



Enhancing Mushroom Detection Using One-Dimensional Convolutional Neural Networks

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Abstract

The classification of mushrooms as either deadly or edible stays a important challenge due to their similar appearances, which can lead to fatal poisonings. The primary difficulty lies in identifying complex patterns in mushroom appearances, such as cap shape, color, and gill structure, which complicate accurate classification. Traditional approaches and even some machine learning (ML) models fail to capture these subtle but important distinctions, leading to misclassifications. To address this issue, this paper proposed a One-Dimensional Convolutional Neural Network (1D-CNN) approach aimed at improving the accurate of mushroom classification. By effectively recognizing complex patterns in the mushroom data set, the proposed approach greatly improves classification accuracy. The model performance evaluated utilizing Precision, Accuracy, Recall, and F1-Score that achieved high scores of 100% across all metrics. These results highlight the strength of deep learning (DL) method, specifically 1D-CNNs, in recognizing with learning complex data patterns. This shows a clear advancement over traditional ML methods and ensemble techniques, establishing the 1D-CNN as a highly reliable tool for mushroom classification that can help reduce mushroom poisoning incidents.

Keywords: Mushroom; One-Dimensional Convolutional Neural Network; Machine Learning; Classification; Deep learning

1. Introduction

Mushrooms are a kind of fungus that grow in a variety of conditions. We frequently see mushrooms on forest floors because they typically favor dark or shaded areas. Mushrooms can be divided into two primary categories: poisonous and edible mushrooms. These types of mushrooms have distinguished features that can be used to identify in nature. Features like a mushroom cap, its color, and its gill are good features to be used to identify poisonous from edible mushrooms. However, it is hard for nonprofessionals to recognize and distinguish such features to identify the mushroom kind. Misidentifying a kind of mushroom can lead to severe repercussions, including fatal poisoning. The difference between deadly and edible mushrooms is very hard to grasp [1].

Classification methods, such as decision tree DT, Support Vector Machine SVM, and many other methods have been applied widely to this problem. However, these methods struggle to recognize the complex patterns within

mushroom features. Due to that, intensive exploration of new and advanced approaches is required to capture complex patterns in the mushroom features [2].

This research presents a one-dimensional convolutional neural network (1D-CNN) as a novel approach to address these challenges. This approach proved its ability to capture complex patterns and recognize mushroom features effectively, providing high identification accuracy. This research aims to investigate this approach in different situations of mushroom types and features and compare this approach with work already presented in this field.

Mushrooms grow in dark and humid places in forests and farms thriving where moisture and organic material are available to live on. They have different shapes and forms, which form their distinct species. According to their properties, including their cap color, stipe color, shape, gill arrangement, volva presence, and many more, a mushroom can be classified. Farmers can identify edible mushrooms from poisonous ones according to the conditions that influence their color or shape. This way is inaccurate and can lead to misidentification of mushroom species that can be poisonous. An instance of that is consuming five pieces of the *Amanita* species' fruiting bodies can result in death [2]. In addition to that, in the USA during the period of 1999 to 2016 around 52 fatalities were reported with 7428 cases of poisoning mushrooms [3]. The type of mushroom differs from zone to zone, allowing for the availability of spores and suitable environmental conditions to grow special mushroom species. Thus, scientists and researchers face difficulty in knowing the species of mushrooms.

Deaths of mushroom eating occur frequently due to misidentification of whether these mushrooms are edible or toxic [4]. For this reason, providing an accurate mushroom classification method is necessary to stop future mushroom deaths. Artificial intelligence (AI), specifically Machine Learning (ML), offers a good solution to this problem. This work proposed a 1D-CNN approach to improving the accuracy of mushroom classification. 1D-CNNs are convenient for issues involving pattern recognition tasks and can better capture the Mushroom dataset's intricate features, leading to better classification performance. The proposed approach is evaluated utilizing metrics like F1-Score, Precision, Recall, and Accuracy to assess model performance. This research uses ML models to provide a robust and accurate tool for mushroom classification and contribute to public safety by reducing the risk of mushroom poisoning.

