

An Analysis of Alopecia Areata Classification Framework for Human Hair Loss Based on VGG-SVM Approach

Shabnam Sayyad¹, Divya Midhunchakkaravarthy², Farook Sayyad³

¹Research Scholar, Computer Engineering Department, Faculty of Engineering, Lincoln University College, Malaysia

Associate Professor, Computer Engineering Department, AISSMSCOE Pune

²Professor, Faculty of Computer Science, Lincoln University College, Malaysia.

³Professor, Dr D Y Patil School of Engineering, Pune India

Email: shabnamfsayyad@gmail.com

DOI: 10.47750/pnr.2022.13.S01.02

Abstract

Artificial intelligence approach is used in this article to make a diagnosis of hair loss. An autoimmune condition known as alopecia areata (AA) results in hair loss in the affected area. The most recent figures show that AA has an incidence of 2% and a frequency of 1 in 1000 people worldwide. For instance, classification is important in the field of medicine because one of the doctor's main objectives is to establish whether or not a patient has a condition. The identification of alopecia areata may be helpful for better prediction and diagnosis. Machine learning (ML) techniques have shown potential in a variety of domains, including dermatology. The dynamic character of illness symptoms is another important factor in the precise diagnosis of a particular disease. After then, as was already mentioned, linked work in the fields of ML and classification of healthy hair & hair disorders. The purpose of this research is to evaluate the efficacy of neural networks in recognising alopecia and non-humans. Healthy hair (HHs) and alopecia areata (AA) have been classified using a framework that will be susceptible to IP, including CLAHE enhancement and segmentation. Then, to increase the precision of the proposed framework, data augmentation (DA) was employed to generate further data. The VGG-19 pre-trained CNN model was then used to extract features. The Support Vector Machine (SVM) classification approach is then used to create an ML model utilising 70% of the images. The remaining images in the collection were used for testing. The suggested VGG-SVM was demonstrated to be 98.31% accurate in the simulation, which used 200 images of HH from the Figaro1k dataset and 68 images of AA from the Dermnet dataset. The proposed VGG-SVM outperformed the current Edge-SVM in terms of accuracy. The findings of our investigation point to the potential for enhanced dermatological prediction.

Keywords: Hair Loss, Deep learning, CNN, Alopecia Areata, VGG-SVM, CLAHE.

1. INTRODUCTION

With AA constituting the vast majority of cases classified as AA, the clinical spectrum of illness can be roughly estimated using this categorization approach up until the most recent edition of the WHO. Therefore, there is no association between subtype and prognosis. Despite the fact that they only make up a small portion of the population overall, ophiasis & AT or AU subtypes are associated with a poor prognosis. The vast majority of cases, ranging from mild to severe scalp hair loss by both favourable & unfavourable prognoses, are categorized into a single subtype [1]. It is essential to apply the SALT (Severity of Alopecia Tool), which has been validated, for determining an AA severity score (0 percent to 100 percent, no hair loss to complete scalp hair loss). The SALT is an essential tool in the clinical investigation of AA because it enables the controlled, objective evaluation of hair loss. [2]. The classification and prediction of a wide range of diseases and ailments has demonstrated the effectiveness of ML techniques. The study of various learning and adapting computer algorithms is known as machine learning (ML). ML algorithms and their sophisticated variations have been used into a number of medical disciplines for diagnostic purposes [3].

The condition known as alopecia results in hair loss on the head and other areas of the body where hair is typically found. Reduced self-esteem brought on by the stressful illness has a negative psychological and social impact on sufferers. The most common subtypes of alopecia are androgenic alopecia (common baldness), androgenetic alopecia (AA), and chemotherapy-induced alopecia (CIA). 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. There are additional unapproved medications that claim to be able to reverse alopecia, even though the FDA has only authorised two

related therapies (minoxidil and finasteride) for the condition. Other products claiming to restore hair loss are not backed up by convincing evidence from controlled scientific tests, preventing their widespread usage and commercialization. Hair develops cyclically in four stages: catagen, anagen, exogen, & telogen.[4,5].

