Principles of Biosignals and Biomedical Imaging - Bioengineering Department

MATLAB Project - Image Processing of Dermoscopic Images [EN]

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Abstract:
This project uses MATLAB to classify 10 skin lesion images as benign or malignant based on their standard deviation and circularity. In order to achieve accurate results, there's a combination image processing and cluster analysis with knowledge on skin cancer and diagnostic techniques, specifically identifying melanomas and distinguishing them from keratosis-like lesions. The project highlights the importance of computer-aided analysis in dermatology and shows the potential for using MATLAB as a tool for image analysis and classification.

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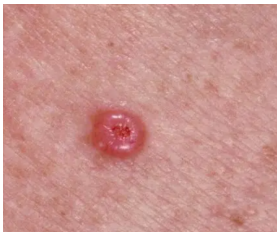
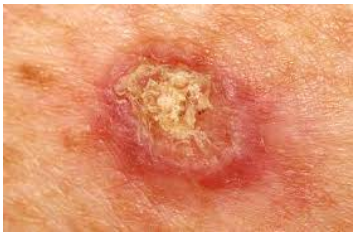
1 Background

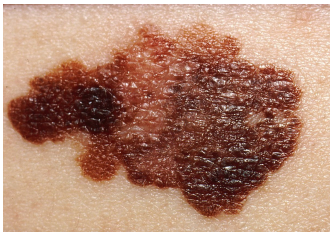
Skin cancer is one of the most common type of cancer in the world. It occurs when cells in the skin mutate and grow uncontrollably, forming a tumor [11]. These mutations are often caused by exposure to ultraviolet (UV) radiation from the sun or other sources, such as tanning beds. Other risk factors include having fair skin, a history of sunburns, a weakened immune system, and exposure to certain chemicals or radiation. There are several different types of skin cancer, including basal cell carcinoma, squamous cell carcinoma, and melanoma [5].



(a) Basal cell carcinoma [2]



(b) Squamous cell carcinoma [1]



(c) Melanoma [4]

Figure 1: Most common types of skin cancer.

Melanoma is the deadliest form of skin cancer, and it is responsible for the majority of skin cancer-related deaths. Unlike other types of skin cancer, which typically develop in sun-exposed areas of the body, melanoma can occur anywhere on the skin [9]. It can also develop in areas that are not exposed to the sun, such as the soles of the feet and the palms of the hands.

One of the challenges of identifying melanoma is distinguishing it from keratosis-like lesions, which are benign growths that can look very similar to melanomas [3]. The **ABCDE rule** is a commonly used method for identifying melanomas.

1.1 ABCDE rule

ABCDE stands for:

- **A**symmetry
- **B**order irregularity
- **C**olor variation
- **D**iameter greater than 6 millimeters
- **E**volution (changes in size, shape, or color over time) [6]

By using this rule, individuals can be more confident in identifying potentially dangerous skin growths and seek medical attention if necessary.

2 State-of-the-Art

Dermoscopy is a non-invasive diagnostic technique that involves the use of a handheld device called a dermatoscope to examine skin lesions for signs of melanoma. It works by illuminating the skin with polarized light and magnifying the area of interest. This allows doctors to see the structure of skin lesions and identify features associated with melanoma, such as irregular borders, uneven color distribution, and abnormal blood vessels.

To enhance the accuracy of dermoscopy, various computer-aided diagnosis (CAD) systems have been developed in recent years. These systems use machine learning algorithms to analyze dermoscopic images and provide diagnostic assistance to dermatologists.

CAD systems typically rely on deep learning models that are trained on large datasets of dermoscopic images with annotations provided by expert dermatologists. The models learn to identify features associated with melanoma and can make predictions about the likelihood of malignancy for a given lesion [8].

There are various techniques used in deep learning models for melanoma detection, including convolutional neural networks (CNNs), recurrent neural networks (RNNs), and hybrid models that combine both [7]. These models have shown promising results in clinical studies and are being integrated into commercial dermatoscopes to assist in the early detection of melanoma.

3 Problem formulation

We are given a dataset of 10 dermoscopic images. Each one is either a keratosis-like lesion (benign) or a melanomas (malignant), there being five of each category.

The ultimate goal here is to analyse each image and determinate its category. For this classification process, we'll have to do image processing as well as cluster analysis.

