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LesionFinder: Development of Pigmented Skin Lesions Segmentation System using thresholds and Morphological Operations

Ximena Morato, Jasenka Quiroz, Rosa Rivera, Alberto Pérez

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Abstract
The project aims to develop a mole and melanoma detection system using Matlab, evaluating segmentation techniques to identify skin lesions. The system focuses on simple and explainable techniques that require low computational resources, such as thresholding and morphological segmentation, to be useful both in clinical practice and in the education of biomedical engineering students. Computational algorithms and image processing techniques can detect abnormalities, including skin lesions. Research in computational methods to analyze skin abnormalities is growing, but current diagnostic accuracy remains insufficient. The methodology includes needs assessment, architecture design, software development, testing and validation. Images from the HAM10000 dataset were used for testing, and the system was validated using metrics such as sensitivity, specificity, and precision, comparing the results with the ImageJ software. The system showed high precision in detecting benign nevi but difficulties with melanomas, suggesting that morphological techniques are insufficient for clinical detection.

Keywords:
Segmentation, benign nevi, melanomas, image processing techniques.

1 Introduction
The skin, a protective organ, has three layers: epidermis, dermis, and hypodermis [1]. Melanocytes in the epidermis produce melanin, leading to moles. Moles, or nevi, are typically benign skin lesions formed by melanocyte accumulation due to sun exposure [2-5]. However, some moles, such as dysplastic nevi, can increase melanoma risk. Melanoma, originating from uncontrolled melanocyte growth, is the most dangerous skin cancer due to its rapid spread [5-8]. Early detection of skin lesions is critical for improving survival rates and patient quality of life by enabling timely and effective treatment interventions [9-12].

Imaging is a vital medical discipline that visualizes the body's interior to diagnose and treat diseases. Computational algorithms can analyze images to detect abnormalities, and image processing techniques can detect skin lesions. Image processing typically involves acquisition, preprocessing, segmentation, feature extraction, and classification [13-16].

The development of computational methods for analyzing skin abnormalities is advancing rapidly. While AI techniques like convolutional neural networks (CNNs) have shown promise in automatically classifying skin cancer, their diagnostic accuracy and ability to detect multiple lesion types remain limited, as noted by Haggenmüller et al. (2021) [17].

Image processing techniques assist dermatologists by providing detailed analyses of skin images, aiding in the early detection of lesions and distinguishing between benign and malignant cases. These methods are also crucial in teledermatology, allowing for remote evaluations using large datasets of clinical images [18]. However, tools like DiaMole, MoleScope, and Dermalogica face limitations such as slow detection times, high costs, and limited accessibility, especially in research environments [19-23]. Additionally, while platforms like Fiji (ImageJ) are useful for biological image analysis, they are not optimized for the specific requirements of 2D dermoscopic image analysis [24-28].

Morphological segmentation techniques are evaluated for their effectiveness in distinguishing benign nevi from melanomas. Also, there are publicly available datasets of skin lesions, such as the HAM10000 dataset, an extensive collection of 10,015 multisource dermoscopic images of common pigmented skin lesions, such as benign keratosis-like lesions and melanoma, developed to validate the detection system [29].

This project aims to develop a mole and melanoma detection system using MATLAB, focusing on the effectiveness of segmentation techniques for identifying skin lesions. The objectives include evaluating segmentation techniques, creating a detection system, identifying design criteria for future research, understanding image processing principles, and presenting the case as an educational tool for students.

