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RESEARCH PAPER

Determining the effect of color spaces on image based disease classification in agaricus bisporus using squeezenet convolutional neural network

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Abstract

Agaricus bisporus, known as the white-capped mushroom, is among the cultivated mushrooms widely grown worldwide due to its high nutritional value and economic yield. However, this species is threatened by various disease agents including fungal, bacterial, viral and abiotic (non-microbial) agents under intensive production conditions. Early diagnosis of the symptoms caused by these diseases is of great importance in terms of preventing yield losses and minimizing the economic losses associated with them. In this study, it was aimed to classify five different diseases and healthy samples seen in *A. bisporus* based on images and to evaluate the effects of different color spaces on the classification accuracy. In this context, classification experiments were conducted on image datasets converted into different color space representations, with the SqueezeNet convolutional neural network (CNN) applied separately to each representation. The findings revealed that the XYZ, RGB and YCbCr color space provided higher classification accuracy compared to other formats in the detection of diseases.

Keywords

Agaricus bisporus, color spaces, deep learning, mushroom diseases, image classification, SqueezeNet Convolutional Neural Network

Introduction

Agaricus bisporus (J.E. Lange) Imbach, commonly known as the white button mushroom, is the most widely cultivated species globally (Royse 2014) and has gained significant commercial importance in Turkey due to its high nutritional value. Although the origin of *A. bisporus* is quite old, its industrial cultivation has gained momentum with the development of modern agricultural techniques (Işık et al. 2004; Sassine 2021). This mushroom species is considered an important part of a healthy diet due to its low calorie content and rich nutrient profile (Sliva 2010; Özkan 2015; B.A.K.A. 2021).

A. bisporus taxonomically belongs to the class Agaricomycetes and is defined by its morphological and genetic characteristics (Berendsen et al. 2010). *A. bisporus* is a macrofungus belonging to the Agaricaceae family and has a rich nutrient profile. It is rich in carbohydrates, fibers, proteins, amino acids, vitamins (especially B vitamins, vitamins C and D) and minerals (potassium, copper, iron, selenium) and low in fat and calories (Jeong et al. 2010; Muszyńska et al. 2011; Pekşen and Eren 2024). The fact that it contains ergosterol (the precursor of vitamin D_2) and antioxidant compounds makes *A. bisporus* stand out as a functional food (Sassine 2021). These properties support the positive effects of *A. bisporus* on

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human health and contribute to its increasing consumption (Royse 2014).

The cultivation of *A. bisporus* requires a more detailed process compared to other mushroom species. Cultivation stages include critical steps such as compost preparation (Pekşen and Eren 2024), mycelial inoculation, cover soil application and climate control (Sezen and Turunçoğlu 2023). Compost is a special medium containing all the nutrients needed by fungi, usually provided from plant-derived organic matter and animal manure (Raj and Antil 2011). The cover soil, which is a mixture of peat and limestone, supports mycelial growth and promotes fungal growth. Careful control of environmental factors such as temperature, humidity, ventilation and light during the cultivation process is of great importance for yield and quality (Berendsen et al. 2010).