There are many different types of alopecia to take into consideration because it can be brought on by a variety of different factors. Alopecia is a condition that is frequently observed in the general population. Examples include androgenic alopecia, AA, CIA, telogen effluvium, anagen effluvium, and traction alopecia. The two forms are scarring alopecia (caused by swelling in response to follicular damage) and the more common non-scarring alopecia (caused by a number of factors including hormones, medications, diet, and certain diseases) [6,7].

An autoimmune illness that causes hair loss on the scalp and in other regions of the body, AA is considered to be benign by medical professionals. The aetiology of the illness remains unknown; some speculate that it is caused by organ-specific immune system infection that is mediated by T cells directed at hair follicles. According to some studies, the disease may be caused by an inherited predisposition or natural circumstances. The disorder is characterised by scattered bald patches across the impacted region, which is often the scalp. If the disease is not controlled, the scalp patches may get larger. Males and females were equally afflicted; however, the illness was more prevalent in infants. When individuals get completely hairless scalps, this is a worsening condition for alopecia areata (alopecia totalis) [8,9].

During the anagen stage, the condition causes hair to be shed off, which is undesirable (anagen arrest). Anagen effluvium is a condition that, like chemotherapy-induced alopecia, may be brought on by certain medications or by chemotherapy itself.[10] The disorder findings in loss of anagen hair, which results in a very lengthy telogen phase that lasts for as long as the patient is receiving therapy for the 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 [11].

There are several types of hair loss, with AA being the most common. Computer-aided identification may help in baldness diagnosis and prognosis, hence the researchers tried to create a DL framework for SALT (Severity of Alopecia Tool). Similarity scores for the scalp and hair loss areas were 0.941 and 0.963, respectively [12]. Texture evaluation was used to distinguish between normal hair and bare scalp in a collection of four view-standardized images of paediatric alopecia areata. The Children's Hospital of Philadelphia Dermatology Hair Clinic collected 250 images from more than 100 kids between the ages of 2 and 21 over the course of a year to evaluate an automated technique for the SALT score [12,13].

2. Literature Review

A substantial number of studies have been carried out employing hair images to identify alopecia areata, according to the results of the literature research (hair disorder). Dermoscopy and scalp photographs have been utilised in previous studies to look at the human body. The bulk of research have taken scalp photos and derived AA-specific skin characteristics from them.

The computational study to identify key genes that were linked with AU or AT based on the whole-genome gene expression of 122 human scalp skin biopsy specimens acquired from the NCBI-GEO GSE68801 collection. Then, using eight different ML methods and important genes identified via bioinformatics analysis, they created a biomarker. Additionally, the Camp database discovered two molecular medicines, azacitidine & anisomycin. Researchers have created high-accuracy models for predicting the likelihood of patients with AA progressing to AT or AU. These models may be beneficial in designing customised treatment plans and clinical care for a wide range of patient populations [14-15].

A Bayesian data assimilation approach is applied, in which the data are included sequentially, to a model of the autoimmune condition alopecia areata, which is characterised by different geographical patterns of hair loss [16]. They demonstrate, using synthetic data in place of simulated clinical observations, that our strategy is generally resilient to variations in parameter estimates. Furthermore, they examine convergence rates for parameters with differing sensitivities, changing observational durations, and varying amounts of noise. According to our findings, this technique performs better when dealing with sparse data, sensitive parameters, or noisy observations. Taken together, we discover that their data assimilation, in combination with their biologically inspired model, gives recommendations for personalised diagnosis & therapy [17].

Acne is regarded to be a T-cell-mediated autoimmune illness that affects hair follicle that is highly heritable. By using allele-specific genome editing with the CRISPR/Cas9 technology, it was possible to construct engineered mice that express the AA risk allele revealed by haplotype sequencing for the MHC region [18]. Finally, functional evaluations were performed on both the mice as well as AA patients who had the risk allele as well as those who did not have the risk allele. The coiled-coil alpha-helical rod protein 1 (CCHCR1) gene was found to have a mutation (rs142986308, p. Arg587Trp) that was the sole non-synonymous variable in AA risk haplotype [19-20].