The project's originality lies in its use of simple, explainable techniques that require low computational resources. Thresholding

Morato Galindo X. R., Quiroz Tapia Ja., Rivera Jiménez R. A.
Biomedical Engineering Department, La Salle University
Mexico City, Mexico.
Email: {xr.moratog, jasenka.quiroz, ra.riveraj}@lasallistas.org.mx

Pérez Sanpablo A.I.
Laboratory of Motion Analysis and Rehabilitation Engineering, National Institute of Rehabilitation
Mexico City, Mexico.
Email: albperezinr@gmail.com

and morphological segmentation techniques, which offer simplicity and computational efficiency, highlight technological innovation. The system aims to facilitate the evaluation of simple methods, such as thresholding and morphological operations to detect skin lesions transparently and explicable for both clinical practice and educational tools for biomedical engineering students. Consequently, the project provides an academic platform for biomedical engineering students to gain medical image processing and data analysis skills. Also, the findings can guide future research and further development of techniques.

2 Methodology

As mentioned, the project aimed to develop an accurate and efficient mole and melanoma detection called LESION FINDER. The methodology involved several key steps:

Needs Assessment and Definition of Requirements: The project identified functional and non-functional requirements, including accurately detecting pigmented lesions, an intuitive user interface, and a high-precision, transparent, and explicable system. The system processes dermoscopic images to identify pigmented skin lesions, with future expansion to other medical images. Specific functionalities include image segmentation using thresholding and morphological operations, quantitative lesion characteristics (size, asymmetry) analysis, saving analyzed images at all stages, and reporting. Finally, DICOM compatibility is also a requirement.

MATLAB was used to implement image processing algorithms, and AppDesigner was used to develop the graphical user interface.
Regarding the experts we consulted for this project, an advisor was sought for information in the field. The advisor in question is an expert in imaging techniques and physical rehabilitation

Architecture Design: It included preprocessing modules, such as a median filter for noise reduction, segmentation modules for border detection, and analysis modules, such as drawing bounding boxes around labeled regions. Display modules involved using axes for graphs and visualizations, tables for numerical data, and shows for processed images.

Software Development: A flow chart guided the development process, involving phases for image reading, processing, analysis, and visualization, see Figure 1. The HAM10000 dataset provided dermatoscopic images of benign nevi and melanomas. Algorithms included converting images to grayscale, thresholding to binary images, and applying morphological operations. Image quality improvement used median filters and morphological operations to reduce noise and improve segmentation.

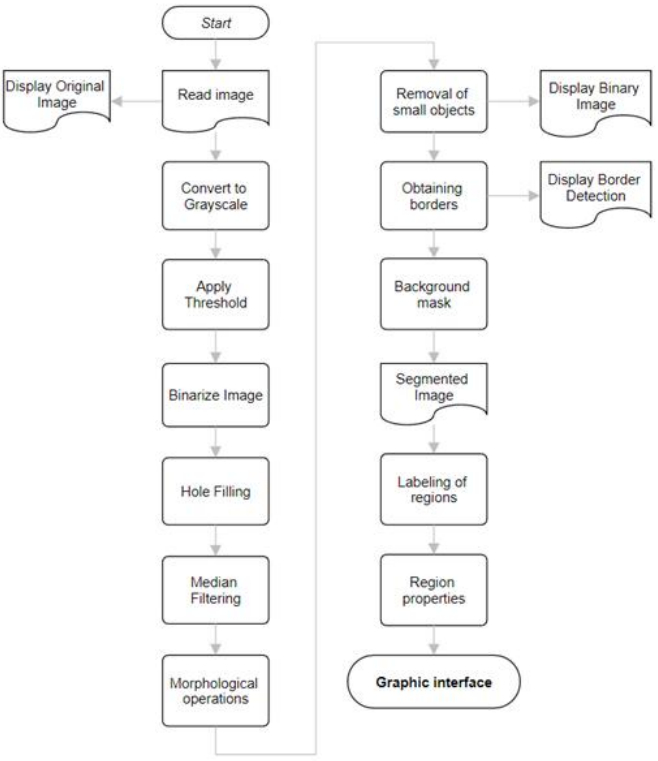

Figure 1. Algorithm's flow chart encompassing image reading, processing, analysis, and visualization phases.

