilized the pre-trained AlexNet model, in combination with a SVM classifier [5]. Similarly using a SVM classifier, Hasan et al. adopted a proposed deep CNN model [6]. Atole et al. transfer learned an AlexNet based architecture with a few fine-tuned parameters [7]. Comparing multiple models, Mathulapransan et al. used ResNet50, ResNet101, DenseNet161 and DenseNet169 models in their study [8]. Kamrul et al. made use of the Inception v3, MobileNet-v1 and Resnet50 architectures [9]. In a more extensive approach, Sethy et al. employed 11 transfer learned networks, performed deep feature extraction and used a SVM classifier [10].

Adding customizations, Mique et al. utilized the Inception-v3 architecture and retrained the final layer on a rice disease dataset [11]. Chen et al. proposed the DENS-INCEP; a fusion of the base DenseNet 201 model with extended Inception modules [12]. Lu et al., proposed a custom CNN inspired by the LeNet and AlexNet models, and compared classifiers like BP, SVM and PSO [13]. A study by Rahman et al., compared fine-tuned transfer learned models like VGG16 and Inception V3 along with a proposed 2 stage architecture [14]. Bhattacharya et al. proposed a custom CNN model for a 2-phase approach to rice disease prediction [15]. The first phase involved classifying healthy and diseased leaves, and the second into 3 classes of rice diseases.

Introducing novel architectures, Sharma et al. proposed a custom CNN that classified 3 classes of rice leaf diseases [16]. Along the same idea, Liang et al. introduced a custom feature extraction architecture, evaluated with a SVM classifier [17].

Exploring other extensions of the base CNN architectures, a study by Ramesh et al. utilized DNNs and KNNs, with K-means clustering based segmented inputs [18]. Comparably, Liu et al. compared an SVM-HOG model with paradigm AlexNet, VGGNet11 based models [19]. Ahmed et al. employed a two-step approach with Faster-RCNN, for region of interest extraction, and a VGG-16 classifying network [20]. Zhou et al. combined Faster R-CNN fusion with FCM-KM for discerning the region of interest as well [21]. In another approach, Kiratiratanapruk et al. compared Faster-RCNN, RetinaNet, YOLOv3 and Mask-RCNN [22].

2.1. Research Gaps and Motivation

In depth review of these publications revealed the following limitations:

- Lack of enough samples, or unbalanced datasets. The under-representation of a particular category of rice disease results in a lack of necessary samples for the model to learn from, utilizing these sample in association with other mismatched categories result in unbalanced datasets that can bias the classification results.
- Lack of standardized datasets. A majority of the studies utilized manually collected images. Due to variance in the samples between studies brought about by factors like lighting, or background color, or quality. It is not correct to take a direct comparison of the results between these studies without considering these factors.
- Low quality images, and color similarity make it difficult for models to identify features properly, and thus do not learn the necessary points for accurate classification.

3. Proposed Work

The following section delineates the proposed model used in this study to classify different categories of rice leaf diseases, from obtained datasets before and after balancing. The major highlight of this research is to develop a Custom transfer learning based architecture for rice disease classification. The block diagram in figure 1 explains the overall work-flow of this study, which is explained in detail in the subsequent sections.

