

## ORIGINAL RESEARCH ARTICLE

# Artificial neural networks algorithms for prediction of human hair loss related autoimmune disorder problem

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### ABSTRACT

In this study, artificial neural networks (ANNs) are being used to diagnose hair loss in patients. An autoimmune condition known as Alopecia Areata (AA) results in hair loss in the affected area. The most recent figures from throughout the world show that AA affects 1 in 1000 persons and has a 2% incidence rate. Based on the look of photographs with healthy hair in the dataset, machine learning techniques were employed to classify the conditions. Before making predictions, each of these ANNs algorithms creates a prediction model using pictures of healthy hair. The aim of this study is to evaluate the accuracy of neural networks for alopecia detection in human subjects. The study presents a classification framework for distinguishing between healthy hairs (HHs) and Alopecia Areata (AA). The framework incorporates Contrast Limited Adaptive Histogram Equalization (CLAHE) enhancement and segmentation techniques to enhance the quality of the images. Additionally, Data Augmentation (DA) is employed to generate additional data and improve the precision of the proposed framework. To extract features from the images, two powerful techniques are utilized. The Visual Geometry Group (VGG), which consists of very deep convolutional networks designed for large-scale image recognition, is employed. VGG networks have proven to be effective in learning complex features directly from data, eliminating the need for manual feature extraction. Additionally, a Convolutional Neural Network (CNN), a deep learning network architecture specifically designed for image processing tasks, is employed. To create a machine learning model for classification, the Support Vector Machine (SVM) approach is utilized. SVM is a widely used algorithm in supervised learning, capable of solving both classification and regression problems. Its versatility and effectiveness make it a suitable choice for the classification task in this study. By combining the CLAHE enhancement, segmentation, data augmentation, feature extraction using VGG and CNN, and classification using SVM, the proposed framework aims to accurately classify HHs and AA cases.

**Keywords:** deep learning; ANNs; feature extraction techniques; Alopecia Areata

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## 1. Introduction

Alopecia Areata is a condition that results in hair loss on the head and other areas of the body where hair is typically found. This illness has a negative psychological and social impact on sufferers. There are several different subtypes of alopecia, but the three that are most frequent are chemotherapy-induced alopecia (CIA), androgenetic alopecia (AA), and androgenic alopecia (common baldness)<sup>[1]</sup>.

Stress, genetics, hormonal imbalances, bad food, particular illnesses, and some medications, such as those used to treat cancer, are only a few of the many factors that contribute to the development of the disorders. Although the Food and Drug Administration (FDA) has only approved two related therapy (minoxidil and finasteride) for the illness, there are more unapproved drugs that claim to be able to

reverse alopecia. Other hair loss restoration solutions are not supported by dependable evidence from rigorous scientific studies, which prevents their broad use and commercialization<sup>[2]</sup>.

The four stages of cyclical hair development are catagen, anagen, exogen, and telogen. Around 90% of the hair on a healthy scalp is produced during the anagen phase of hair development, also known as the active phase, which lasts for years<sup>[3]</sup>. The anagen period gets shortened with each cycle, which causes the growth of villus hair, which is weaker hair. The stages that follow anagen are characterized by hair recession, and hair on a healthy scalp is typically shorter in length<sup>[4]</sup>.

Extensive research has been conducted using photographs of hair to identify Alopecia Areata, a hair disorder<sup>[4,5]</sup>. Dermoscopy and scalp pictures have been used in earlier studies to investigate the human body. The bulk of researchers have taken scalp photos and extracted skin characteristics diagnostic with AA<sup>[5]</sup>.

ScalpEye is an intelligent scalp inspection and diagnostic solution based on deep learning. Utilizing advanced technology, ScalpEye can accurately identify and diagnose four common scalp hair symptoms, namely folliculitis, dandruff, oily hair, and hair loss<sup>[6]</sup>. This retrospective study looked into a number of well-known object identification models, but in the end decided to use the ScalpEye system's Faster R-CNN with Inception ResNet v2 Atrous model for picture recognition<sup>[7]</sup>.