Testing and Validation: A comprehensive validation and testing plan was implemented, including software setup, user manuals, and data preparation. The HAM10000 dataset was split into benign and malignant lesions. Individual modules involving grayscale conversion, filter application, segmentation accuracy, and edge detection were bench- tested. The complete system was tested for module integration and report generation. Quantitative metrics like sensitivity, specificity, accuracy, and Dice index were calculated using confusion matrices. The system was validated by evaluating and comparing its performance (sensitivity, specificity, accuracy, precision, Dice index) with ImageJ in identifying benign nevi and melanomas. For these comparisons, each pixel from the images was classified into two classes (lesion or background) using the results obtained using ImageJ as the true classes and the ones obtained by LESION FINDER as the predicted classes using the confusionmat MATLAB function. The confusion matrix was calculated to oversee the comparison of the images and evaluate the application's performance using ImageJ as a reference. It calculated the sensitivity, specificity, accuracy, and the Dice index=0.90. For validation the following cases were used:

- Case 1: Identification of a known benign nevi case alone
- Case 2: Identification of a known Melanoma case alone
- Case 3: Identification of benign nevi and melanoma in a sample of 50 images selected randomly from the HAM10000 database.
- Case 4: Pilot study with a user with expertise in medical image processing and teaching who interacted anonymously and independently with the system to identify 5 cases of nevi and melanomas and conducted qualitative validation of transparency, explainability, and usability (time and usage errors). This pilot study validated the system in a controlled environment with a limited dataset. Testing protocol and the application's user

manual were provided as additional material. This study involved installing the application, performing tests on subsets of images, recording processing times, and identifying transparency, explicability, and any performance errors to make further adjustments.

3 Results

The project successfully developed a graphical interface for a pigmented skin lesions detector using MATLAB's App Designer. The interface includes several functional buttons to select, process, and save images at all processing stages, see Figure 2.

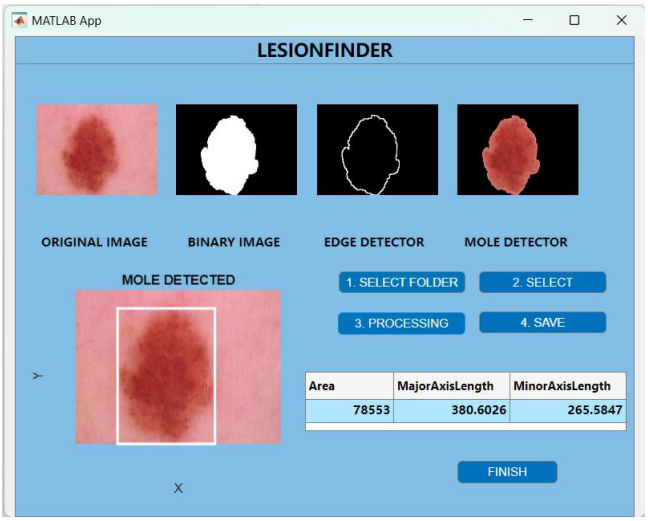

Figure 2. Graphical User Interface.

When pressing the button "Select Folder", a dialog box will open where you will select the folder of the images you want to process.

To choose an image to analyze, you must press the button "Select" which opens a dialog box for the user to select a folder in the computer between Melanomas or Melanocytic nevi. It gets a JPEG file list from which one can be selected. Once selected, the program is going to store and display it.

To begin the image processing, you must press the button "Processing", which is going to display at the top of the app the binary image, the edge detection and the segmented image.

To save the images, you must press the button "Save", which is going to ask you where to save them; it is going to save 4 files: the original, binary, border, and detection images.

To close the app, you must press the button "Finish" at the bottom of the app.

As mentioned in the methodology, confusionmat in MATLAB was used to calculate the confusion matrix to oversee the image comparison. In each case, sensitivity, specificity and dice index are calculated with the mentioned methodology.