3. Proposed Methodology

In addition to great variability in hair loss at the time of first commencement of hair loss, AA is also distinguished by extreme variability in the length, amount, and pattern of hair loss within a single episode of the illness. Millions of individuals all over the globe are affected by the illness, which is particularly prevalent in families with alopecia areata. Because of the diverse and unexpected nature of spontaneous re-growth, as well as the absence of a consistent response to different medications, it has been challenging to develop and perform clinical studies in AA. There are two types of alopecia that affect both men and women in the same way. In both children and adults, it is a problem. The peak age of incidence is between 20 and 50 years old. Women's hair loss undergoes more periodic variations than men's hair loss. Women's hair volume decreases with age, and some individuals are born with thin and sparse hair; this is natural and does not need the use of specific products. Hair loss may be caused by no. of different circumstances. Variables such as illness, hormonal changes, medication usage, environmental factors, and genetics may all contribute to full hair loss. These situations need medical intervention or surgical intervention.

We utilised 200 photos of HHs from Figaro1k dataset & 68 pictures of AA from Dermnet dataset for this study. The Dermnet dataset [2] has a total of 68 hair photos of AA, which were retrieved. As trial photographs, we looked at skin ailments from different parts of the globe. Dermnet was the location where we took the photos. We took into consideration skin infection pictures that included the natural components. It has been shown that the precision of the suggested framework varies depending on the skin disease being studied. Alopecia areata is one of the twenty-three types of dermatological illnesses included by the Dermnet database. The following diseases are represented by disease images: seborrheic, 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

It was possible to obtain a total of 200 healthy hair pictures from the Figaro1k dataset [1] using this method. Figaro1k is a freely accessible dataset that contains photos of several types of hair, including straight, wavy, & curly hair types. The dataset has been subjected to a normalising method to verify that size & aspect ratio of each picture are similar across the board.

A collection of unconstrained view photos comprising varied hair textures is required to conduct hair analysis in wild. The scarcity of open and freely available databases prompted us to develop also make publicly available Figaro1k, an extension of Figaro, annotated novel multi-class image database for hair analysis in the wild that includes 150 images of each class (wavy, straight, kinky, curly, dreadlocks, short, & braids; each containing 150 images). Because the photos are of varying sizes and aspect ratios, a normalising technique has been implemented: the normalisation factor used is set in such a way that the maximum squared area inscribed in the hair region is reduced to 227×227 pixels, which is the smallest possible size.



Figure. 2 Sample images of damage and healthy hair

Figure 2. shows the sample images for health hair. Table 3.1 represents the data categories with their labeled. here, Alopecia Aretha is labeled as ‘0’ while Healthy Hairs is labelled as ‘1’

Table 1. Data labeling

Category	Label
Alopecia Aretha	0
Healthy Hairs	1

In this study, we offer a framework that includes practical application in accurately identifying AA and healthy hairs utilizing hair photos, as opposed to earlier work, which has been conducted only using scalp & skin images. Our idea is based on the practical use of ML and DL methods, which have shown promise in several fields of dermatology and also may play a main role in identifying AA to improve prediction and diagnosis. We suggest a categorization scheme for healthy hairs and AA, as well as a method for determining the severity of the condition. We used 200 healthy hair photos from the Figaro1k dataset as well as the 68 alopecia areata hair images from the Dermnet datasets which are publicly obtainable. Firstly, we processed our input images, and image pre-processing including histogram equalization (CLAHE). When it comes to CNNs, one of the most often utilized pre-processing approaches is data augmentation, which involves increasing the amount of the training dataset by performing several alterations to the original input data. DA is a technique for reproducing instances from a training set by incorporating different forms of transformations, such as translation, rotation, and various types of symmetries, among others. Noise & overfitting are reduced in sensitivity of the training as a result of such procedures. The CNN model (e.g. VGG16) is selected to build the model architecture. From each input sample picture, feature extraction was performed using the layered VGG-16 deep learning algorithm, which was applied to each output sample image. After then, the classification approaches, such as SVM, are utilized to train an ML model on the remaining pictures, which account for 70% of the total. Testing was carried out using the leftover picture collection that had been left over. The extraction of picture features is the first and most important stage in the process of image classification. Many different kinds of features may be used to achieve the goal of picture classification, including colour & shape characteristics, statistical features of pixels, and transform coefficient features. Aside from that, several researchers have employed algebraic features to aid in the identification and classification of images. In many cases, a vector or multi vectors are produced as the result of the feature extraction of an image. In this study, an image is retrieved & processed using the CNN-VGG-16 Model.