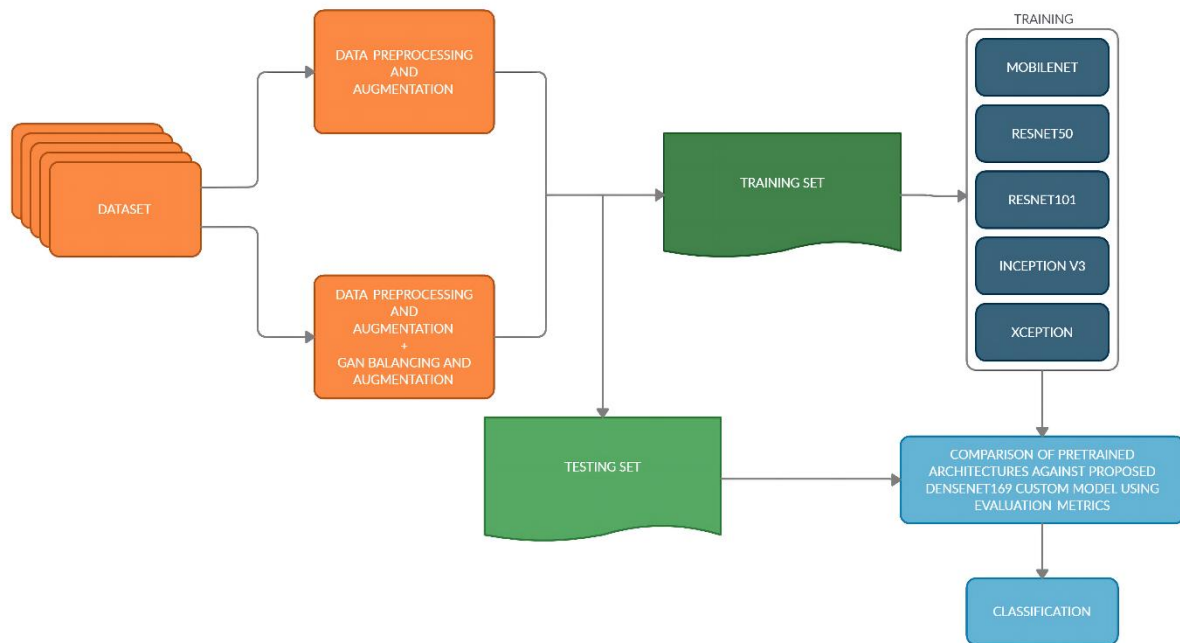


Figure 1. Work-flow of the proposed system.

3.1. Data acquisition

Three open-source datasets were used in this study, detailed in table 1.

Table 1. Details of datasets used.

Dataset	Number of Samples	Train:test Split	Classes
Rice Leaf Diseases [23]	120	80:20	Bacterial leaf blight, Brown spot, Leaf smut
Rice Diseases Image Dataset [24]	2092	75:25	Brown spot, Hispa, Leaf Blast, Healthy
Leaf Diseases Dataset [25]	8293, 12496 (after balance)	80:20	Bacterial Leaf Streak, Brown Spot, False Smut, Sheath Blight

3.2. Augmentation and Pre-processing

In this study, data augmentation was used as a strategy to implement transformations for the improvement of feature visualization, and for addressing the imbalanced dataset problem as well. Initially all images underwent transforms using the Albumentations augmentation library to address the issues of color similarity discussed in section 2 [26].

From the survey of other literatures in section 2, one of the most common drawbacks reported was the unavailability of a balanced dataset with enough samples. Using this as motivation, we have explored the use of the Style-GAN2 architecture with adaptive discriminator augmentation (ADA) [27]. This is used to create more samples for the Bacterial leaf streak and the Rice false smut class of the Leaf Diseases dataset, achieving a balanced distribution [25]. After the augmentation the number of samples in the Bacterial leaf streak class increased to 2976 from 776, and the Rice false smut class to 3056 from 1056; taking the total number of images in the dataset to 12496 from 8293.

3.3. Transfer learning models and proposed RiceDenseNet

Classic pre-trained architectures were compared against the customized classification model proposed in this study to illustrate its efficacy. These architectures include MobileNet, ResNet50, ResNet101, Inception V3, and Xception [28], [29], [30], [31]. With the base DenseNet, model each layer receives inputs from the preceding layers, and then passes its feature-maps to all layers in subsequence, which results in very deep inputs [32].

This study proposes the RiceDenseNet, based on the Densenet-169 model with customizations to the classification head, as illustrated in figure 2. Initial modifications include employing Max pooling for the overall base network. This was followed by custom additions of Average pooling, Dense, Dropout and Batch Normalization layers to the classification head in order to make it more specific to our datasets. As a result, a total of 54,393,924 parameters for a specific input size of (224, 224, 3).

Furthermore, the layers of the RiceDenseNet, except the additional layers we added, are frozen for certain number of epochs during the training process. From this point, the model was fine-tuned by unfreezing the top half of architecture. In addition to this, the learning rate was reduced, to update higher-order feature representations and make it more specific to the task at hand.