The computational analysis used the whole-genome gene expression of 122 human scalp skin biopsy samples from the collection to identify important genes associated with AA<sup>[7]</sup>. Then, they developed a biomarker utilising eight distinct Machine Learning (ML) techniques and significant genes discovered through bioinformatics research. Additionally, azacitidine and anisomycin, two molecular drugs, were found in the Cmap database<sup>[8]</sup>. Researchers have developed highly accurate algorithms to predict the likelihood of patients having androgenetic alopecia (AA). These advanced models have the potential to assist in creating personalized treatment plans and clinical care for diverse patient populations<sup>[8]</sup>. Acne is thought to be a highly heritable, T-cell-mediated autoimmune condition that attacks the hair follicle. The AA risk allele identified by haplotype sequencing for the Major Histocompatibility Complex (MHC) area might be expressed in modified mice by applying allele-specific genome editing with the Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR/Cas9) technology<sup>[9]</sup>. Finally, functional assessments were carried out on both mice and AA patients who carried the risk allele as well as those who did not. The single non-synonymous variable in the AA risk haplotype was discovered to be a mutation in the coiled-coil alpha-helical rod protein gene<sup>[10]</sup>.

In order to simulate the autoimmune disease Alopecia Areata, which is characterised by various geographical patterns of hair loss, a Bayesian data assimilation approach is used<sup>[11]</sup>. They show that our technique is often resistant to fluctuations in parameter estimates by employing synthetic data instead of simulated clinical observations. They also look at convergence rates for parameters with different sensitivity, variable observational times, and variable noise levels. Our results show that this method performs better in the presence of sparse data, delicate parameters, or noisy observations. Together, we find that their data assimilation and physiologically inspired model provide suggestions for individualised diagnosis and treatment<sup>[12]</sup>.

Protein-protein interactions have played a crucial role in unraveling the functional connections between source proteins and target proteins. Through the study of these interactions, researchers have discovered the involvement of these molecules in a wide range of physiological processes, including protein metabolism and signal transduction<sup>[13]</sup>. Therefore, the inconsistent expression of these critical proteins would affect their normal level and would cause abnormalities in hair formation. Alopecia, which is frequently referred to as hair loss, is a complex, polygenetic condition that affects millions of men and women worldwide<sup>[14]</sup>.

During the anagen stage, a condition known as anagen effluvium can disrupt the regular hair growth cycle, resulting in unwanted hair shedding or thinning (referred to as anagen arrest). Anagen effluvium can be triggered by certain medications or chemotherapy, similar to chemotherapy-induced alopecia. This disorder

leads to the loss of anagen hair and extends the telogen phase significantly, which can persist throughout the duration of the patient's treatment for the underlying condition. Another factor thought to be responsible for the illness is excessive use of pharmaceuticals such as birth control pills, blood thinners, acne, & diuretics treatments. The disease may be reversed & hair can regrow after the time of up to three months in the majority of cases; nevertheless, the problem can be permanent, causing psychological distress and harming the patient's sensitivity to appearance<sup>[15]</sup>.

Machine learning and deep learning strategies are widely employed to identify alopecia in humans and assess the accuracy of feature extraction methodologies. These advanced computational approaches leverage algorithms to analyze diverse datasets, including clinical images, genetic information, and patient records. By utilizing techniques such as support vector machines (SVM), random forests, artificial neural networks (ANNs), and convolutional neural networks (CNNs), researchers can extract meaningful features and improve the precision of alopecia detection. These strategies play a crucial role in enhancing diagnostic capabilities, prognosis assessment, and treatment planning in the field of dermatology. Different machine learning techniques have been used in dermatology to provide accurate diagnoses and predictions. Estimation models are built using healthy hair photos in all these machine learning approaches<sup>[16]</sup>.