A. bisporus is an important source of income and contributes to rural development in both developed and developing countries (Chang and Miles 2004). The intensive cultivation of edible mushrooms predisposes to the emergence of various pests and diseases under certain environmental conditions. This can make mushroom cultivation an economically risky activity (Prasad and Singh 2020). Commonly cultivated species such as *Agaricus bisporus* (white caps), *Pleurotus* (oyster mushrooms) and *Lentinula edodes* (shiitake mushrooms) are susceptible to various fungal, bacterial and viral pathogens (Prasad and Singh 2020; Zhang et al. 2022). In this case, various fungal, bacterial and viral diseases in mushroom cultivation pose a serious threat to this sector (Basim and Basim 2018; Amin et al. 2021; Sutradhar et al. 2021; Zhang et al. 2022). When commercially important fungi such as *A. bisporus* are attacked by these pathogens, yield losses occur and product quality decreases (Amin et al. 2021; Zhang et al. 2022). Fungal diseases such as dry blister disease (caused by *Lecanicillium fungicola*), wet blister disease (*Mycogone perniciosa*), green mold disease (*Trichoderma aggresivum*) and cobweb disease (*Cladobotryum* spp.) are considered a serious threat to this industry (Fletcher and Gaze 2007; Berendsen et al. 2010; Öztürk et al. 2017; Prasad and Singh 2020; Sutradhar et al. 2021; Sharma et al. 2024). *Pseudomonas tolaasii* is a widespread bacterial disease (Amin et al. 2021), which is the primary cause of brown spot disease of white caps (Basim and Basim 2018), leading to significant yield losses worldwide (Amin et al. 2021). This disease, known as La France disease and caused by different virus complexes, slows down mycelial development, reduces yield and causes deformities in caps (Elibüyük 2007), and viral diseases such as fungal virus X (MVX) can cause degeneration of mycelium, deformation of fruit bodies and yield losses (Grogan et al. 2003; Zhang et al. 2022). These diseases not only reduce yield, but also cause economic losses by shortening shelf life and reducing marketability (Amin et al. 2021). Therefore, the control and management of fungal diseases is of vital importance for mushroom growers.

A. bisporus remains a primary focal point of mycological and agricultural research, ranging from the optimization of cultivation conditions (Sharma et al. 2007) to the etiology and management of various pathogens (Berendsen et al. 2010; Basim and Basim 2018; Amin et al. 2021). In particular, brown spot disease caused by *Pseudomonas tolaasii*, along with diverse fungal (Sutradhar et al. 2021) and viral agents (Zhang et al. 2022), represents the most significant challenge to the industry. Given the substantial economic impact of these diseases on yield and product quality, research has increasingly shifted toward utilizing genetic and molecular techniques to elucidate disease mechanisms and develop resistant cultivars (Amin et al. 2021; Zhang et al. 2022). Such advancements are critical for ensuring the long-term sustainability and economic efficiency of mushroom cultivation.

Dry blister disease (*Lecanicillium fungicola*)

Dry blister disease is a disease caused by the fungus *Lecanicillium fungicola* (Preuss) Zare & W. Gams (formerly *Verticillium fungicola*) and causes significant economic losses in *Agaricus bisporus* cultivation (Zare and Gams 2008; Fletcher and Gaze 2007). The disease usually starts with brown spots or streaks on the upper part of the mushroom stem and cap in mild infections. These spots turn grayish after sporulation (Albayrak et al. 2024). In dry blister disease, many localized, light brown, sunken spots appear on mature sporophores. These spots may merge into irregular brown spots and white fungal spore masses, or a gray moldy cover may form on the surface (Marlowe and Romaine 1982; Prasad and Singh 2020). In the later stages of the disease, infected hats shrink, become leathery in spotted areas, dry and crack (Marlowe and Romaine 1982).

Wet blister disease (*Mycogone perniciosa*)

Wet blister disease is an important disease caused by the fungus *Mycogone perniciosa* and causes serious economic losses in *Agaricus bisporus* cultivation (Albayrak et al. 2024). Wet blister disease is characterized by the formation of tumor-like, irregular fungal masses in infected young pinheads (up to 6 mm), which do not show organ differentiation (Sharma and Kumar 2000; Umar et al. 2000). In advanced cases, a cottony, white mold growth can be observed on these tumor-like masses (Sharma and Kumar 2000). A white, fluffy mold forms on infected areas, which over time turns the fungus into a soft mycelial ball. In the early stages of the disease, a brown-amber colored liquid emerges from the fungus. These structures, which are initially white, turn brown in time and start to rot (Albayrak et al. 2024).