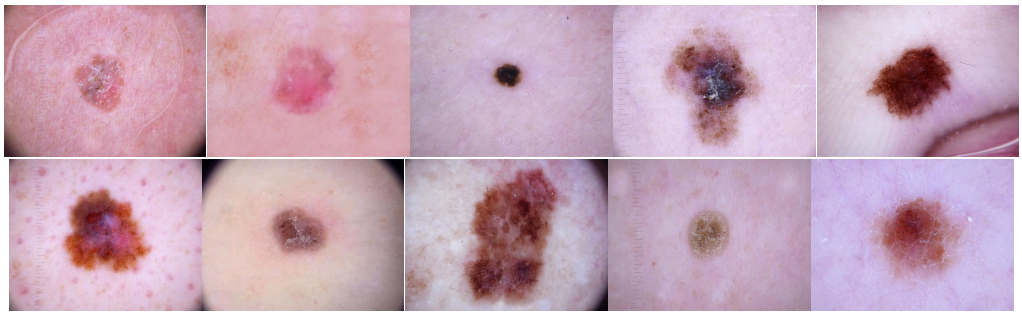


Figure 2: 10 dermoscopic images present in the *Data* folder

Up next, we present the results for each step of image processing.

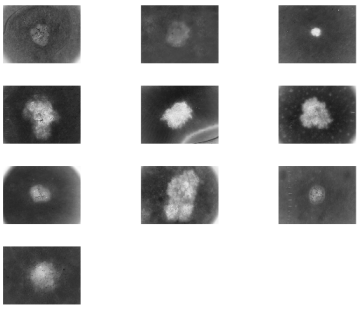


Figure 3: Dataset: Reversed Images

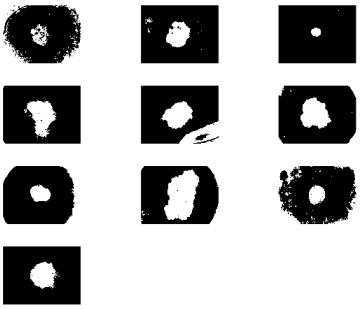


Figure 5: Thresholding: Thresholded Images

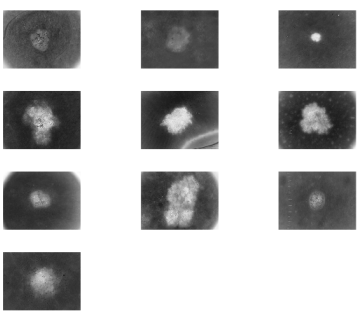


Figure 4: Denoising: Filtered Images

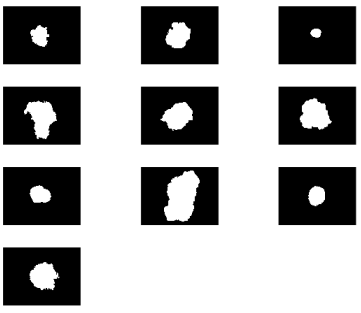


Figure 6: Morphological Operations: Masked Images

4 Methods and Algorithms

In this study, we implement a classic image processing pipeline to classify dermoscopy images into two classes: benign (keratosis-like lesions) and malignant (melanomas). The pipeline consists of the following steps:

4.1 Dataset

We use MATLAB's `imageDatastore` and `readall` functions to import all the .jpg images from our working directory. We then convert the images to grayscale and invert them.

```
% Define the folder path where the images are stored
folderPath = 'Data';

% Create an imageDatastore object to read all the .jpg images from the folder
imds = imageDatastore(folderPath, 'FileExtensions', '.jpg');

% Read all the images and convert them to grayscale and invert them
imds = readall(imds);
imds = cellfun(@(x) imcomplement(rgb2gray(x)), imds, 'UniformOutput', false);

% 'UniformOutput' is set to false to tell cellfun every output of the cell
% may not be uniform in size or shape (can have different data types)

% Display all inverted images in grayscale
figure;
for i = 1:numel(imds)
    subplot(4, 3, i);
    imshow(imds{i});
end
```

4.2 Denoising

We use a Gaussian filter to remove noise from the images.

```
% Define the standard deviation and filter size of the Gaussian filter
sigma = 1;
filterSize = 5;

% Apply a Gaussian filter to each image in the cell array
imds_filtered = cellfun(@(x) imgaussfilt(x, sigma, 'FilterSize', filterSize), imds, 'UniformOutput', false);

% Display all the denoised images in a loop
figure;
for i = 1:numel(imds_filtered)
    subplot(4, 3, i);
    imshow(imds{i});
end
```