4. Proposed Algorithm

- Step 1. Collect the dataset of Dermnet as well as Figaro -1K.
- Step 2. Perform pre-processing using CLAHE.
- Step 3. Perform feature extraction using VGG 16 model.
- Step 4. Apply data augmentation to perform shift, shear, zoom, flip operations on image data.
- Step 5. Split dataset into training and test.
- Step 6. Perform classifications using the SVM algorithm.
- Step 7. Evaluate the obtained results in different performance metrics.
- Step 8. Generate confusion matrix using radial-based function

5. Results

In this study, experiments were conducted using Intel (R) Core(TM) i7-5820K processor running at 3.30GHz with 64 GB of RAM & 1 Titan X Pascal with 12 GB of RAM, as well as Keras or TensorFlow framework for Python. Python was used to implement the source code & pre-trained models’ technique. Jupyter platform was utilized for implementing the methodology in python. Importing all necessary libraries NumPy, pandas, matplotlib, os, sklearn, TensorFlow etc. Our research team utilised data from the Figaro1k dataset, which included 200 pictures of HHs, and data from the Dermnet dataset, which included 68 images of AA hairs. Because just a few of significant features from an entire picture are picked and the information received through feature selection is more succinct, this preprocessing phase allows for smaller data sizes. Traditionally, the rate of classification is calculated during the testing phase of the process. In both the testing (30 %) & training (70 %) phases, the same processes of feature extraction & classification are used.

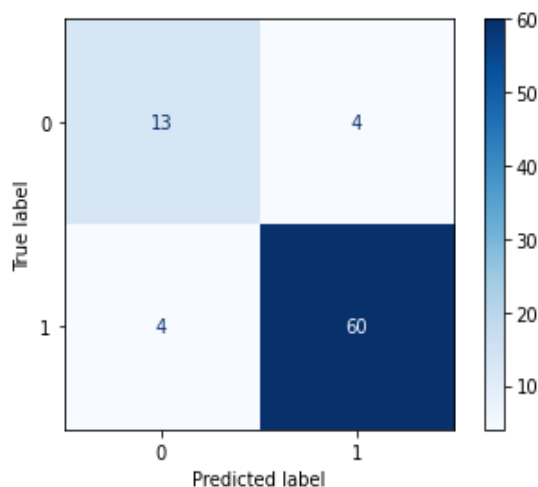


Figure 3. Confusion Matrix of baseline method (Edge-SVM)

A confusion matrix is a method of measuring the performance of DL classification. As an instance, consider a table that enables you to evaluate the performance of a classification model on a set of test data for which the true values have been established. Although the concept of a "confusion matrix" is straightforward, some of its language may be a bit difficult to grasp. The confusion matrices generated over the test data are shown in Figure 3 and 4 for baseline (Edge-SVM) and proposed method(VGG-SVM), respectively.

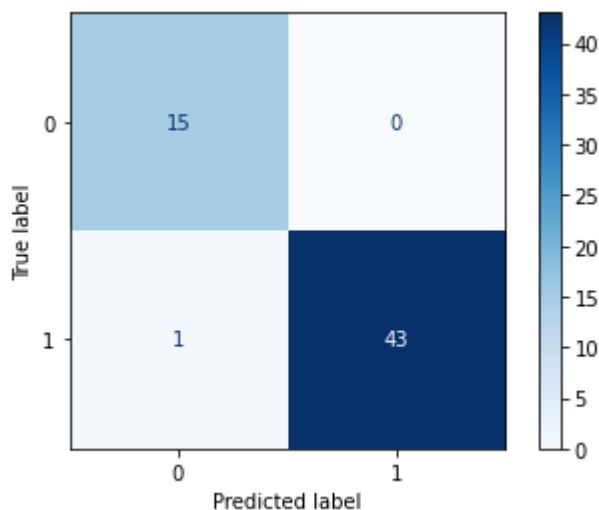


Figure 4. Confusion Matrix of proposed method (VGG-SVM)

	precision	recall	f1-score	support
0	0.76	0.76	0.76	17
1	0.94	0.94	0.94	64
accuracy			0.90	81
macro avg	0.85	0.85	0.85	81
weighted avg	0.90	0.90	0.90	81

Figure 5. Classification report of SVM classifier for baseline (Edge-SVM)

Figure 5 depicts the classification report of SVM classifier for baseline work. It shows the precision, recall, and f1-score having 76% value that are same for all three metrics to Alopecia Aretha images while 94% value for healthy hairs that are same for all three metrics.