Spider web disease (*Cladobotryum dendroides*)

Spider web disease is a serious disease caused by *Cladobotryum mycophilum* that can cause significant yield losses in

white-capped mushroom (*Agaricus bisporus*) cultivation (Chakwiya et al. 2015; Zuo et al. 2016). The first symptoms of the disease are the appearance of small, white spots on the cover crop soil. These spots spread to the nearest fungi through a fine, gray-white mycelium network, creating a cobweb-like appearance (Sharma 1994; Prasad and Singh 2020). As the infection progresses, the mycelium can cover the surface of the fungi and cause rotting. The disease is usually more common in fall and winter (Carrasco et al. 2016). The disease agent is a soil-dwelling fungus and is usually transmitted to crops through soil contamination, spores, crop residues or farm workers. Spores are easily spread by air currents, workers' hands, tools, clothing and splashing water (Sharma 1994).

Bacterial brown spot disease (*Pseudomonas tolaasii*)

Pseudomonas tolaasii is the causal agent of brown spot disease in *Agaricus bisporus* cultivated worldwide. This pathogen starts by forming slightly sunken brown lesions on the surface of the fungus (Fletcher and Gaze 2007; Basim and Basim 2018). In later stages, these lesions coalesce to cover large parts of the infected pileus and can lead to tissue decay (Wells et al. 1996; Basim and Basim 2018,). Under favorable conditions, such as high humidity and poor ventilation, this decaying tissue can emit a foul odor (Basim and Basim 2018). Also, depending on the time of infection, deformations such as twisting of the stems and curvature of the caps can be observed. Depending on the severity of the cases, crop losses can be up to 100% (Amin et al. 2021).

Crocodile skin (Non-Microbial Causes)

Deviations from optimum growing conditions can cause various physiological abnormalities in the development of fungi. Fluctuations in abiotic factors such as substrate moisture, pH, temperature, carbon dioxide concentration, airflow and relative humidity create an unfavorable environment for fungi, leading to both yield and quality losses. These factors can adversely affect the development of the fungal mycelium as well as encourage the proliferation of competitive molds and pests. Deformations, such as cracks due to fluctuations in temperature and humidity, show the direct impact of abiotic stress on the crop (Sharma et al. 2007). Crocodile skin starts with small, brown or gray spots on the surface of the mushroom cap. These spots grow and merge over time to form a cracked and scaly appearance. This causes the outer surface of the fungus to dry and harden, forming a typical crocodile skin-like texture (North and Wuest 1993). This condition is not caused by a microbial infection but by environmental factors (Fletcher and Gaze 2007). Factors such as irregular irrigation, inadequate ventilation and sudden changes in temperature can create stress on the surface of the mushroom cap and promote the formation of such cracks. Furthermore, nutrient imbalances and compost quality problems also contribute to such physiological disorders (Fletcher and Gaze 2007).

A. bisporus is exposed to numerous fungal, bacterial, and abiotic disease threats under intensive cultivation conditions. Among these, green mold caused by *Trichoderma aggressivum* is one of the most difficult diseases to diagnose and necessitates the use of artificial intelligence–based approaches. This is primarily because the white mycelia of the pathogen at the early stage are visually indistinguishable from those of *A. bisporus* itself (Šašić Zorić et al. 2023; Djisalov et al. 2024). The disease is typically recognized only after the formation of dark green spores, at which point yield losses can reach between 60% and 100% (Šašić Zorić et al. 2023). Another critical disease, dry bubble caused by *Lecanicillium fungicola*, initially manifests as small brown lesions on the cap or as deformities on the stipe known as "blow-out" under mild infections; however, these symptoms can easily be confused with other fungal spots (Berendsen et al. 2010; Amin et al. 2021). Wet bubble disease, caused by *Mycogone perniciosa*, leads to the formation of undifferentiated, tumor-like masses on young pins and produces characteristic amber-colored droplets at advanced stages (Amin et al. 2021; Albayrak et al. 2024). Bacterial blotch disease, caused by *Pseudomonas tolaasii*, results in sunken brown lesions on the cap, whereas an abiotic disorder known as "crocodile skin" creates a scaly and cracked appearance due to environmental factors, often mimicking pathogenic symptoms (Basim and Basim 2018). Conventional visual inspection methods require a high level of expertise to differentiate these symptoms, and intervention is often delayed until the symptoms become pronounced (Djisalov et al. 2024). Therefore, deep learning models such as SqueezeNet have become critically important for enabling early and accurate diagnosis by analyzing subtle textural and color variations that are not discernible to the human eye (Theerthagiri et al. 2024).