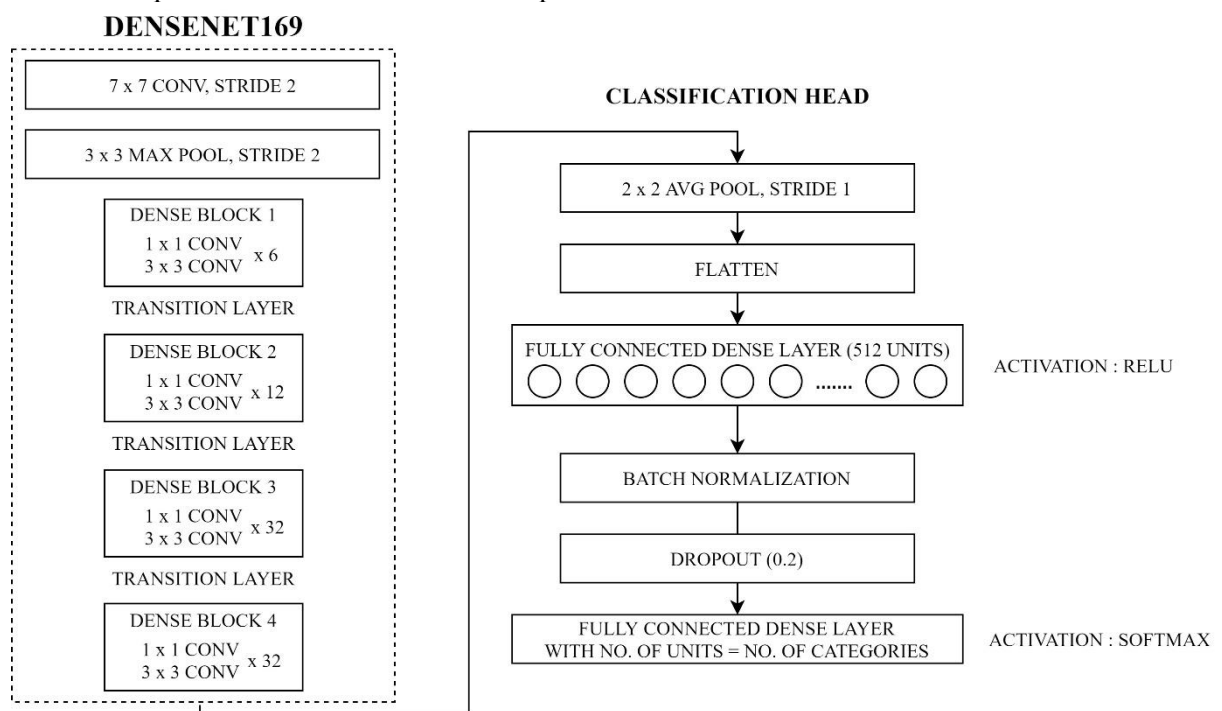


Figure 2. Block diagram illustrating the proposed customizations to the RiceDenseNet architecture.

4. Results and Discussion

4.1. Environmental Setup

All experiments were conducted in a Python 3 environment on the Keras and Tensorflow frameworks. Experiments were conducted in a Ryzen 2700X CPU and GeForce GTX 1660 Ti GPU for one of the datasets [24]. A Tesla K80 GPU was used for the other two [22],[23].

4.2. Performance Analysis

The metrics used in this study to measure the performance of the proposed models and other techniques include: Accuracy, F1 score, Precision, and Recall. The evaluation of the proposed model considered each of the three datasets, as mentioned in section 3.1. The datasets were compared with paradigm transfer learned models to draw a comparison to the better performance that our customization brings. These models include MobileNet, ResNet 50, ResNet 101, Inception V3, and Xception. In this evaluation the proposed RiceDenseNet outperformed all tested architectures, as illustrated in table 2 and figure 3.

As our primary dataset for evaluation, the results of testing the proposed model on the Leaf Diseases Dataset [25], has provided the highest accuracy, 97.71%, outperforming the accuracies reported in the studies discussed under section 2.

