POLITECNICO DI TORINO



ICT For Smart Societies

ICT for Health (Lab 2) Prof. Monica Visintin

MOLES

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Chapter 1

Purpose of the laboratory

1.1 Introduction and Data-Set

The main purpose of this laboratory is to write an algorithm that helps doctors in the analysis of moles' photos. Five features have to be taken into account in order to state whether a mole is a melanoma or not:

A) Asymmetry; B) Border; C) Color; D) Diameter; E) Evolution.

The aim of our algorithm is an accurate reproduction of the mole's border by considering three categories of moles: **Low Risk Moles**, **Medium Risk Moles** and **Melanomas**. Initially, the photos will be converted into images made of three or more color clusters by using K-means in scikit-learn (quantization of the image with different levels of color). Once the image is converted into a binary representation, we will cancel the noise, fill the holes in the mole and smooth-out the resulting shape of which we intend to calculate the perimeter. The initial image conversion is shown below in figure [1.1].

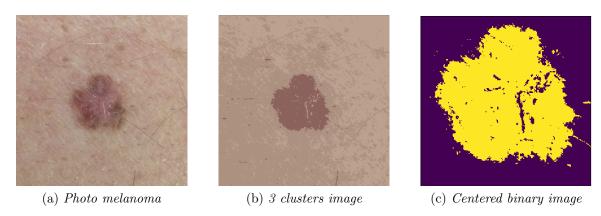


Figure 1.1: Conversion of a photo into a binary image with a final centralization

Chapter 2

Description of the algorithm

2.1 Image finishing

First of all, the algorithm eliminates the noise from the binary image: the noise consists in a number of scattered pixels that are not useful to outline the shape of the mole. The binary image used is a matrix called subset (see figure [2.1]) made of 0's [purple] and 1's [yellow]. We cancel the noise by analyzing, pixel by pixel, which value is more likely to recur, according to the nearest pixels. The key elements of this process are an initialized counter (cnt = 9) and the 8 nearest pixels that surround the pixel that is being analyzed. Every time a pixel near the one we are focusing on is different, the counter is decreased by one and if it goes down to 3, the pixel color is inverted (the number 3 is considered to be the threshold). Below in figure [2.2] we can see the "before and after" the cleaning process; we still need to eliminate the holes and "islands" that surround the main element of the image. To do so, we will use an approach similar to the one we have just illustrated, as we will see in section [2.2]

```
cnt = 9

if subset[i][j+1] != subset[i][j]:
    cnt -= 1

if subset[i+1][j] != subset[i][j]:
    cnt -= 1

if subset[i+1][j-1] != subset[i][j]:
    cnt -= 1

if subset[i+1][j+1] != subset[i][j]:
    cnt -= 1

if subset[i-1][j] != subset[i][j]:
    cnt -= 1

if subset[i-1][j-1] != subset[i][j]:
    cnt -= 1

if subset[i][j-1] != subset[i][j]:
    cnt -= 1

if subset[i][j-1] != subset[i][j]:
    cnt -= 1

if cnt <= 3:

    if subset[i][j] = 0:
        subset[i][j] = 1

    else:
        subset[i][j] = 0</pre>
```

Figure 2.1: Core of the cleaning algorithm



(a) Binary image



(b) Noiseless version

Figure 2.2: Cleaning of the image's noise

2.2 Filling holes and eliminating the "islands"

The algorithm is based on the same principle of the one in section [2.1], however we will examine the matrix in a different way and we will refer to a lower threshold in the counter for the conversion of a pixel's color. We will start by examining each quarter of the image, from the centre to the opposite angle (islands elimination) and vice-versa (holes filling) (see figure [2.3a]). For the islands elimination we start exploring from out of the mole's shape taking for granted that portions of yellow pixels, found during the process, have to be considered "islands" and so, in need for a conversion. The same idea comes handy for filling the holes but this time we start examining the image from the centre, taking for granted that portions of purple pixels need to be converted. The conversion is always made by counting what is the color majority around the pixel in analysis but this time we set less "hard" conditions by initializing the counter equal to 8 and the threshold equal to 4, doing so we are able to convert bigger areas.

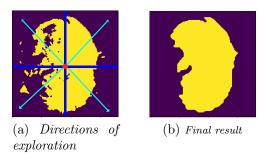


Figure 2.3: Image result

2.3 Finding the image perimeter

For the perimeter we have used a very simple approach. With the aid of a structuring element such as the one in figure [2.4], we will check each 3×3 section of the subset[i][j] and verify if the central pixel, the circled one in figure [2.4], is surrounded by 4 other ones; if so, the central one (yellow), becomes a 0 (purple). The calculation of the perimeter and of the area of the mole is made by simply counting the ones in the binary image. The perimeter of the equivalent circle, with the same area, is given by the formula [2.1].

Figure 2.4: Structuring element

$$Perimeter_{circle} = 2\sqrt{\pi \cdot Area_{mole}}$$
 (2.1)

The final process consists in determining the ratio between the perimeter of the mole and the perimeter of the circle with the same area of the binary image.