The results of the validation for each case are as follows:

- Case 1: To validate the detection of a known benign nevi case alone, an image from the HAM10000 dataset was loaded and processed with the software, then the result was compared with a segmented image obtained with ImageJ, see Figure 3. The results of the evaluation metric are Sensitivity=1, Specificity=0.95, Dice Index=0.93.

Figure 3. Segmented image comparison. a) Original image, b) ImageJ segmented image, c) LESION FINDER segmented image.

- Case 2: To validate the detection of a known melanoma case alone, an image from the HAM10000 dataset was loaded and processed with the software, then the result was compared with a segmented image obtained with ImageJ, see Figure 4. The results of the evaluation metric are Sensitivity=1, Specificity=0.95, Dice Index=0.93.

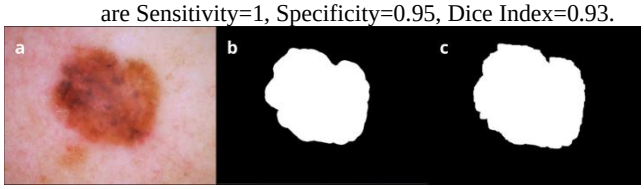

Figure 4. Segmented image comparison. a) Original image, b) ImageJ segmented image, c) LESION FINDER segmented image.

- Case 3: To make a comparison of segmetationn resulsts, 50 representative images from the HAM10000 dataset were selected, then this sample was loaded and processed with the software; then teh sample was loaded and processed with ImageJ. Finally, both results were compared obtaining the sensitivity=0.99, specificity=0.95, accuracy=0.96, and the Dice index=0.90.
- Case 4 Pilot study: To validate the system in a controlled environment, a user with medical/biomedical knowledge used the system without any prior training to evaluate its accuracy and performance through individual tests with 5 images from the benign nevus folder and 5 images from the melanoma folder. For each test, the user recorded the time it took to process the images and identified any incorrect lesion detection.

In the qualitative analysis, the user highlighted the system's transparency, explainability, usability (time = 0.74±0.35 seconds), and noted the errors observed during lesion detection, see Table 1.

Table 1. Case 4. Usability results (time and usage errors).

Benign nevus		
Test	Time (seconds)	Incorrect object of interest
Test 1	0.7865	No
Test 2	1.0367	No
Test 3	0.5672	No
Test 4	0.9815	No
Test 5	0.5296	No
Melanomas		
Test	Time (seconds)	Incorrect object of interest

Test 1	0.5763	Two areas instead of one. Heal as injury and injury too big
Test 2	0.3148	Four areas. Three healthy injuries, plus one injury with adequate size.
Test 3	0.6866	No
Test 4	1.5414	No
Test 5	0.4529	Six areas. Five are healthy as injury, plus an injury of adequate size.

The system accurately detected benign nevi with high detection accuracy, and well-defined lesion borders were obtained in the segmentation process. Quantitative metrics were perfect: Sensitivity = 1.0, Accuracy = 1.0, Dice Index = 1.0. Detection of melanoma posed challenges. The system's sensitivity was 1.0, but the accuracy was 0.36, and the Dice index was 0.53. Segmentation errors were noted (60% of cases), with false positives in three tests due to non-uniform skin color and lighting problems during image capture.

4 Discussion

The system demonstrated high precision and sensitivity in detecting benign nevi but struggled with melanoma identification. This issue isn't due to system programming errors, as comparisons with ImageJ, a robust analysis platform, yielded similar results with up to 0.96 precision. Therefore, relying solely on morphological segmentation for clinical melanoma detection is unfeasible.

Error analysis helped identify patterns and common causes, guiding specific segmentation algorithms and methodology adjustments.