Additionally, k fold cross validation of the proposed model was conducted on each of the datasets, as well as the GAN augmented dataset, explained in section 3.2. The achieved cross validation results, in table 3 and figure 4, are quite impressive and bolster the use of GAN augmentation to improve classification accuracy. With the base dataset, our model achieved 98.38% average accuracy, while the use of GAN augmentation resulted in an improved 98.79% average accuracy for 10 folds.

Table 2. Comparison of different transfer learning architectures.

Dataset used	Model	Accuracy	F1 score	Precision	Recall
Rice Leaf Diseases [23]	MobileNet	0.875	0.8928	0.9166	0.875
	ResNet 50	0.3333	0.3611	0.4166	0.3333
	ResNet 101	0.5	0.2777	0.4166	0.2083
	Xception	0.8333	0.7809	0.9444	0.7083
	InceptionV3	0.7916	0.6539	0.8333	0.5833
	Proposed RiceDenseNet	0.9166	0.9166	0.9166	0.9166
Rice Diseases Image Dataset [24]	MobileNet	0.5101	0.4873	0.5242	0.4599
	ResNet 50	0.3780	0.2202	0.4045	0.1700
	ResNet 101	0.3658	0.3313	0.3825	0.2960
	Xception	0.5833	0.5735	0.6006	0.5500
	InceptionV3	0.5813	0.5760	0.5931	0.5606
	Proposed RiceDenseNet	0.6646	0.6675	0.6824	0.6540
Leaf Diseases Dataset [25]	MobileNet	0.9133	0.9127	0.9148	0.9108
	ResNet 50	0.9410	0.9403	0.9408	0.9398
	ResNet 101	0.9458	0.9464	0.9469	0.9458
	Xception	0.9446	0.9455	0.9477	0.9434
	InceptionV3	0.9133	0.9148	0.9164	0.9132
	Proposed RiceDenseNet	0.97713	0.97714	0.97714	0.97714