Deep learning and machine learning

There are many studies in the literature where various Deep Learning and Machine Learning based methods have been successfully applied for the detection of diseases seen in plants. These studies are generally carried out to classify disease symptoms on images obtained from plant parts such as leaves, fruits and stems. Methods such as Convolutional Neural Networks (CNN), Transfer Learning, Support Vector Machines (SVM) and Artificial Neural Networks (ANN) are widely preferred; these approaches attract attention with their high accuracy rates, especially in image-based diagnosis systems. Early diagnosis of leaf diseases that cause yield loss in agricultural products is of great importance in terms of preserving product quality. In this context, deep learning-based approaches offer effective solutions, especially in automatic

diagnosis systems based on image data. Recent research has particularly highlighted the efficiency of lightweight architectures. For instance, Theerthagiri et al. (2024) conducted a study on the detection and classification of maize leaf diseases using various deep learning models. They reported that the SqueezeNet architecture, a compressed Convolutional Neural Network, is an effective diagnostic method offering both rapid processing times and high accuracy. Al-Khateeb (2024) used SqueezeNet based deep learning method for the detection of olive crop diseases. Image-based deep features extracted with SqueezeNet architecture were trained with two different machine learning models, ANN and SVM. As a result of the experiments, ANN model showed the highest performance with 92.9% accuracy rate, while SVM model achieved 85.5% accuracy. Similarly, Alado (2024) achieved a high accuracy rate of 92% in identifying Cassava leaf diseases using the SqueezeNet architecture, reinforcing that its lightweight structure is highly suitable for agricultural tasks. Furthermore, Koklu et al. (2023) successfully applied deep features from SqueezeNet for the classification of soybean seed defects. This success of the SqueezeNet architecture in agricultural diagnostics has also been confirmed in the current literature by Jagdev et al. (2025); researchers achieved high accuracy rates using this architecture in the classification of tomato leaf diseases. This result shows that SqueezeNet, despite its lightweight and optimized structure, can exhibit high performance in agricultural image classification tasks and is a suitable deep learning architecture for such applications. Nath et al. (2025) demonstrated that deep learning architectures offer significantly higher accuracy and processing speed in diagnosing brinjal fruit diseases compared to traditional methods.

Albayrak et al. (2025) classified the diseases seen in *Agaricus bisporus* using image data with pre-trained deep learning models and carried out the analysis of the diseases. In the study, they used a special dataset consisting of images collected with a specially designed portable imaging device under uniform white light conditions.

Currently, the methods used to detect *Agaricus bisporus* diseases present several limitations in terms of effectiveness, cost, and time. Visual inspection, the most commonly used approach, is entirely subjective and remains insufficient for diagnosis before the pathogen reaches the sporulation stage (Šašić Zorić et al. 2023; Djisalov et al. 2024). Culture-based methods require the pathogen to be grown on selective media, a process that is time-consuming and may take several days to weeks (Šašić Zorić et al. 2023). Similarly, microscopy-based techniques necessitate waiting until the sporulation stage to examine spore structures (Šašić Zorić et al. 2023). Although molecular methods such as PCR, RT-PCR, and MNP provide highly sensitive results, they are not well-suited for field applications due to their reliance on expensive equipment, the need for skilled personnel, and their susceptibility to inhibitors present in compost, which may lead to false-negative results (Šašić Zorić et al. 2023; Djisalov et al. 2024; Liu et al. 2025). In contrast to laboratory-based techniques such as PCR, image-based analysis systems can perform detection within seconds using images captured by a standard smartphone camera. The SqueezeNet architecture employed in this context enables real-time operation on mobile and embedded devices by delivering high accuracy with a reduced number of parameters (Theerthagiri et al. 2024; Kiran et al.,2026).