The following sections are organized as follows: Section 2 provides a list of related studies about mushroom classification methods and their limitations. Section 3 explains the 1D-CNN methodology, containing data preprocessing and model architecture. Section 4 presents the experimental setup, performance metrics, and results, with a comparative analysis, and discusses the implications and findings. While Section 5 concludes with key findings and future research directions.

2. Related Works

Several studies have been presented on the classification of edible and poisonous mushrooms. Researchers have employed various techniques and compared them to find the best method. This section shows multiple previous studies related to our presented work done via several researchers.

Wang et al. [5] presented an automated toxicity classification approach based on visual characteristics. The proposed approach regards toxicity designation as a binary classification issue. First, instinctive and efficiently available appearance mushroom datasets, like the color and cap shape, were taken as attributes. Second, the missing values data in any attribute were processed using two methods. After all, three classification techniques containing multigrained cascade Forest (gcForst), LR, and SVM are utilized. Compared with the LR and SVM techniques, the gcForest technique performed better, with an accuracy of 98%.

Chitayae et al. [6] proposed an intelligent approach for identifying different types of mushrooms utilizing DT and KNN algorithms. The study compared the performance of these techniques to determine which was more effective for mushroom classification. Experimental testing, conducted using the UCI Mushroom dataset, demonstrated the effectiveness of both approaches. However, the DT method outperformed KNN, achieving a higher accuracy of 91.93%, making it the more suitable technique for classifying mushroom species. Ortega et al. . [7] proposed a practical approach based on ML techniques: NB, LR, DT, and KNN. The DT technique is the most effective ML technique for predictive modelling. The results obtained from the decision tree technique show its effectiveness, as the accuracy exceeded 88%.

Kousalya et al. [8] proposed an effective model based on ML techniques due to its ability to classify mushroom types. NB, DT, SVM, and LR are four comparisons of the best categorization algorithms available in data mining. At the same time, the investigation method used a WEKA tool to compare the four models. The *Agaricus* and *Lepiota* mushroom data were employed to perform the investigations. The source of the dataset utilized is acquired from the Kaggle website. The DT algorithm has the highest performance compared with the other used algorithms. The DT algorithm shows a high accuracy of 93.34%.

Siddique et al. (2023) investigate utilizing a Genetic Algorithm (GA) as a Feature Selection (FS) method for a classification issue, precisely the mushrooms classification issue. The RF technique is utilized as the ML classifier, and GA is compared with correlation as the FS method. The experimental results show that GA performs better than correlation-based FS. However, GA has restrictions in their relevancy to distinct optimization difficulties, appropriate parameter setup requirements, and longer times. Despite these disadvantages, GA is better than other FS methods, specifically correlation-based methods. This investigation highlights the significance of determining proper FS methods for optimisation approaches to enhance their performance and reach improved results [9].

Morshed et al. [10] explored different kinds of mushrooms and employed efficient FS methods associated with practical ML-based classification approaches to predict the edibility of mushrooms through investigation with nine distinct ML techniques and twenty selected attributes. The ML techniques are RBF SVM, linear SVM, KNN, RF, DT, NN, Quadratic Discriminant Analysis (QDA), NB, and Adaptive Boosting. The result demonstrates that the best model (KNN) achieved significantly better accuracy at 99%.

Singh et al. [11] presented multiple ML techniques to predict mushroom types. The ML techniques are LR, KNN, Support Vector Classifier (SVC), RF, DT, and Gradient Boosting Classifier (GBC). The RF shows the highest accuracy ratio at 99.38%.

Sahu et al. [12] presented five distinct ensemble-learning techniques for classifying unhealthy and healthy Agaricus Mushrooms based on their physical features. The techniques that are used in this model are Bagging, RF, Gradient Boosting (GB), eXtrem Gradient Boost (XGBoost), and Adaptive Boosting (AdaBoost). Ensemble models can underestimate the errors developed by single models. As an experimental result, performance is excellent compared to the single classifier. Here, Adaboost indicates the highest accuracy, 95.35%, with 10-fold cross-validation.

While these studies achieved respectable results, most were limited by their inability to fully capture intricate features in mushroom data, which are necessary for precise classification. In contrast, DL models, particularly CNN, have demonstrated superior performance in learning complex patterns from high-dimensional data. This study builds on this idea by applying a 1D-CNN model, which has the potential to outperform traditional ML methods by effectively capturing subtle differences between deadly and edible mushrooms.