4.3 Thresholding

We use Otsu's method to obtain binary masks that separate the background (skin, black) from the foreground (lesion, white).

```
% Apply Otsu's method to each image to obtain threshold values
thresholds = cellfun(@(x) graythresh(x), imds_filtered);

% Apply the obtained threshold values to each image to obtain binary masks
imds_binary = cellfun(@(x, t) imbinarize(x, t), imds_filtered, num2cell(thresholds), 'UniformOutput', false);

%imshow(imds_binary{1})
% Display all the denoised images
figure;
for i = 1:numel(imds_binary)
    subplot(4, 3, i);
    imshow(imds_binary{i});
end
```

4.4 Morphological Operations

We clean the pre-processed masks by performing binary dilation, border clearing, small object removal and hole-filling within the lesion masks if needed.

```
% Apply morphological operations to each binary mask
% disk-shaped structuring element with radius 3
se = strel('disk', 3);
for i = 1:numel(imds_binary)
    % Perform binary dilation
    imds_binary{i} = imdilate(imds_binary{i}, se);
```

```
52
53      % Perform border clearing
54      imds_binary{i} = imclearborder(
            imds_binary{i});
55
56      % Perform small object removal (<100
            pixels)
57      imds_binary{i} = bwareaopen(imds_binary{
            i}, 100);
58
59      % Perform hole-filling
60      imds_binary{i} = imfill(imds_binary{i},
            'holes');
61
62      % Keep only largest connected component
63      imds_binary{i} = bwareafilt(imds_binary{
            i}, 1);
64  end
65
66  % Show the cleaned and refined binary masks
67  figure;
68  for i = 1:numel(imds_binary)
69      subplot(4, 3, i);
70      imshow(imds_binary{i});
71  end
```

4.5 Feature Extraction

We multiply the grayscaled and inverted images with the final binary masks obtained from the previous step. We then compute the standard deviation of the intensity distribution of each lesion and use `regionprops` to obtain the circularity of each mask.

```
72  % Loop through each image
73  for i = 1:numel(imds)
74
75      % Multiply with binary mask
76      imds_masked = double(cell2mat(imds(i)))
            .* double(cell2mat(imds_binary(i)));
77
78      % Compute standard deviation of
            intensity distribution
79      std_intensity(i) = std(double(
            imds_masked(:)));
80
81      % Use regionprops to obtain circularity
            of mask
82      stats = regionprops('table', imds_binary
            {i}, 'Circularity');
83      circularity(i) = stats.Circularity;
84  end
85
86  % Concatenate the features into a matrix and
        display it
87  features = [std_intensity', circularity']
```

4.5.1 Output:

Image	Std dev	Circularity
"image0.jpg"	24.9175	0.4417
"image1.jpg"	32.7166	0.6175
"image2.jpg"	25.5942	0.9227
"image3.jpg"	55.5259	0.3276
"image4.jpg"	64.3821	0.6384
"image5.jpg"	56.5298	0.6349
"image6.jpg"	32.6795	0.7812
"image7.jpg"	75.1156	0.5627
"image8.jpg"	27.2339	0.8406
"image9.jpg"	47.7586	0.3981

(See note[1]).

4.6 Data Visualization and Analysis

We perform k-means clustering to automatically separate the two classes (benign / malignant lesions). We use `scatter` to plot both features simultaneously in the 2D feature plane along with the corresponding estimated class label.

```
88  % Set the number of clusters (2 for benign/
        malignant)
89  k = 2;
90
91  % Perform k-means clustering on the features
92  [idx, centroids] = kmeans(features, k);
93
94  % Plot the results
95  figure;
96  scatter(features(idx==1,1), features(idx
        ==1,2), 40, 'filled', 'DisplayName','
        Benign','MarkerFaceColor','#77AC30');
97  hold on;
98  scatter(features(idx==2,1), features(idx
        ==2,2), 40, 'filled', 'DisplayName','
        Malignant','MarkerFaceColor','r');
99  scatter(centroids(:,1), centroids(:,2), 150,
        'x', 'Linewidth', 4, 'DisplayName','
        Centroids');
100 legend();
101 title('Malignant vs. Benign Lesions')
102 xlabel('Standard Deviation');
103 ylabel('Circularity');
```

[1] This isn't exactly the output, but to have a more explicit result the data is presented as shown in the table.

5 Validation and Testing

In this first part, before coming to conclusions, we apply the methods previously described to a validation dataset. We selected two images from reliable sources that were certain to be either melanomas or keratosis-like lesions, and identified as such. From here, we looked at the k-means clustering results and plot in order to verify the validity of the given approach.