While most artificial intelligence models in the literature rely only on RGB inputs, this study aimed to determine the effect of different color spaces on classification success using deep learning. Deep learning-based image classification approaches offer significant advantages over traditional methods in the detection of *Agaricus bisporus* diseases. Deep learning-based image classification approaches offer significant advantages over traditional methods in the detection of fungal diseases. In particular, they can generate results in seconds by automatically extracting features from images, thus providing a significant speed advantage compared to laboratory-based analyses. Furthermore, since they only require camera and software infrastructure, they reduce costs and enable large-scale applications. Comparing different color spaces can improve model accuracy by allowing for more distinct differentiation of disease symptoms. The proposed approach enables the development of consistent and fully automated diagnostic systems in this field, reducing human error.

Color spaces that achieved a high accuracy rate in distinguishing visually similar diseases such as *Lecanicillium fungicola* and *Cladobotryum dendroides* were identified in this study. This system, operating under field conditions, allows growers to quickly quarantine infected areas, thus preventing disease spread and minimizing yield losses.

The continuation of the study includes the creation of the dataset, the creation of the deep learning model, and the findings obtained for the purpose of predicting these different types of fungal diseases from images, respectively.

Material and method

Data collection

The photographic data utilized in this study were obtained from mushroom specimens cultivated under controlled conditions in the production rooms of the Mushroom Cultivation Program at Korkuteli Vocational School. The cultivation process was conducted in accordance with standard commercial mushroom farming protocols, ensuring all necessary environmental and hygiene parameters were maintained. Disease symptoms were initially observed following the first flush period. From that point onward, photographs were systematically captured at regular intervals to document disease progression and to compile a representative image dataset for analysis.

The study contains 21 images from the Healthy category, 40 images from the *Lecanicillium fungicola* category, 40 images from the *Mycogone perniciosa* category, 45 images from the *Cladobotryum dendroides* category, 40 images

from the *Pseudomonas tolaasii* category, and 40 images from the Crocodile skin abiotic disorder category, totaling 226 images.

The images were collected with a 12 MP smartphone camera in a mushroom growing area under the same lighting conditions. The collected images were cropped so that only the mushrooms remained in the image.

Each image was taken from approximately the same distance (25 cm) and under similar conditions. A density was observed among the sporophores developing after primordia formation, with an average distance of 2–5 cm between them. Different diseased and healthy *Agaricus bisporus* could be located at various positions within the production room; therefore, images for each class were collected to encompass the specific mushroom along with a portion of its immediate surroundings. The camera was not fixed at any specific location; rather, in line with the goal of practical disease identification, mushroom photographs were captured without the use of any formal image-acquisition setup.

In mushroom growing environments, rare or irregular diseases are inherently unavoidable. Since these diseases do not occur with the same frequency in each production period, creating a balanced and large dataset is practically difficult. In this study, to mitigate the effects of data scarcity, the generalization ability of the model was enhanced using data augmentation. According to the defined settings, each image can be randomly rotated between -20° and +20° and randomly reflected on the horizontal axis in each training cycle. Thus, although the dataset does not physically grow, the model becomes more generalizable and robust by viewing different variations of the same images.

These collected RGB formatted images were converted to HSV, NTSC, XYZ and YCbCr color spaces to create a total of five different data sets. For each different color formatted set, 70% of the data collected from each class was used in the training of the network and the remaining part was used in the testing phase. Data augmentation was applied to the images in the data set during training. Fig. 1 below shows sample RGB formatted images for each class. Fig. 2 shows sample images with different color spaces for fungi belonging to the Crocodile skin abiotic disorder class.