The primary objective of this retrospective study is to evaluate the effectiveness of a neural network in accurately identifying human alopecia and determining its presence. The proposed VGG-SVM model offers clinical specialists a valuable second opinion, assisting them in making well-informed decisions regarding the presence of this condition in patients. Obtaining a second opinion is crucial due to various factors that influence the diagnosis process, such as population growth, environmental pollution, increased demand for proper healthcare, and a shortage of medical professionals to address the needs of an aging population. Furthermore, the accuracy of a diagnosis heavily relies on the dynamic nature of symptoms associated with the illness. Hence, the present study aims to assess the accuracy of neural networks in detecting alopecia in human individuals.

## 2. Materials and methods

AA is characterized by considerable variability in the length, amount, and pattern of hair loss during a single episode of the illness, in addition to great variability in hair loss at the time of first beginning. The disorder, which affects millions of people worldwide and is especially common in families with Alopecia Areata, is widespread. It has been difficult to design and carry out clinical investigations in AA due to the varied and unpredictable nature of spontaneous re-growth as well as the absence of a consistent response to various treatments. There are two forms of alopecia that have an identical effect on both sexes. It is a problem in both kids and adults.

VGG is a part of the Department of Science and Engineering at Oxford University. It has generated a number of convolutional network models for face recognition and image classification from VGG16 to VGG19. Models for advanced object recognition are built using the VGG architecture. Along with ImageNet, the VGGNet, which was developed as a deep neural network, beats baselines on numerous tasks and datasets. It is also one of the most frequently employed image recognition architectures right now.

The SVM algorithm's objective is to establish the best line or decision boundary that can divide n-dimensional space into classes, allowing us to quickly classify fresh data points in the future. A hyperplane is the name given to this optimal decision boundary. SVM selects the extreme vectors and points that aid in the creation of the hyperplane. Support vectors, which are used to represent these extreme instances, form the basis for the SVM method.

For this investigation, we used 68 images of AA and 200 images of healthy hairs from the Figaro1k dataset. There are 68 images of AA hair that were extracted from the DermNet dataset<sup>[17,18]</sup>. In this study, we conducted an analysis of skin issues in individuals worldwide using sample images sourced from DermNet.

The images included various dermatological conditions, with a particular focus on skin infections treated with natural remedies. The accuracy of the proposed framework was found to vary depending on the specific skin condition being investigated. Among the twenty-three different types of dermatological conditions listed in the DermNet database, Alopecia Areata was one of the conditions included in the study. Disease images were used to illustrate several other conditions as well, including seborrheic dermatitis, eczema keratoses, bullous disease, poison ivy, psoriasis, and tinea ringworm. Example pictures for AA are shown in **Figure 1**.



**Figure 1.** Sample images of Alopecia Aerate (Picture courtesy of DermNet database <http://www.dermnet.com>).

In this study, we utilized the Figaro1k dataset<sup>[19]</sup> to obtain a total of 200 images representing healthy hair. The Figaro1k dataset is a publicly available resource that consists of images showcasing individuals with diverse hairstyles, including straight, wavy, and curly hair. To ensure consistency in the size and aspect ratio of each image, a normalization process was applied. Normalization involves organizing the data in a database to maintain uniformity.

To conduct hair analysis in different environments, it is crucial to have a diverse collection of images with various hair textures and unrestricted field of view. To address the limited availability of open and freely accessible databases, we utilized Figaro1k, an extension of Figaro, which is an annotated multi-class image library specifically designed for hair analysis in different environments. The Figaro1k dataset includes 150 images for each hair class, including wavy, straight, kinky, curly, dreadlocks, short, and braids, resulting in a total of 150 images per class.

To ensure consistency across the dataset, a normalization approach was implemented to account for variations in image sizes and aspect ratios. The normalization factor was adjusted to reduce the maximum squared area within the hair region to  $227 \times 227$  pixels, which served as the standardized size.