2.4 Result examples

The figures below ([2.5], [2.6] and [2.7]) are an example of each mole category. The video shows an animation of the proposed algorithm: <u>YouTube</u>

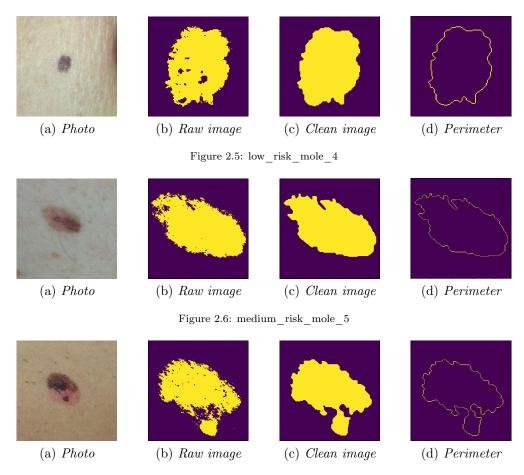


Figure 2.7: melanoma 17

2.5 Data Results and comments

The ratios obtained are shown in table [2.1]. An analysis of the results clearly reveals that the border alone is not sufficient to categorize the moles, as some numbers overlap between categories. However, there could be a correlation between the border's indentation and the presence of skin cancer, as ratios are generally higher in case of melanomas than in case of low and medium risk moles. The mole low_risk_4 (figure [2.5]), with a ratio of 1.043 (very close to the average ratio of medium risk moles in table [2.2]), could in all likelihood belong to the medium risk category; therefore it is evident that the border was not the only criterion used to categorize it. The same could

be said for the mole $medium_risk_5$ (figure [2.6]), whose ratio is 1.266, higher than the mean value of the melanomas (see table [2.2]). Figure [2.7] shows $melanoma_17$ (figure [2.7]), whose border is rather irregular, consistently with its ratio of 1.509. Finally, we can state that the evaluation of a mole's perimeter and the computation of its ratio with a circumference of the same area is a useful instrument when combined with the other four criteria of the "ABCDE" method and, of course, with a medical examination.

Image	Mole	Circle	Ratio
low_risk_1	326	326.68	0.997
low_risk_2	327	360.34	0.935
low risk 3	281	254.19	1.105
low_risk_4	273	261.53	1.043
low_risk_5	252	246.87	1.020
low_risk_6	278	287.74	0.966
low_risk_7	215	195.09	1.102
low_risk_8	324	301.27	1.075
low_risk_9	184	203.29	0.905
low_risk_10	129	138.65	0.930
low_risk_11	192	202.83	0.946
medium_risk_1	117	128.84	0.908
medium_risk_2	323	333.57	0.968
medium_risk_3	160	169.30	0.945
medium_risk_4	183	185.18	0.988
medium_risk_5	651	513.98	1.266
$medium_risk_6$	357	315.11	1.132
medium_risk_7	671	636.05	1.054
medium_risk_8	429	419.49	1.022
medium_risk_9	295	235.72	1.251
medium_risk_10	421	388.51	1.083
medium_risk_11	608	591.37	1.028
medium_risk_12	405	432.27	0.936
medium_risk_13	293	291.26	1.005
medium_risk_14	336	349.65	0.960
medium_risk_15	325	320.75	1.013
medium_risk_16	471	483.03	0.975

Image	Mole	Circle	Ratio
melanoma_1	396	392.07	1.010
$melanoma_2$	335	312.97	1.070
$melanoma_3$	460	353.35	1.301
$melanoma_4$	472	400.43	1.178
melanoma 5	472	356.15	1.325
melanoma 6	982	773.31	1.269
melanoma 7	726	697.93	1.040
melanoma_8	523	429.46	1.217
$melanoma_9$	728	570.98	1.274
melanoma_10	619	573.45	1.079
melanoma 11	500	446.40	1.120
melanoma 12	582	584.82	1.195
melanoma_13	559	471.53	1.185
melanoma 14	438	421.08	1.040
melanoma_15	573	485.92	1.179
melanoma_16	450	388.21	1.159
$melanoma_17$	663	439.23	1.509
melanoma_18	700	723.07	1.368
melanoma_19	565	534.37	1.057
melanoma_20	730	652.42	1.118
$melanoma_21$	475	373.88	1.270
melanoma 22	461	460.42	1.001
melanoma 23	1542	654.30	2.356
melanoma 24	797	659.74	1.208
melanoma_25	293	295.27	1.292
melanoma_26	498	444.72	1.119
melanoma 27	306	237.77	1.286

Table 2.1: Tables with the perimeter of the mole, of the equivalent circle and the ratio of the perimeters

Image	Average of the ratios	Standard deviation of the ratios
Low Risk	1,002181	0,0717
Medium Risk	1,033375	0,1044
Melanoma	1,197248	0,2646
All categories	1,108957	0,2155

Table 2.2: Average and Standard Deviation for each category of moles