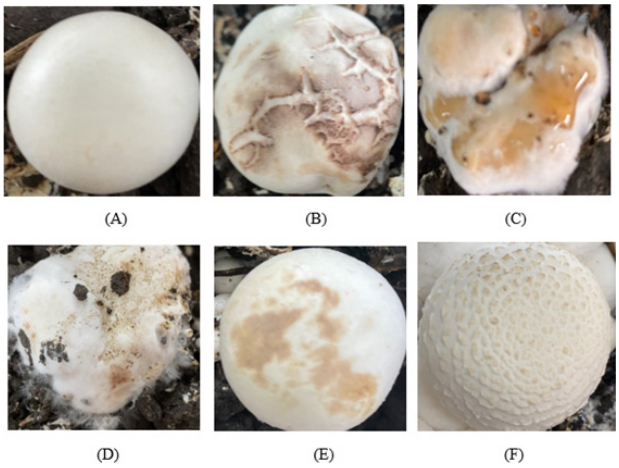

Figure 1. Example fungi images belonging to the classes. **a.** Healthy; **b.** *Lecanicillium fungicola;* **c.** *Mycogone perniciosa;* **d.** *Cladobotryum dendroides;* **e.** *Pseudomonas tolaasii*; **f.** Crocodile skin abiotic disorder.

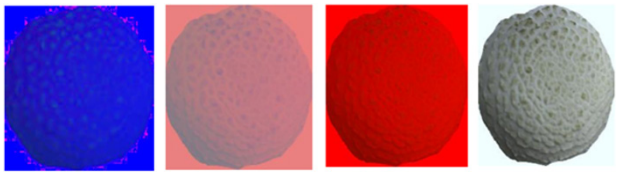

Figure 2. Sample images in color spaces for the Crocodile skin abiotic disorder class.

SqueezeNet convolutional neural network

In the proposed study, SqueezeNet model is used for the detection of fungal diseases. SqueezeNet model focuses on sensitivity with fewer parameters, and this model design emphasizes more sensitivity than other convolutional neural network models. This model is a lightweight and fast convolutional neural network model used in deep learning and is designed to provide high performance especially in limited computational resources. The basic structure of the network consists of blocks called "fire module"; these blocks first reduce the input feature maps with "squeeze" layers, then expand this information with "expand" layers to extract more complex features. In this study, 'InitialLearnRate' was set to 1e-4, 'MaxEpochs' to 20, and 'MiniBatchSize' to 8.

Thus, high accuracy can be achieved with fewer parameters with the model. In the study, the last classifier layer of the pre-trained SqueezeNet was restructured according to the number of classes in accordance with our dataset (Theerthagiri et al. 2024).

Results

5-fold cross-validation was performed in this work. Confusion matrices obtained with the SqueezeNet model for different color spaces in the classification of fungal diseases from images are given in Fig. 3. The obtained average success rates with different performance metrics for different color spaces are given in Table 1.

When the table is examined, it is seen that the high performance of RGB, XYZ, and YCbCr color spaces is quite similar. This shows that the model already makes good use

Table 1. Cross-Validation success rates for the different color space formats.

Color spaces	Mean accuracy	Precision	Recall	F1
RGB	%88.93	0.9085	0.8892	0.8956
HSV	%81.89	0.8265	0.8164	0.8186
NTSC	%85.41	0.8585	0.8497	0.8533
XYZ	%88.95	0.9054	0.8948	0.8970
YCbCr	%90.26	0.9179	0.9106	0.9126