**Figure 2** presented in this study displays a set of sample photographs representing healthy hair. Unlike previous research that primarily focused on analyzing scalp and skin photos, our study introduces a novel and practical framework for accurately identifying Alopecia Areata (AA) and healthy hair in images of individual hair strands. By shifting the focus to hair-specific images, we aim to provide a more comprehensive and specialized approach to hair analysis and diagnosis.



**Figure 2.** Sample images of healthy hair (Picture courtesy of Figaro1k database <http://projects.i-ctm.eu/it/progetto/figaro-1k>).

The proposed framework harnesses the power of machine learning and deep learning techniques, which have shown great promise in various domains of dermatology. These techniques enable the automated analysis of large datasets, extracting meaningful patterns and features that can aid in the accurate identification of hair disorders, including AA. By leveraging the capabilities of these advanced algorithms, we can improve the precision and efficiency of AA detection, contributing to significant advancements in the field of dermatology.

One of the primary objectives of our framework is to enhance the prediction and diagnosis of AA. Alopecia Areata is an autoimmune condition characterized by hair loss in patches, which can have a profound impact on an individual's physical appearance and emotional well-being. Early and accurate detection of AA is crucial for initiating appropriate treatment strategies and improving patient outcomes. Through the utilization of machine learning and deep learning models, our framework aims to identify AA with high accuracy, enabling timely intervention and management.

In addition to the classification system that distinguishes between AA and healthy hair, our methodology also incorporates a technique to assess the severity of the condition. Understanding the extent and severity of AA is essential for tailoring personalized treatment plans and monitoring the progression of the disorder over time. By analyzing various features and patterns within the hair images, our framework provides valuable insights into the severity of the condition, enabling healthcare professionals to make informed decisions and offer appropriate interventions.

The use of machine learning and deep learning techniques in dermatology has revolutionized the field, offering new avenues for accurate and efficient diagnosis. These approaches have demonstrated remarkable capabilities in analyzing complex and diverse datasets, identifying subtle patterns, and making accurate predictions. By applying these techniques specifically to hair images, we aim to bridge the gap in previous research, which predominantly focused on scalp and skin analysis.

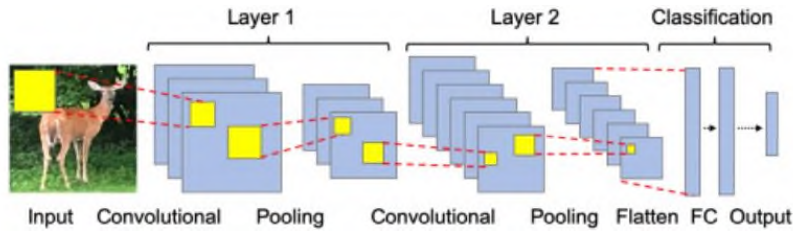
The practical application of our framework in clinical settings can greatly benefit both healthcare professionals and patients. By automating the process of AA identification and severity assessment, our approach offers a reliable and standardized method for diagnosing this hair disorder. This not only saves time but also reduces the subjectivity associated with manual evaluations. Moreover, our framework serves as an additional tool that clinical specialists can utilize to obtain a second opinion, enhancing the accuracy and confidence in the diagnosis process.

In conclusion, our study presents a practical framework for accurately identifying AA and healthy hair in images of individual hair strands. Leveraging machine learning and deep learning techniques, we offer a comprehensive approach to enhance the prediction, diagnosis, and severity assessment of AA. This framework holds significant potential for improving patient outcomes, advancing research in the field of dermatology, and paving the way for more personalized and effective interventions in the management of AA and other hair disorders.

When it comes to architecture, ANN is distinguished by having convolutional layers & pooling them as



shown in **Figure 3**. An ANN model’s convolutional layers are its fundamental construction blocks. Images having these convolutional layers in them are fed into the system, and the learned filters are used to extract essential information. After the convolutional layer comes to the pooling layer, which is a new layer used to build down-sampled feature maps.