These 2 selected images corresponded to different clusters indeed. The benign known lesion (Fig. 8) is associated with Cluster 1 (left) and the selected malignant lesion (F. 9) is part of Cluster 2 (right). From here, we could assume that Cluster 1 corresponds to benign lesions and Cluster 2 to malignant ones. The parameters chosen for image processing were the following:

- Denoising - Gaussian filter sigma: 1
- Denoising - Gaussian filter filterSize: 5
- Morphological Operations - disk-shaped element radius: 3
- Morphological Operations - maximum number of pixels for object removal: 100

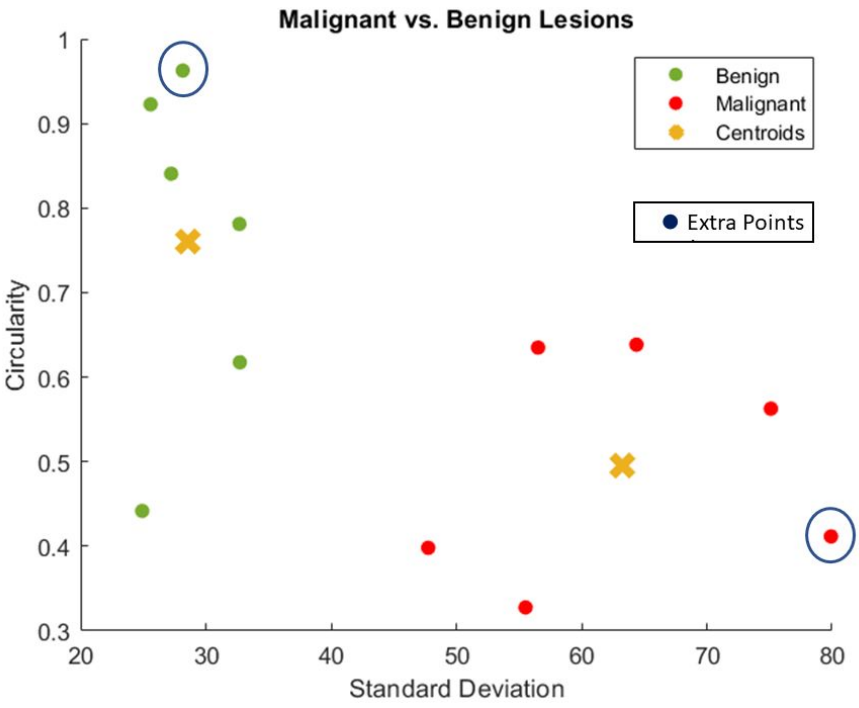


Figure 7: Plot using given dataset plus 2 selected images

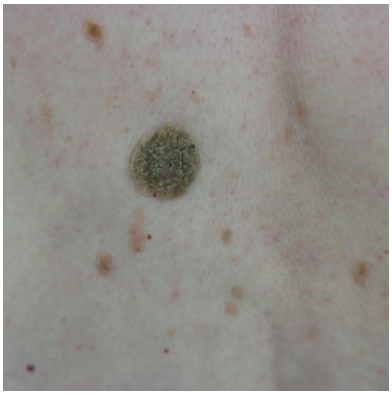


Figure 8: Benign-known

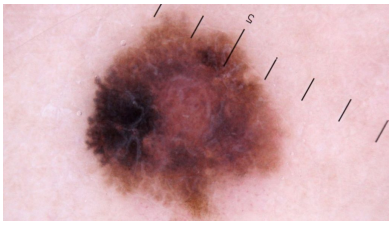


Figure 9: Malignant-known

Based on the results of k-means clustering, the two clusters correspond to benign and malignant lesions. The cluster with a lower standard deviation and higher circularity values (Cluster 1 on the left) is most likely to correspond to benign lesions (keratosis-like lesions) while the cluster with a higher standard deviation and lower circularity values (Cluster 2 on the right) is most likely to correspond to malignant lesions (melanomas). This assumption is not only based on the association with the Benign-know and Malignant-know images and its clusters. This conclusion is based on the following observations:

- Circular lesions, which tend to have higher circularity values, are more likely to be benign (keratosis-like lesions).
- Lesions with a larger spread of color values, which tend to have higher standard deviation values, are more likely to be malignant (melanomas).
- The ABCDE rule 1.1 suggests that malignant lesions tend to have asymmetry, irregular borders, uneven color, larger diameter, and evolving features [10]. Cluster 2, which has lower circularity and higher standard deviation values, is more likely to correspond to malignant lesions based on these criteria.