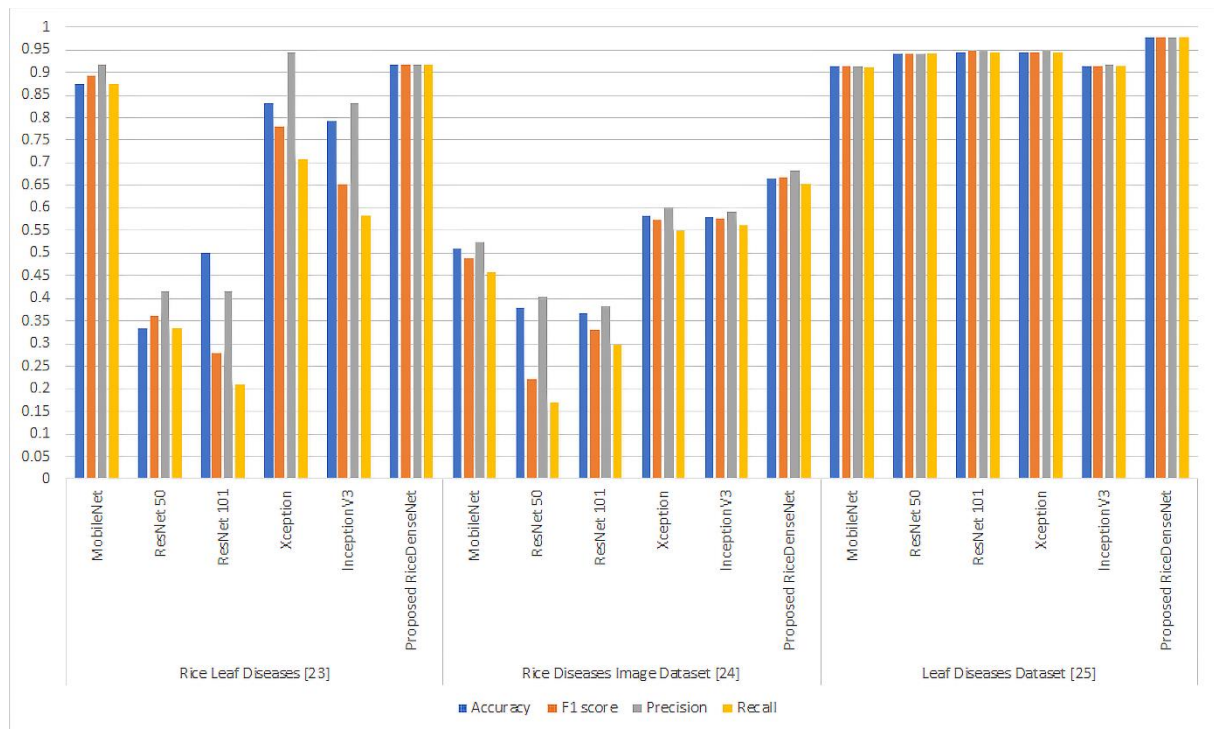


Figure 3. Comparison of different transfer learning architectures.

Table 3. Observations of cross validation folds on all 3 datasets used.

Dataset	Model	Number of folds	Accuracy	F1 score	Precision	Recall	Loss
Rice Leaf Diseases [23]	Proposed RiceDenseNet	5	0.8666	0.8678	0.8694	0.8666	0.4223
Rice Diseases Image Dataset [24]	Proposed RiceDenseNet	10	0.6257	0.6140	0.6715	0.5682	0.9800
Leaf Diseases Dataset [25]	Proposed RiceDenseNet	10	0.9838	0.9840	0.9844	0.9836	0.0493
Leaf Diseases Dataset [25]	RiceDenseNet+ GAN augmented dataset	10	0.9879	0.9879	0.9883	0.9876	0.0346

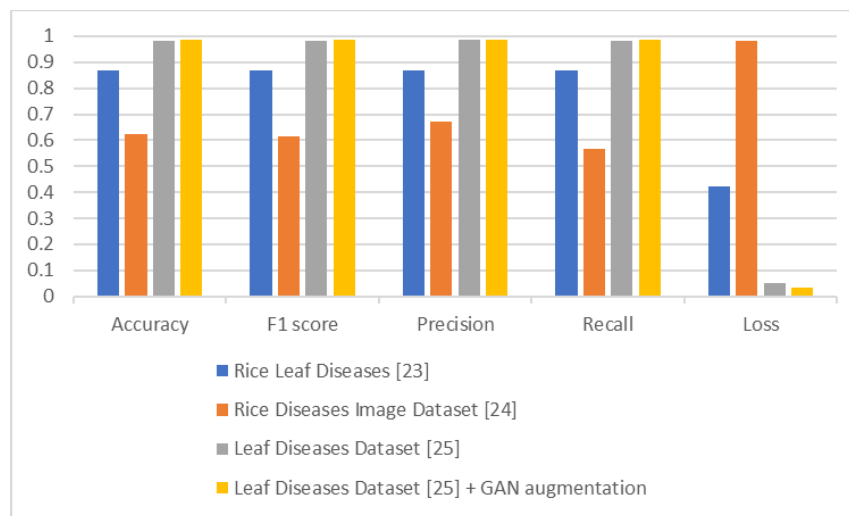


Figure 4. Comparison of average results for cross validation folds on all 3 datasets used.

5. Conclusion

The advantages of an automated rice disease detection system can prove of much value to agricultural organizations and cultivators. This work has proposed an innovative technique to detect rice diseases efficiently, and accurately classify them. Three datasets of varying sizes and multiple paradigm classification architectures have been used, to compare the performance of the proposed model. Noticeably the accuracy of the proposed model and every other architecture compared, was slightly unsatisfactory for the dataset the Rice Disease Image Dataset, due to relatively lower quality of images. This work has also addressed the unbalanced dataset problem as well, by utilizing a GAN architecture to generate more samples for specific classes. This in the best of our knowledge is the highest accuracy reported for the classification of rice leaf diseases using CNN based deep learning techniques. This approach can be carried forward with future improvements, like integrating more categories of rice diseases and designing low-computational requirement models that can be implemented at low costs.

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