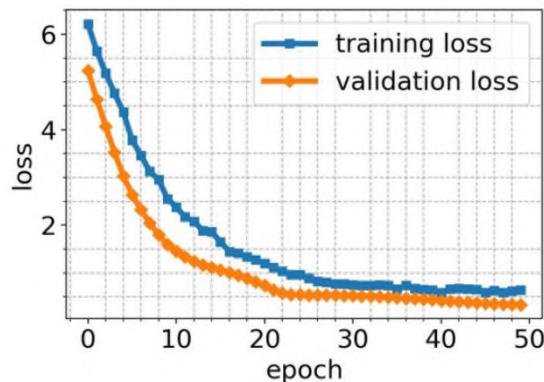
**Figure 3.** An example of ANN architecture.

The ANN model was trained using the optimal hyperparameters determined through grid search, as shown in **Table 1**. The dataset was split into a train-test-split of 70%–30%, with 105 randomly selected images used for training and 45 random images reserved for testing. Preprocessing steps were applied to the dataset, and the ANN model was trained using the training dataset. Finally, the performance of the model was evaluated using the test dataset.

**Figure 4** illustrates the training loss and validation loss of the neural network plotted against the number of epochs for various datasets.

**Table 1:** Hyperparameters of ANN model.

Hyperparameters	Values
Batch size	6
Epoch	50
Kernel size	$3 \times 3$
Pooling size	$2 \times 2$
Activation function	ReLU



**Figure 4.** Training and validation loss.

### 3. Results

In this study, the algorithm testing was conducted using a Titan X Pascal with 12 GB of RAM and an Intel (R) Core (TM) i7-5820K processor operating at 3.30 GHz. The implementation of the algorithm was done using the Python Keras or TensorFlow framework<sup>[20]</sup>. The pre-trained models were utilized by implementing the Python technique on the Jupyter platform.

To facilitate the implementation and analysis of the algorithm, various libraries such as Sklearn,

TensorFlow, Numpy, Pandas, and Matplotlib were imported. These libraries provided the necessary functionalities for data manipulation, model training, evaluation, and visualization.

For the experimental evaluation, two datasets were employed by our research team. The Figaro1k dataset consisted of 200 photographs of healthy hair (HH), while the DermNet dataset contained 68 images of Alopecia Areata (AA) hair. These datasets served as the basis for training and testing the algorithm.

To optimize the computational efficiency and improve the performance of the algorithm, a feature selection technique was applied. This technique helped to extract and retain only the most important elements from the images, resulting in more concise information representation. This preprocessing step also led to smaller data sizes, which facilitated the subsequent stages of the algorithm.

During the testing phase, the rate of categorization or classification accuracy, was calculated to assess the algorithm’s performance. Both the feature extraction and classification procedures were employed during both the training (70%) and testing (30%) stages of the algorithm, ensuring comprehensive evaluation.

By utilizing the specified hardware setup, implementing the algorithm using Python and its associated libraries, and leveraging the Figaro1k and DermNet datasets, the algorithm’s performance and effectiveness in classifying HH and AA hair images were assessed and analyzed.

Accuracies are expressed as a percentage of properly categorized samples, whereas error rates are a measure of how often incorrect classifications occur in the data. Accuracy is defined as the number of properly-identified samples divided by the total sample number<sup>[21]</sup>.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FN + FP} = \frac{TP + TN}{P + N} \quad (1)$$

In this study, edge detection was employed to identify curves in an image that exhibit rapid changes in intensity, serving as an indication of potential features in the image. A classification framework was then developed to differentiate between healthy hairs and Alopecia Areata using hair images. The features extracted from these images included color, texture, and shape. The classification process was performed using a support vector machine (SVM), resulting in a method referred to as Edge-SVM, which leverages machine learning techniques<sup>[22]</sup>.