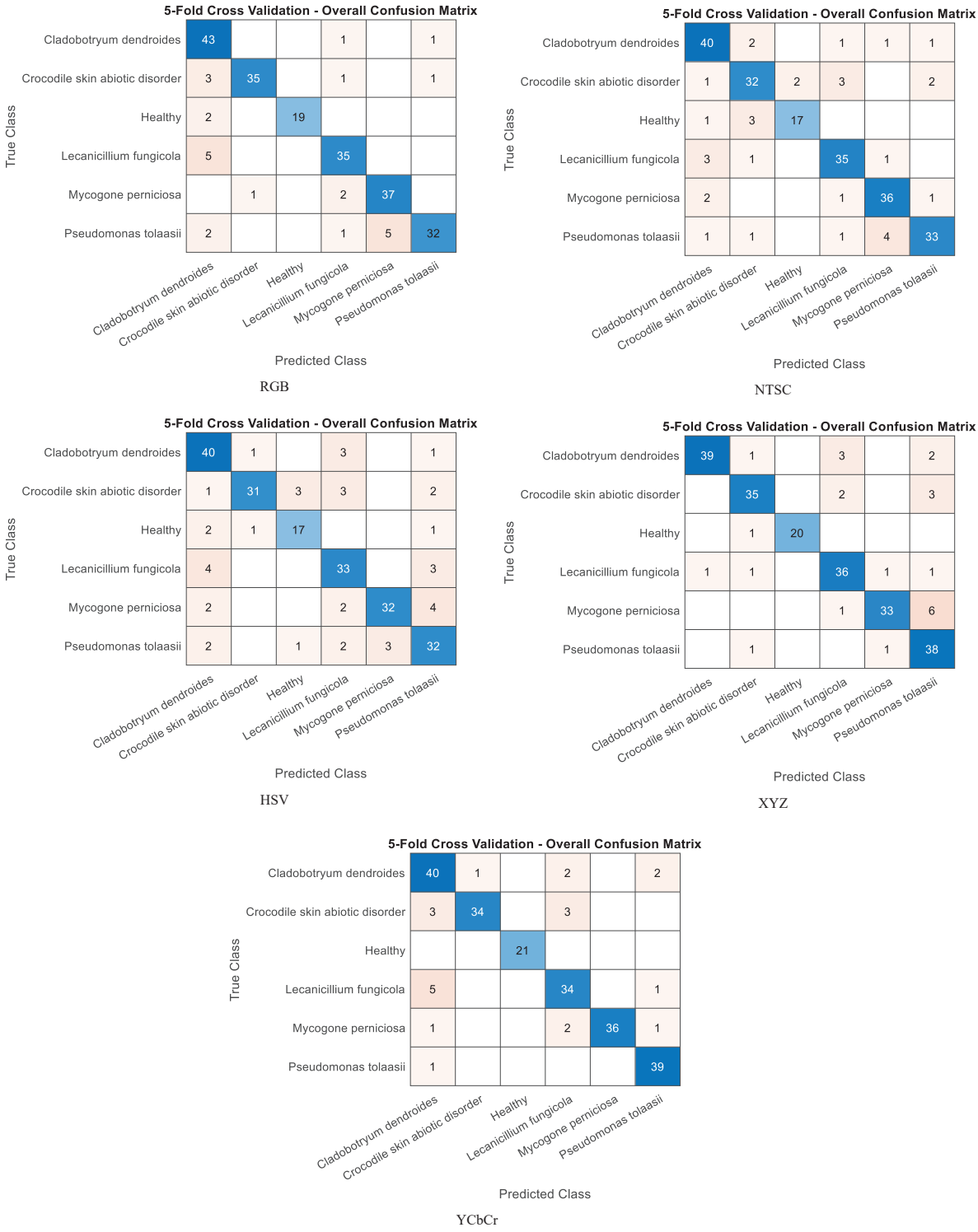

Figure 3. Confusion matrices obtained in different color space formats.

of color information for these three color spaces. YCbCr provides the most balanced results, with a slight advantage, especially in terms of precision, recall, and F1-score. RGB, on the other hand, demonstrates a strong baseline by producing competitive results even without any conversion.

The high precision values in the XYZ and YCbCr color spaces indicate that the vast majority of samples classified as positive by the model are indeed correct. This provides a critical advantage, especially in applications where false positives are costly. Thanks to the better separation of color and brightness components in XYZ and YCbCr, the model learns distinguishing features more clearly, which contributes to increased precision. As a result, these two color spaces allow the model to work more selectively and reliably.