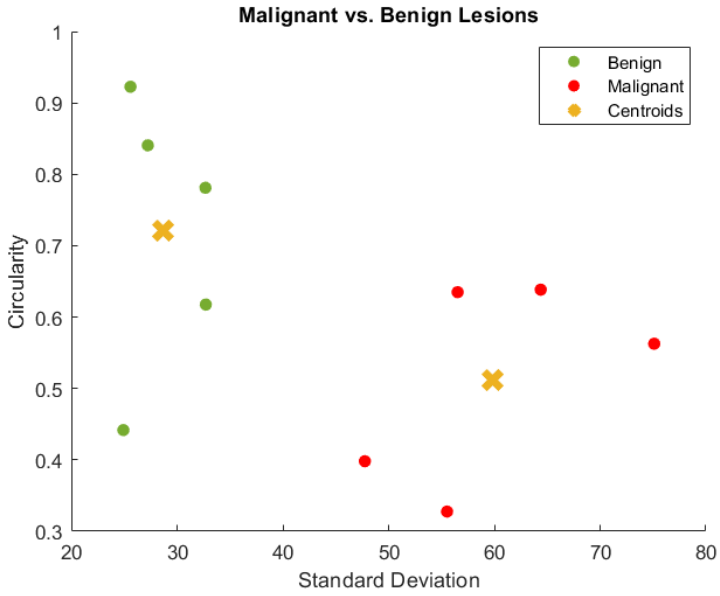
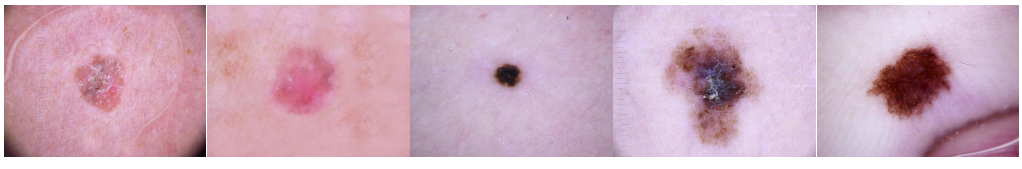
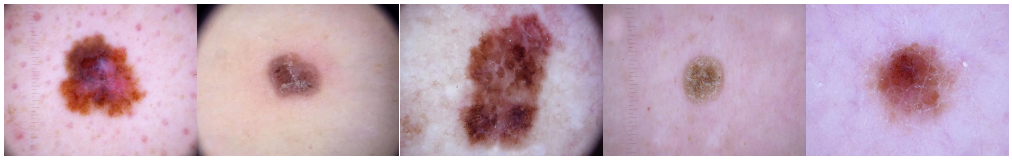


Figure 10: Final plot and results for the 10 dermoscopic images present in the *Data* folder

Together with the table obtained from step 4.5.1, we can finally classify the images with a high degree of confidence, looking at graph 5, as **"benign"** or **"malignant"**:



(a) Benign **(b)** Benign **(c)** Benign **(d)** Malignant **(e)** Malignant



(f) Malignant **(g)** Benign **(h)** Malignant **(i)** Benign **(j)** Malignant

Figure 11: Classification of images in "benign" or "malignant".

6 Conclusions

To sum up, we have used MATLAB to analyze a set of skin lesion images to classify them as benign or malignant based on their standard deviation and circularity. We first plotted the data points on a scatter plot and identified two distinct clusters, which we further analyzed using the ABCDE rule. Our analysis indicates that benign lesions tend to have a lower standard deviation and higher circularity, while malignant ones tend to have opposite features.

This project demonstrates the potential of using MATLAB for image analysis and classification tasks. By leveraging the power of MATLAB's built-in functions, we were able to quickly and accurately analyze a large dataset of skin lesion images and make meaningful classifications.

It is important to note that our analysis was based solely on two features and further research could be done to incorporate other features that may increase the accuracy of the classification. Future work may also include applying more advanced machine learning techniques such as the ones referred in section 2 to improve the accuracy of classification.

References

[1] [Accessed: 13-Apr-2023]. 2020. URL: ballaratskincancer.com.au/squamous-cell-carcinoma-scc/.

[2] [Accessed: 11-Apr-2023]. 2022. URL: skinsight.com/skin-conditions/basal-cell-carcinoma-bcc/.

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