	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 (VGG-SVM)

Figure 6 depicts the classification report of SVM classifier for proposed work. It shows the precision is 100%, recall is 94%, and f1-score having 97% value to Alopecia Aretha images while 98% precision, 100% recall & 99% f1-score value for healthy hairs for all respective three metrics.

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

Table 2 represents the final classification results that have utilized similar ML (Edge-SVM) methods but the proposed method (VGG-SVM) has shown higher accuracy, sensitivity and specificity.

6. Conclusions

Alopecia areata is a disease that affects millions of people worldwide. The body's autoimmune system starts attacking hair follicles, which stops them from operating correctly and prevents new hair growth from happening. This disorder leads to hair loss. Doctors frequently perform tracheoscopies and biopsies on patients to test out other options before deciding if AA is the cause or not. 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 an urgent need to find and test new approaches in order to better classify and diagnose alopecia areata. A variety of medical specialties have used advanced ML algorithms and their advanced variations to diagnose patients. In dermatology, many ML techniques have been applied to make precise diagnosis and prognoses. SVM has been used to develop a method for categorising photographs of healthy hair in the priceless work in order to distinguish between human hair images. Based on the look of healthy hair images in the dataset, the conditions were classified using SVM and KNN machine learning algorithms. As far as we are aware, none of the ML techniques have been combined. 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 initially applied the CLAHE data pre-processing approach. The healthy hair image dataset's features are extracted using VGG-19, and the classification of the hair image data is done using AA & SVM. Python has been used to simulate these two datasets of hair picture data, and experiments have been run with various performance measures. According to the results, the data analysis using SVM showed a 98.31% accuracy rate. In addition to accuracy, the proposed approach also possesses 100% sensitivity and 97.72% specificity, both of which are greater than the standard method. It has been called an intelligent HH picture analysis system that can identify between AA and HHs using hair photos, making it the first of its kind.

REFERENCES

1. T. Alkarakatly, S. Eidhah, M. Al-Sarawani, A. Al-Sobhi and M. Bilal, "Skin Lesions Identification Using Deep Convolutional Neural Network," 2019 International Conference on Advances in the Emerging Computing Technologies (AECT), 2020, pp. 1-5, doi: 10.1109/AECT47998.2020.9194205.
2. A. A. Adegun and S. Viriri, "FCN-Based DenseNet Framework for Automated Detection and Classification of Skin Lesions in Dermoscopy Images," in IEEE Access, vol. 8, pp. 150377-150396, 2020, doi: 10.1109/ACCESS.2020.3016651.
3. J. Kawahara and G. Hamarneh, "Fully Convolutional Neural Networks to Detect Clinical Dermoscopic Features," in IEEE Journal of Biomedical and Health Informatics, vol. 23, no. 2, pp. 578-585, March 2019, doi: 10.1109/JBHI.2018.2831680.
4. A. Kwasigroch, A. Mikołajczyk and M. Grochowski, "Deep neural networks approach to skin lesions classification — A comparative analysis," 2017 22nd International Conference on Methods and Models in Automation and Robotics (MMAR), 2017, pp. 1069-1074, doi: 10.1109/MMAR.2017.8046978.
5. T. Majtner, S. Yildirim-Yayilgan and J. Y. Hardeberg, "Combining deep learning and hand-crafted features for skin lesion classification," 2016 Sixth International Conference on Image Processing Theory, Tools and Applications (IPTA), 2016, pp. 1-6, doi: 10.1109/IPTA.2016.7821017.
6. LeCun Y, Haffner P, Bottou L, Bengio Y. Object recognition with gradient-based learning. In: Shape, Contour and Grouping in Computer Vision Lecture