3. Research Methodology

This research aims to apply the 1D-CNN method to classify and detect the Mushroom dataset into two classes (deadly and edible). This proposed 1D-CNN approach applied a five-step process in this analysis: the first step is dataset utilization description, the second step is data preprocessing, the third step is splitting data into training and testing, observed by the 1D-CNN model, and the last step is evaluation. The investigation steps for the presented method are illustrated in Figure 1.

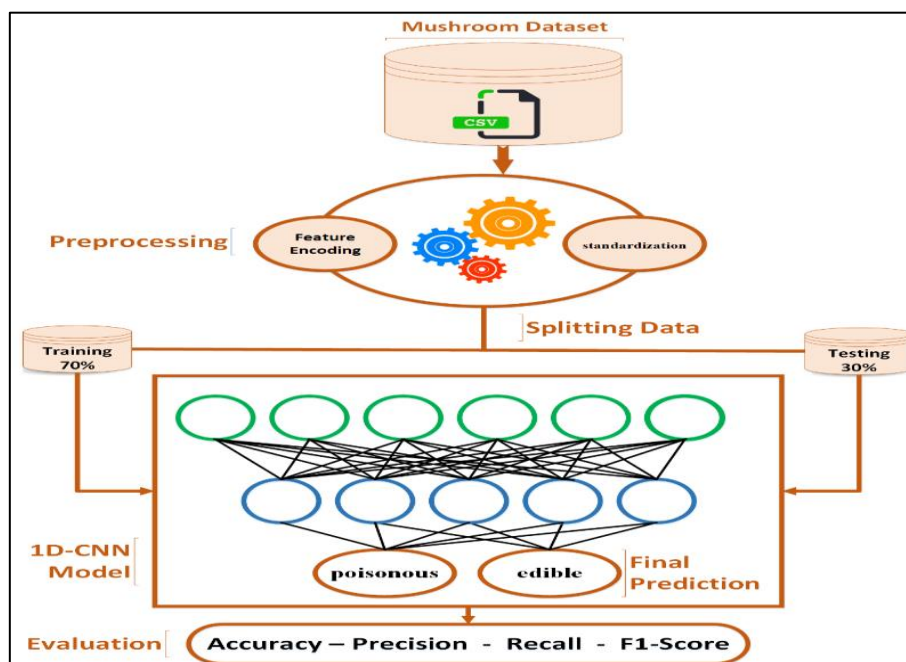


Figure 1. Proposed method.

4. Dataset Description

This study utilized the available mushroom dataset [13]. The data set is composed of 8124 instances, each with 22 features. Each mushroom species is recognized as a class of poisonous and edible. These instances are distributed as 3916 poisonous and 4208 edible mushrooms, as seen in Figure 2.

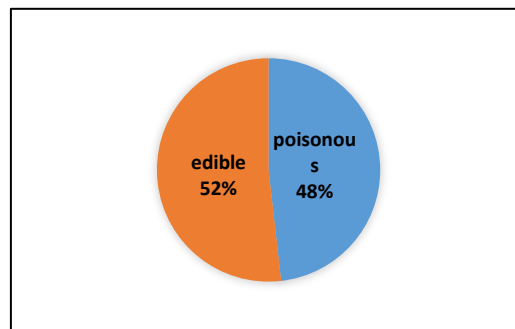


Figure 2. Composition of class content

As shown in Table 1 summarizes the features, which are utilized for categorizing mushrooms.

Table 1: Features description of the mushroom dataset

Feature	values
gill-color	n=brown, b=buff, h=chocolate, g=gray, r=green, o=orange, p=pink, u=purple, e=red, w=white, y=yellow, k=black
Cap-surface	g=grooves, s=smooth, y=scaly, f=fibrous
Cap-color	b=buff, c=cinnamon, g=gray, r=green, n=brown
Bruises	no=f, t=bruises
Odor	n=none, p=pungent, s=spicy, m=musty, l=anise, c=creosote, y=fishy, f=foul, a=almond
gill-attachment	d=descending, f=free, n=notched, a=attached
gill-spacing	d=distant, w=crowded, c=close
gill-size	n=narrow, b=broad
Cap-shape	c=conical, x=convex, f=flat, k=knobbed, s=sunken, b=bell
stalk-root	c=club, u=cup, e=equal, r=rooted, b=Bulbous, missing=?
stalk-shape	t=tapering, e=enlarging
spore-print-color	n=brown, b=buff, h=chocolate, r=green, u=purple, w=white, y=yellow, k=black
stalk-color-below-ring	b=buff, c=cinnamon, g=gray, o=orange, p=pink, e=red, y=yellow, w=white, n=brown
stalk-color-above-ring	b=buff, c=cinnamon, g=gray, o=orange, p=pink, e=red, y=yellow, w=white, n=brown
ring-number	o=one, t=two, n=none