As can be seen from these confusion matrices, it is possible to obtain full accuracy in images with different color spaces, especially for some disease classes. This can provide higher success by converting to an effective color space, especially in determining some disease types.

Discussion

Accurate and early identification of fungal diseases in *Agaricus bisporus* cultivation is essential to reduce yield losses and ensure economic sustainability in mushroom production. In this study, a deep learning-based diagnostic framework was proposed using the lightweight SqueezeNet convolutional neural network architecture to classify six distinct classes five disease types and one healthy condition based solely on image data. A unique contribution of this research lies in its systematic investigation of different color space conversions (RGB, HSV, NTSC, XYZ, and YCbCr) and their effect on classification performance, which remains an underexplored area in fungal disease diagnostics.

In this study, similar and high success rates were obtained for RGB, XYZ, and YCbCr color spaces. The superior performance of XYZ and YCbCr color spaces is largely due to their better separation of chrominance and luminance information. This separation allows the model to be less affected by light variations and learn more meaningful features. In YCbCr, the separation of brightness and color difference components produces more noise-resistant and balanced results, while XYZ, offering a more linear color representation closer to human vision, demonstrates its ability to capture color differences more consistently. This finding suggests that the selection of an appropriate color space plays a pivotal role in enhancing feature representation and model sensitivity, particularly for visually similar diseases like *Lecanicillium fungicola* and *Cladobotryum dendroides*. The perceptual uniformity and component decorrelation characteristics of the XYZ format likely contributed to this superior performance.

In contrast, HSV and NTSC color spaces have been observed to have lower success rates. In the HSV color space, the sensitivity of the Hue component to lighting variations and its instability at low saturation levels may have caused the performance decrease. The fact that the NTSC color space provides a lower success rate compared to RGB but a higher success rate compared to HSV may be due to its different representation of color components. It is considered that the YCbCr color space more effectively represents disease-related color changes due to its ability to separate brightness and color components, and therefore achieves higher accuracy.

Another critical strength of the study is the simplicity of its data acquisition process. Images were captured under controlled lighting using a standard smartphone camera, without the use of specialized imaging hardware or preprocessing techniques beyond cropping. This emphasizes the robustness and practicality of the model for in-field applications, aligning with the goals of precision agriculture and low-cost diagnostic tool development.

In methodological terms, the findings validate the potential of lightweight CNN models like SqueezeNet for agricultural diagnostics, particularly in settings with limited computational resources. While previous studies (Theerthagiri et al. 2024; Alado 2024) have reported promising results using SqueezeNet in classifying plant leaf diseases, this study extends those insights to fungal pathogens and highlights the role of image representation through color space conversion. The results support the broader thesis that domain-specific optimization of input features can significantly impact deep learning performance in agricultural contexts.

Conclusion

This study demonstrates that deep learning models, particularly the SqueezeNet CNN architecture, can effectively classify fungal diseases in *Agaricus bisporus* using simple image-based data. Among the color spaces evaluated, YCbCr, XYZ and RGB was identified as the most effective in enhancing classification accuracy. The ability to achieve high performance using smartphone images without extensive preprocessing confirms the feasibility of deploying such systems in real-world mushroom production environments.

These findings underline the importance of incorporating color space considerations into model design for agricultural diagnostics and support the development of accessible, field-deployable decision support systems for mushroom growers. As a practical implication, growers could utilize mobile applications or embedded systems leveraging this approach for on-site disease monitoring.

For future research, it is recommended to explore multi-input CNN architectures that can process different color space representations concurrently, integrate multisensory data for improved diagnosis, and adopt explainable AI techniques to increase user trust and model transparency. The establishment of open-access, annotated datasets and mobile-compatible tools would further advance the integration of AI into mushroom cultivation practices.

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Additional information

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The authors have declared that no competing interests exist.

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Data availability
The datasets generated and/or analyzed during the current study are available from the corresponding author on reasonable request.