Notes in Computer Science, vol 1681. Berlin; Heidelberg: Springer (1999). p. 319–45. doi: 10.1007/3-540-46805-6_19

7. Litjens G, Kooi T, Bejnordi BE, Setio AAA, Ciompi F, Ghafoorian M, et al. A survey on deep learning in medical image analysis. *Med Image Anal.* (2017) 42:60–88. doi: 10.1016/j.media.2017.07.005
8. Erickson BJ. Magician's corner: how to start learning about deep learning. *Radiol Artif Intell.* (2019) 1:e190072. doi: 10.1148/ryai.2019190072
9. Chollet F. *Deep Learning with Python*. Shelter Island: Manning Publications Company (2018).
10. Cullell-Dalmau M, Otero-Viñas M, Manzo C. Research techniques made simple: deep learning for the classification of dermatological images. *J Invest Dermatol.* (2020) 140:507–14.e1. doi: 10.1016/j.jid.2019.12.029
11. Perez F, Avila S, Valle E. Solo or ensemble? Choosing a CNN architecture for melanoma classification. In: *Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition Workshops*. Long Beach, CA (2019).
12. He K, Zhang X, Ren S, Sun J. Deep residual learning for image recognition. *Proc IEEE Comput Soc Conf Comput Vis Pattern Recognit.* (2016) 2016-Decem:770–8. doi: 10.1109/CVPR.2016.90
13. Gutman D, Codella NCF, Celebi E, Helba B, Marchetti M, Mishra N, et al. Skin lesion analysis toward melanoma detection. In: *A Challenge at the International Symposium on Biomedical Imaging (ISBI) 2016, hosted by the International Skin Imaging Collaboration (ISIC) (2016)*.
14. Marchetti MA, Codella NCF, Dusza SW, Gutman DA, Helba B, Kalloo A, et al. Results of the 2016 international skin imaging collaboration international symposium on biomedical imaging challenge: comparison of the accuracy of computer algorithms to dermatologists for the diagnosis of melanoma from dermoscopic images. *J Am Acad Dermatol.* (2018) 78:270–7.e1. doi: 10.1016/j.jaad.2017.08.016
15. Codella NCF, Gutman D, Celebi ME, Helba B, Marchetti MA, Dusza SW, et al. Skin lesion analysis toward melanoma detection: a challenge at the 2017 International symposium on biomedical imaging (ISBI), hosted by the international skin imaging collaboration (ISIC). In: *2017 IEEE 15th International Symposium on Biomedical Imaging (ISBI 2017)*. New York, NY: IEEE (2017). p. 168–72.
16. S Sayyad, F Sayyad, D Mithunchakravati “Deep Review On Alopecia Areata Diagnosis for Hair Loss Related Autoimmune Disorder Problem” *International Journal of Applied Pharmaceutics*, Volume 14, (2022) p.8-12. doi: 10.22159/ijap.2022.v14ti.19.
17. E. Bernardis and L. Castelo-Soccio, “Quantifying Alopecia Areata via Texture Analysis to Automate the SALT Score Computation,” *J. Investig. Dermatology Symp. Proc.*, 2018, doi: 10.1016/j.jisp.2017.10.010.
18. G. Fabbrocini, M. Cantelli, A. Masarà, M. C. Annunziata, C. Marasca, and S. Cacciapuoti, “Female pattern hair loss: A clinical, pathophysiologic, and therapeutic review,” *International Journal of Women’s Dermatology*. 2018, doi: 10.1016/j.ijwd.2018.05.001
19. Han SS, Kim MS, Lim W, Park GH, Park I, Chang SE. Classification of the clinical images for benign and malignant cutaneous tumors using a deep learning algorithm. *J Invest Dermatol.* (2018) 138:1529–38. doi: 10.1016/j.jid.2018.01.028
20. Codella N, Rotemberg V, Tschandl P, Celebi ME, Dusza S, Gutman D, et al. Skin lesion analysis toward melanoma detection 2018. In: *A Challenge Hosted by the International Skin Imaging Collaboration (ISIC)*. Washington, DC (2019).