veil-type	u=universal, p=partial
veil-color	o=orange, y=yellow, w=white, n=brown
stalk-surface-below-ring	y=scaly, k=silky, s=smooth, f=fibrous
Habitat	l=leaves, m=meadows, p=paths, u=urban, w=waste, d=woods, g=grasses
ring-type	e=evanescent, f=flaring, l=large, n=none, p=pendant, s=sheathing, z=zone, c=cobwebby
stalk-surface-above-ring	y=scaly, k=silky, s=smooth, f=fibrous
Population	c=clustered, n=numerous, s=scattered, v=several, y=solitary, a=abundant

5. Preprocessing

Preprocessing is essential in converting datasets into a format suitable for DL. It directly affects the learning model and enhances efficiency. It directly influences the learning model and enhances efficiency. We employed two preprocessing operations: standardization and label encoding.

Standardization: - is a transforms data to have a mean of 0 and the standard deviation of 1, ensuring consistent scale across features [14].

Label Encoding: - is to switch categorical labels into numerical values, assigning each unique category a corresponding integer [15],[16].

6. Splitting data

In ML and DL, the data is usually split into two parts: testing and training. This step confirms the creation of data models and methodologies that employ data models. The training part is utilized to develop and train the model. The testing part is utilized after the training is complete. The testing and training data correspond to ensure that the absolute model functions accurately. In this study split the data set into 30% for testing and 70% for training.

7. Proposed 1D-CNN architecture

In this investigation, we employed 1D-CNN for binary classification [17],[18]. The 1D-CNN model includes an output layer (L₁₃), input layer(L₀), and multiple hidden layers (L₁ ~ L₁₂), which include multiple parts like a one-dimensional Convolutional Layer (1D-CL), Batch Normalization Layer (BNL), one-Dimensional Max Pooling Layer (1D-MPL), Flatten Layer (FL), Fully Connected Layer (FCL), and Dense Layer. The parameters utilized in the proposed 1D-CNN model are shown in Table 2. The proposed 1D-CNN model architecture is shown in Figure 3.

Table 2: The 1D-CNN model parameters

Layer	Kernel Size	Output Shape	No. of Parameter
Conv1D	2	(21,8)	24
Max pooling 1D	2	(20,8)	0
Batch Normalization	-	(20,8)	32
Conv1D	2	(19,16)	272
Max pooling 1D	2	(18,16)	0
Batch Normalization	-	(18,16)	64

Conv1D	2	(17,32)	1056
Max pooling 1D	2	(16,32)	0
Batch Normalization	-	(16,32)	128
Conv1D	2	(15,64)	4160
Max pooling 1D	2	(14,64)	0
Dropout	0.5	(14, 64)	0
Flatten	-	896	0
Dense	-	64	57408
Dense	-	32	2080
Dense	-	2	66