Furthermore, the proposed method utilized a VGG-SVM approach, employing machine learning techniques to achieve the final classification results. These results were compared to those obtained from other machine learning techniques, and the performance of the proposed method demonstrated higher accuracy, sensitivity, and specificity. The findings are presented in **Table 2**, highlighting the superior performance of the proposed approach in accurately classifying healthy hairs and Alopecia Areata cases.

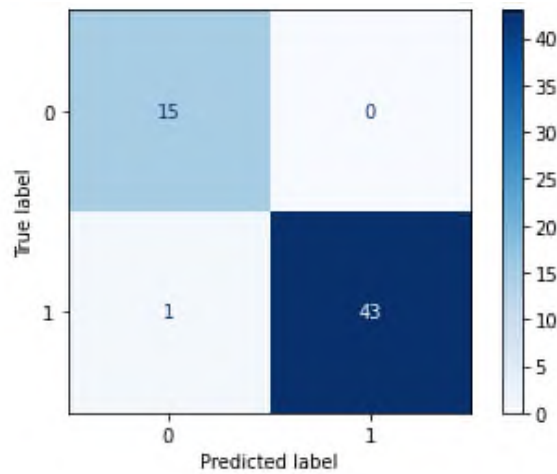
**Table 2.** Performance comparison between baseline and proposed method.

Metrics	Baseline (edge-SVM)	Proposed (VGG-SVM)
Accuracy	90.12	98.31
Sensitivity	73.68	100
Specificity	95.16	97.72

The confusion matrices generated over the test data are shown in **Figure 5** for proposed method.

**Figure 6** showcases the classification report of the SVM classifier for the proposed work. The report reveals that the classifier achieves high performance in terms of precision, recall, and f1-score for both Alopecia Areata (AA) images and healthy hair images. Specifically, for AA images, the precision is 100%, indicating a high proportion of accurately classified AA cases. The recall, also known as sensitivity, is 94%, indicating the classifier’s ability to correctly identify a significant proportion of AA cases. The f1-score, which

combines precision and recall, is 97%, reflecting the overall performance of the classifier in correctly classifying AA images.



**Figure 5.** Confusion matrix of proposed method.

	precision	recall	f1-score	support
0	1.00	0.94	0.97	16
1	0.98	1.00	0.99	43
accuracy			0.98	59
macro avg	0.99	0.97	0.98	59
weighted avg	0.98	0.98	0.98	59

**Figure 6.** Classification report of SVM classifier for proposed.

Similarly, for healthy hair images, the SVM classifier demonstrates excellent performance. The precision is 98%, indicating a high proportion of accurately classified healthy hair cases. The recall, also known as sensitivity, is 100%, suggesting the classifier’s ability to correctly identify all healthy hair cases. The f1-score for healthy hair images is 99%, reflecting the overall performance of the classifier in correctly classifying healthy hair.

These results demonstrate the effectiveness of the SVM classifier in accurately classifying both AA and healthy hair images, as indicated by high precision, recall, and f1-score values across all respective metrics

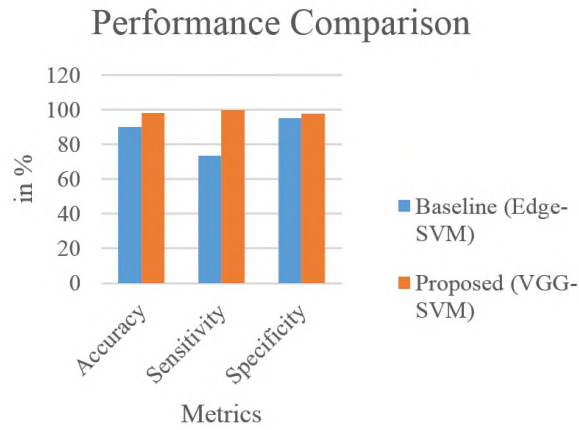
A bar graph comparing the baseline method with the suggested way is shown in **Figure 7**. Our suggested framework, the first of its type, has a special feature that uses hair images to categorize AA and healthy hairs. The accuracy of the suggested intelligent system for analyzing images of healthy hair using VGG-16 and SVM classifier was 98.31%. In addition to accuracy, the suggested approach boasts a 100% sensitivity rate and a 97.72% specificity rate.