Benign Nevus are well-defined, and confined to the epidermis or dermis, with slight variation in size and shape. They have a homogeneous distribution of melanin, resulting in uniform color and texture, facilitating easy identification and segmentation. Uniform pigmentation allows clear threshold differentiation from surrounding skin. Well- defined edges facilitate morphological techniques like erosion and dilation for refining segmentation. On the other hand, melanomas have disorganized, atypical melanocyte growth, invading both the epidermis and dermis, with significant size and shape variations. Melanin distribution is irregular, creating a mottled appearance and making accurate segmentation difficult with thresholding and morphological techniques. Heterogeneous pigmentation complicates thresholding, leading to incomplete or incorrect segmentations. Irregular borders hinder effective morphological methods, and lighting effects during image capture can introduce shadows and reflections, further complicating accurate segmentation. However, strategies can be implemented to mitigate these limitations and improve results. Combining morphological techniques with advanced preprocessing and feature detection methods can refine segmentation results. Using a more extensive and diverse dataset for training and validating the system with CNNs would include images with variability in lighting, contrast, and skin type.

5 Conclusion

Segmentation techniques using thresholds and morphological operations effectively detect benign nevi but struggle with melanomas, fulfilling the study's objectives. Grayscale and binary conversion simplify image processing, reducing computational complexity. Future improvements include integrating advanced techniques to increase accuracy and clinical application. Although this system has limitations for clinical use, it can be incorporated into biomedical engineering curricula to teach image processing and promote research.

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7 References

[1] Arenas R. La piel. Capítulo 1. Serrano H. Dermatología: Atlas, diagnóstico y tratamiento (Séptima Edición). México: Mc Graw Hill; 2019. Páginas 1-4.

[2] Actinic keratosis (A precancerous condition). Johns Hopkins Medicine. Homepage, https://www.hopkinsmedicine.org/health/conditions-and- diseases/actinic-keratosis, last accessed 2024/07/06.

[3] Keratosis pilaris - Symptoms and causes - Mayo Clinic. Homepage, https://www.mayoclinic.org/diseases-conditions/keratosis-pilaris/symptoms- causes/syc-20351149, last accessed 2024/02/17.

[4] Buendía A, Mazuecos J, Camacho F. Anatomía y fisiología de la piel. Conejo-Mir J, Camacho F. Manual de Dermatología (Segunda Edición). Páginas 2-27. Homepage, https://www.berri.es/pdf/MANUAL%20DE%20DERMATOLOGIA%E2%80%9A%202%20Vols.%20(Tapa%20Dura)/9788478856282

[5] Thawabteh, A. M., Jibreen, A., Karaman, D., Thawabteh, A., & Karaman, R. (2023). Skin Pigmentation Types, Causes and Treatment—A Review. Molecules/Molecules Online/Molecules Annual, 28(12), 4839. https://doi.org/10.3390/molecules28124839

[6] American Cancer Society. Cáncer de piel: Lunares comunes, nevos displásicos y el riesgo de melanoma Homepage, https://www.cancer.gov/espanol/tipos/piel/hoja-informativa-lunares, last accessed 2024/02/25.

[7] Aris M. Origen del melanocito normal y maligno. Acta bioquím. clín. Latinoam. 2009; volumen (43): n3. Homepage, http://www.scielo.org.ar/scielo.php?script=sci_arttext&pid=S0325- 29572009000300007, last accessed 2024/02/25.

[8] American Cancer Society. Todo sobre el cáncer: ¿Qué es el cáncer de piel tipo melanoma? Homepage, https://www.cancer.org/es/cancer/tipos/cancer-de-piel- tipo-melanoma/acerca/que-es-melanoma.html, last accessed 2024/02/25.

[9] American Cancer Society. Diccionario de cáncer del NCI: Niveles de Clark Homepage, https://www.cancer.gov/espanol/publicaciones/diccionarios/diccionario- cancer/def/niveles-de-clark, last accessed 2024/02/25.