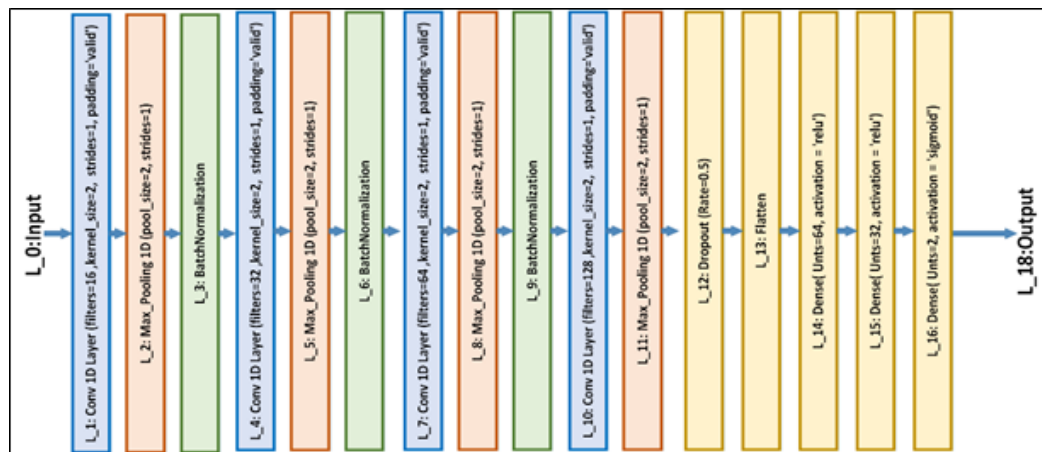


Figure 3. Proposed 1D-CNN model architecture

L_0: The input layer is the input data of the completely neural network. The input data format contains 8,124 instances, each with 22 features, and is input to the CL.

L_1, L_4, L_7, L_10: The convolutional layers (CL). The filters are specified to 16, 32, 64, and 128, individually. The kernel size is specified as 2, and the padding is specified as "valid". The strides are specified to 1.

L_2, L_5, L_8, L_11: The Max pooling layers. The pool size is specified to 2. The strides are specified to 1. They are sandwiched among the previous 1D_CL and employ the maximum value per cluster of neurons at the previous layers.

L_3, L_6, L_9: The batch normalization layers. Via placing after 1d_MPL, they can assist in unravelling the issue of problem in confluence in the operation of network training. Moreover, it delays the overfitting to a particular extent.

L_12: The dropout rate is selected to 0.5 to avoid over-fitting efficiently.

L_13: The flatten layer. The two-dimensional inputs are repositioned to the one-dimensional inputs in the change from the CL to the fully connected layers.

L_14, L_15, L_16: The dense layers are three with units assigned to 64, 32, and 2, respectively. The two activation functions are assigned to 'relu' and 'sigmoid'.

L18: The output layer, with two units, represents the two classes edible and poisonous.

The proposed approach employs the Keras framework. While the learning rate is (0.0001) and the optimizer Adam, the batch size for model testing and training is specified as 22, and the model's epoch is specified as 30.

8. Evaluation

This task is a binary classification; the subsequent performance values are examined: F1-Score, Precision, Recall, and Accuracy as shown in Table 4. Meanwhile, we illustrate the results figures to evaluate the model's performance from considerable angles [19],[20],[21].

Confusion matrix: Multiple combinations of actual and predicted results exist [22],[23],[24]. In a binary classification scheme, there are four various sequences of the findings, which are indicated as FN (False Negative), FP (False Positive), TP (True Positive), and TN (True Negative). Hence, the CM, as displayed in Table 3 [25],[26],[27].

Table 3: Confusion Matrix

Mushroom Dataset		Predicted	
		edible	poisonous
Actual	edible	TP	FN
	poisonous	FP	TN

Table 4: Formulas for Performance Metrics [28]

Evaluation	Formulas
Recall	$\frac{TP}{FN + TP}$
Precision	$\frac{TP}{(FP + TP)}$
F-measure	$\frac{2 \times (Precision * Recall)}{Precision + Recall}$
Accuracy	$\frac{TP * TN}{total\ number\ of\ cases}$

9. Result and Discussion

As shown in Table 5, the proposed 1D-CNN approach demonstrated exceptional performance in classifying mushrooms into deadly and edible categories, achieving perfect scores across all evaluation metrics. Specifically, the model attained a recall, accuracy, F1-score, and precision of 100%, highlighting its ability to accurately identify deadly mushrooms while minimizing false positives. These results signify the efficiency of the 1D-CNN approach in capturing intricate patterns from the Mushroom dataset, surpassing traditional methods.