To evaluate the robustness of the proposed method, various experiments can be conducted, including testing the method on diverse datasets with different hair types, lengths, and colors. Additionally, introducing controlled variations, such as noise or outliers, can help assess the method’s resilience to such challenges.

Scalability can be evaluated by measuring the method’s performance on progressively larger datasets and monitoring its computational requirements. This can involve analyzing execution time, memory usage, and system resources as the dataset size increases.

The proposed method demonstrates robustness by consistently delivering accurate results under various conditions, while also showcasing scalability by efficiently handling larger datasets and accommodating future expansion.





**Figure 7.** Comparative bar graph for different metrics.

## 4. Conclusions

Doctors sometimes perform tracheoscopies and biopsies on patients to eliminate alternative possibilities to ascertain whether the cause is AA. The uncertainty surrounding the number of tests that will be required for an accurate diagnosis to be established, however, is one of the drawbacks of these diagnostic processes. There is a critical need for new techniques to be found and tried to enhance the classification and diagnosis of Alopecia Areata. A wide range of medical fields has used sophisticated ANN algorithms and their advanced variations to diagnose patients.

Numerous ANN approaches have been used in dermatology to produce accurate diagnosis and prognoses. This study presents a novel technique for categorizing images of healthy hair into multiple classes using Support Vector Machines (SVM). The proposed approach focuses on accurately classifying and organizing photographs based on various hair characteristics and attributes. By employing SVM, a powerful machine learning algorithm, we aim to enhance the classification accuracy and efficiency of the hair categorization process. SVM and machine learning techniques were used to classify the conditions based on the appearance of healthy hair photos in the dataset. Each of these machine learning techniques builds a prediction model from images of healthy hair before making predictions. To the best of our knowledge, none of the ANN techniques have yet been applied in tandem with DL on images of human hair. The results of the present study allow us to create a categorization system for HHs and AA using hair pictures. To improve the contrast of the input sample photos with the features extraction technique, this framework first applied the CLAHE data pre-processing approach.

The healthy hair image dataset's features are extracted using VGG, and the classification of the hair image data has been done using AA & SVM. On these two datasets of hair photos, simulation was carried out using Python, and several performance indicators were tested the results showed that the data analysis performed using SVM had a 98.31% accuracy rate. Additionally, a comparison between the baseline and the suggested method was made, and a bar graph was created. The classification framework is reliable and efficient when it comes to classifying two different sets of hair photos. Along with accuracy, the proposed technique also outperformed the baseline method in terms of sensitivity and specificity, both of which are 100%. It has been called an intelligent HHs image analysis system that uses hair photographs and is the first of its kind to be able to discern AA from HHs.

The suggested VGG-SVM was demonstrated to be 98.31% accurate in the simulation, which used 200 images of HHs from the Figaro1k dataset and 68 images of AA from the DermNet dataset. The Figaro1k and DermNet datasets are renowned as the most extensive publicly available datasets for deep learning models in skin disease classification. These datasets provide a comprehensive collection of images and information

related to various skin conditions, enabling researchers and practitioners to develop and evaluate advanced algorithms for skin disease analysis.

## Author contributions

Conceptualization, SS and FS; methodology, SS; software, SS; validation, SS and FS; formal analysis, SS; investigation, SS; resources, FS; data curation, FS; writing—original draft preparation, FS; writing—review and editing, FS; visualization, FS; supervision, SS.

## Conflict of interest

The authors declare no conflict of interest.

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