[10] IDERMA, La importancia de la prevención Homepage,

https://www.iderma.es/es/blog.cfm/ID/14383/ESP/la-importancia-prevencion-y- deteccion-precoz-cancer-piel.htm, last accessed 2024/07/01.
[11] American Academy of Dermatology. Find skin cancer: how to perform a skin self- exam Homepage, https://www.aad.org/public/diseases/skin-cancer/find/check-skin, last accessed 2024/07/20.
[12] Skin Cancer Foundation. Early Detection: Overview Homepage, https://www.skincancer.org/early-detection/, last accessed 2024/07/20.
[13] Meyer-Baese A, Schmid V. Chapter 1 - Introduction. Pattern Recognition and Signal Analysis in Medical Imaging (Second Edition). Elsevier Inc. 2014, Pages 1- 20
[14] Instituto de Medicina. Dermatología: ¿QUÉ ES LA DERMATOSCOPIA DIGITAL? Homepage, https://www.egr.es/que-es-la-dermatoscopia-digital/, last accessed 2024/07/06.
[15] Nazari S, Garcia R. Automatic Skin Cancer Detection Using Clinical Images: A Comprehensive Review. Life (Basel). 2023 Oct 26;13(11):2123. doi: 10.3390/life13112123. PMID: 38004263; PMCID: PMC10672549.
[16] Martínez Martínez, Á. (2014). Clasificación de imágenes dermatoscopias [Trabajo de Fin de Grado, Universidad Politécnica de Madrid]. Archivo Digital UPM. https://oa.upm.es/33039/1/TFG_alvaro_martinez_martinez.pdf
[17] Haggenmüller S, et al. Skin cancer classification via convolutional neural networks: systematic review of studies involving human experts. Eur J Cancer. 2021 Oct; 156:202-216. doi: 10.1016/j.ejca.2021.06.049. Epub 2021 Sep 8. PMID: 34509059.
[18] Esteva, A., Kuprel, B., Novoa, R. A., Ko, J., Swetter, S. M., Blau, H. M., & Thrun, S. (2017). Dermatologist-level classification of skin cancer with deep neuralnetworks. Nature, 542(7639), 115–118. https://doi.org/10.1038/nature21056
[19] Liu S, Chen Z, Zhou H, He K, Duan M, Zheng Q, Xiong P, Huang L, Yu Q, Su G, Zhou F. DiaMole: Mole Detection and Segmentation Software for Mobile Phone Skin Images. J Healthc Eng. 2021 Jun 2;2021:6698176. doi: 10.1155/2021/6698176. PMID: 34188791; PMCID: PMC8195635.
[20] Dermalogica. Face mapping explained | Dermalogica®. Homepage, www.dermalogica.com/blogs/living-skin/face-mapping-skin-analysis, last accessed 2024/07/06.
[21] Olveres, J., et al. (2021). What is new in computer vision and artificial intelligence in medical image analysis applications. Archivo Digital UNAM. http://lapi.fi- p.unam.mx/wp-content/uploads/qims-11-08-3830What-is-new-in-cv-and-ai.pdf
[22] MoleScope Homepage, https://www.dermengine.com/es/molescope-ii, last accessed 2024/07/20.
[23] FotoFinder: Detección de cáncer de piel Homepage https://www.fotofinder.de/es/tecnologia/deteccion-del-cancer-de-piel, last accessed 2024/07/20.
[24] ITK-SNAP Homepage, http://www.itksnap.org/pmwiki/pmwiki.php, last accessed 2024/07/06.
[25] Schindelin, J., Arganda-Carreras, I., Frise, E. et al. Fiji: an open-source platform for biological-image analysis. Nat Methods 9, 676–682 (2012). https://doi.org/10.1038/nmeth.2019
[26] 3D Slicer image computing platform Homepage, https://www.slicer.org/, last accessed 2024/07/06.
[27] SkinVision Homepage, https://www.skinvision.com, last accessed 2024/07/20.
[28] OsiriX DICOM Homepage, https://www.osirix-viewer.com, last accessed 2024/07/20.
[29] Tschandl, P. et al. The HAM10000 dataset, a large collection of multi-source dermatoscopic images of common pigmented skin lesions. Sci. Data 5:180161 doi: 10.1038/ sdata.2018.161 (2018).