Table 5: Evaluation results

	Precision	Recall	F1-score	Accuracy
Proposed 1D-CNN	100%	100%	100%	100%

Figure 4 shows the confusion matrix of the proposed 1D-CNN approach and highlights its exceptional performance in classifying mushrooms into deadly and edible categories. The model correctly identified 1272 instances of deadly mushrooms (True Positives) and 1166 instances of edible mushrooms (True Negatives), with no instances of misclassification (False Negatives and False Positives both at 0). This perfect classification accuracy indicates that every mushroom in the dataset was accurately categorized, demonstrating the model is robust precision and reliability. Such flawless performance is crucial for applications where accurate detection of mushrooms is necessary for public health and safety.

Confusion matrix of proposed 1D-CNN			
TARGET \ OUTPUT	Edible	Poisonous	SUM
Edible	1272 52.17%	0 0.00%	1272 100.00% 0.00%
Poisonous	0 0.00%	1166 47.83%	1166 100.00% 0.00%
SUM	1272 100.00% 0.00%	1166 100.00% 0.00%	2438 / 2438 100.00% 0.00%

Figure 4. Proposed model confusion matrix of proposed 1D-CNN

The proposed 1D-CNN model was rigorously evaluated using a range of performance metrics: Accuracy, F1-Score, Precision, and Recall. The model achieved high scores of 100% across all these metrics, indicating its exceptional performance in distinguishing between deadly and edible mushrooms.

The confusion matrix revealed no instances of misclassification, with both edible and poisonous mushrooms correctly identified. These results suggest that the 1D-CNN model is highly effective at capturing the intricate patterns within the mushroom dataset. However, while these findings are promising, they also raise the question of whether the model might be overfitting the dataset. To address this concern, cross-validation was performed, which confirmed the robustness of the model.

Figure 5 shows the training loss with validation loss, while Figure 6 shows the curve of training accuracy with validation accuracy.

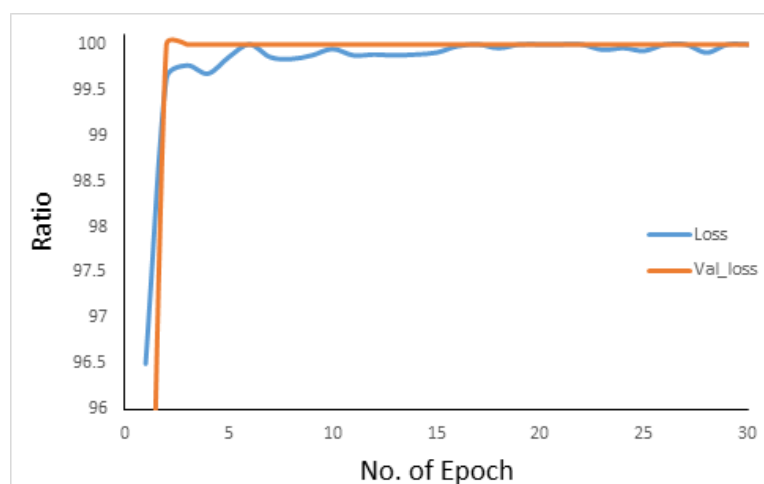


Figure 5. The curve of training and validation accuracy.

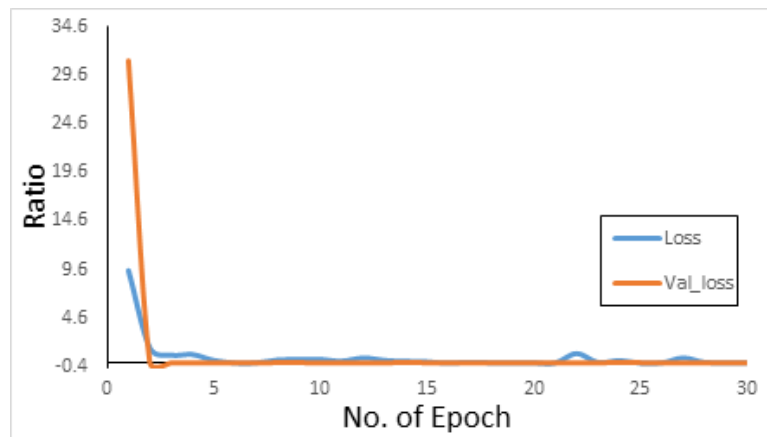


Figure 6. The curve of training and validation loss.

The results of the proposed work show the exceptional performance of 1D-CNN in classifying mushrooms, achieving a perfect accuracy of 100%. This surpasses the accuracy achieved by several state-of-the-art studies that have applied several ML and ensemble learning techniques to the same task as shown in Table 5.

Singh et al. [11] explored several classifiers including LR, KNN, SVC, DT, RF, and Gradient Boosting Classifier (GBC). RF has achieved a high accuracy of 99.38%. Similarly, Kousalya et al. [8] applied NB, DT, SVM, and LR, with the DT yielding a high accuracy of 93.34%.

Sahu et al. [12] investigated ensemble learning techniques, combining RF, Bagging, GB, XGBoost, and AdaBoost. The Gradient Boosting method achieved a high accuracy of 95.35%. Morshed et al. [10] proposed an array of classifiers including LSVM, KNN, RBF SVM, DT, RF, NN, AB, NB, and QDA, with KNN achieving a high accuracy of 99%.

Additionally, Siddique et al. [9] combined Genetic Algorithms with RF, achieving an accuracy of 89.12%, while Ortega et al. [7] used LR, NB, DT, and KNN, with DT achieving a high accuracy of 88.2%. Chitayae et al. [6] applied KNN and DT, achieving 91.93% accuracy with DT, and Wang et al. [5] proposed SVM, LR, and multigrained cascade Forest (gcForest), with gcForest achieving an accuracy of 98.27%.

In comparison to these studies, our proposed 1D-CNN model not only meets but exceeds the highest reported accuracies, indicating a significant improvement in the classification of mushrooms. The perfect accuracy achieved by our model underscores the capability of DL techniques, particularly 1D-CNNs, in effectively capturing and learning complex patterns in data. This demonstrates a robust advancement over traditional ML methods and ensemble techniques, making the 1D-CNN a highly reliable tool for mushroom classification.

Table 5: A comparative result of the proposed model with related studies

References	Year's	Methods	Accuracy
Chitayae et al. [6]	(2020)	KNN	89.61%
		DT	91.93%
Wang et al. [5]	(2020)	LR	95.45%
		SVM	96.2%
		gcForest	98.27%
Ortega et al. [7]	(2020)	LR	87.8%
		NB	86.5%
		DT	88.2%

		KNN	87.9%	
Kousalya et al. [8]	(2022)	NB	62.09%	
		DT	93.34%	
		SVM	89.77%	
		LR	86.35%	
Singh et al. [11]	(2023)	LR	83.69%	
		KNN	98.76%	
		SVC	93.66%	
		DT	97.96%	
		RF	99.38%	
		GBC	93.29%	
Morshed et al. [10]	(2023)	KNN	99%	
		LSVM	68%	
		RBF SVM	95%	
		DT	75%	
		RF	79%	
		NN	96%	
		Adaptive Boosting	81%	
		NB	61%	
		QDA	74%	
Siddique et al. [9]	(2023)	Genetic Algorithm + RF	89.12%	
Sahu et al. [12]	(2024)	Ensemble Learning Techniques	RF	84.08%
			Bagging	85.79%
			GB	95.35%
			XGBoost	90.06%
			AdaBoost	88.58%
Proposed model	(2025)	1D-CNN	100%	

The results demonstrate that the 1D-CNN model excels at distinguishing between edible and poisonous mushrooms, achieving flawless accuracy across all major evaluation metrics. The confusion matrix analysis reveals that the model effectively classifies both toxic and safe mushrooms, without any false positives or negatives.

While this performance is ideal for preventing mushroom poisoning, additional testing on larger and more diverse datasets is needed to evaluate the model's ability to generalize. It is also crucial to account for real-world conditions, where environmental factors could alter the appearance of mushrooms, introducing variations that were not present in the training data.

10. Conclusion

This paper shows the ability of utilizing a 1D-CNN for mushroom classification achieved high scores across all metrics. The proposed model ability to capture complicated patterns within the mushroom dataset surpasses that of traditional ML approaches. These results show that 1D-CNNs are a highly reliable tool for mushroom classification, particularly in applications where public health and safety are at risk. Future work should focus on testing the model on more different datasets, containing mushrooms from different regions and environmental conditions, to further evaluate its strength. Additionally, integrating real-time image analysis with this model could enable more practical applications, such as mobile apps for mushroom identification in the field.

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