POLITECNICO DI TORINO

ICT for Health

Report Laboratory 2

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1 Introduction

Melanoma is the most dangerous type of skin cancer that develops from the pigment-containing cells known as melanocytes. Melanomas typically occur in the skin, but may rarely occur in the mouth, intestines or eye. Sometimes they develop from a mole with changes such as an increase in size, irregular edges, change in color, itchiness or skin breakdown.

ICT can be extremely useful in mole diagnosis. Having a software able to detect abnormalities saves time for the doctor and the patients. In fact, patients would not need to go to the hospitals for analysis, because they could send to the doctor a simple photo of the mole, and doctors can rely on machines doing basics analysis. It is important to say however, that machines cannot replace the doctor, that is fundamental in supervising the software results.

In the diagnosis of melanoma, five features are considered: A asymmetry; B border; C color; D diameter; E evolution. Forming the abbreviation ABCDE , easy to remember.

2 ICT in mole diagnosis

The scope of this lab is to analyze borders of a set of moles and melanomas starting from the its photography. The work outline includes the following steps idea is to: highlight the darkest part of the image, corresponding to the mole; find the contour of this darkest part; evaluate the length of the found contour (perimeter of the mole) and evaluate the ratio between the perimeter of the mole and the perimeter of the corresponding circle with the same area. In fact, this last calculation gives us an approximative information about the analyze mole: the lower the ratio (more regular mole's shape) if the ratio is very low, this means that the mole shouldn't be a melanoma, otherwise it should be.

2.1 The data set

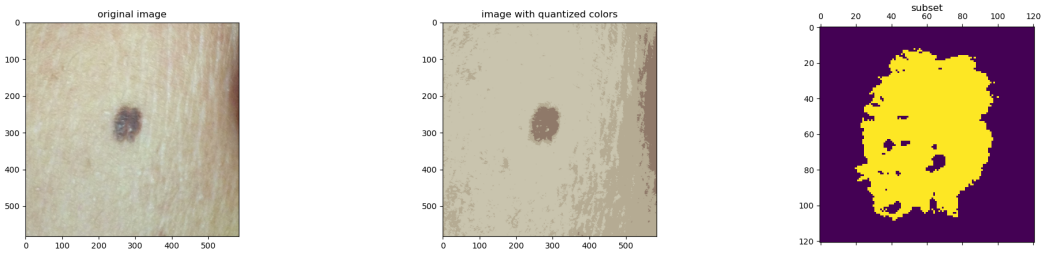
The software implemented in this place focuses on moles' border calculation. In particular, the irregularity of the mole border can be sign of abnormalities of that mole. The more the border is irregular, the higher the risk of melanoma.

The dataset is composed by 58 images of moles with different melanoma gravity risk level: low level, medium level and melanoma. For each of those, the border of the mole is isolated and compared to the perimeter of a circle with the same area, to check irregularity.

2.2 Algorithm

2.2.1 Preprocessing

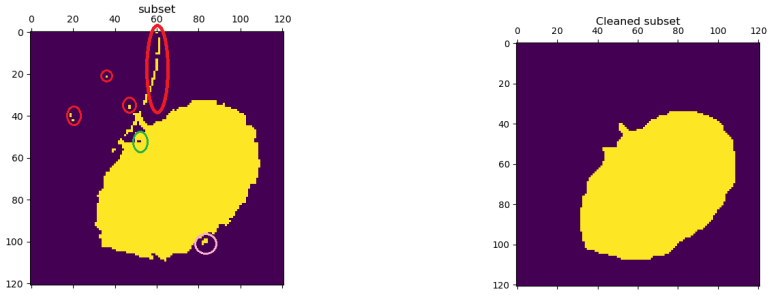
First of all each photo is converted into quantized images(figure 1b) by using K-means in scikit-learn tool in python. The level of quantization depends on the image itself. Once done, the image is converted in binary representation: 1 indicates the mole (yellow pixels) and 0 represents the skin (violet pixels) (figure 1c).



(a) (b) (c)

Figure 1: moles

The problem is that the image is not always 'clean': the mole sometimes contains violet pixels (caused by reflected light) and the skin sometimes contains yellow pixels (cause by some darker zones). Hence, data cleaning is required.
The data cleaning process is made by analyzing pixel by pixel. It is divided in three parts: **noise removal**, **island correction** and **hole filling**. The **noise** consists in a number of scattered pixels that are not useful to outline the shape of the mole; the **the islands** are errors related to dark skin detected as mole; the **the holes** are errors related to light reflected on the mole (image 2a reports the three kind of errors).



(a) (b)

Figure 2: 2aExample of dirty image. The red circle highlights scattered pixels (noise); the green circle highlights hole error and pink circle highlights island error. The figure refers to the image: $'low_risk'_3$. Example of cleaned image (2b). The image refers to the image 2b

Part I: noise removal.
For each pixel the nearest neighbors are considered:

- for the 4 corners' pixels: if the pixel in question has value 1 and at least two of its tree neighbors are 0 also the pixel in question should be 0, so it is modified from 1 to 0 (and vice versa).
- for the frame pixels: if the pixel in question has value 1 and at least four of its five neighbors are 0 also the pixel in question should be 0, so it is modified from 1 to 0 (and vice versa).
- for the internal pixels: if the pixel in question has value 1 and at least six of its eight neighbors are 0 also the pixel in question should be 0, so it is modified from 1 to 0 (and vice versa).

Part II and III : island correction and hole filling.
This part is carried out exactly like the first one, but the threshold in the number of neighbors to consider is lower. This makes sense because the scattered yellow

pixels are completely surrounded by violet pixels, hence the number of neighbor with opposite value is higher.

In the end, the cleaned image shows up as reported in the image 2b

2.2.2 Perimeter calculation

Having at this point the cleaned image, it was possible to proceed with the perimeter calculation. The used approach is a basic one: for each pixel, again the neighbors are considered; if the pixel in yellow (value 1) and all the 4 neighbors are also yellow, it is considered as an internal pixel (internal to the mole), and, in another matrix, at the same position of the pixel in question, value 0 is assigned. Instead, if the yellow pixel has at least one violet neighbor this means that that pixel is a perimeter pixel and nothing happens. In the end, the image that is obtained shows up as in figure 3 where the inner part of the mole is completely removed and only the perimeter stands.

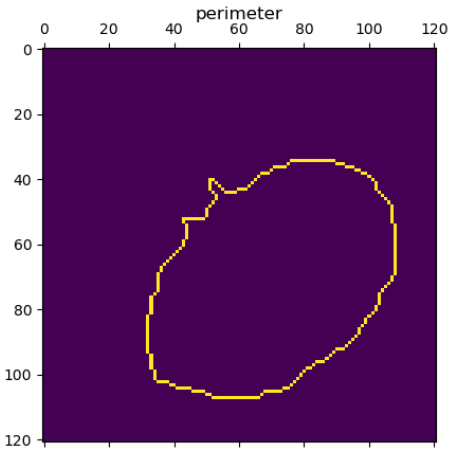


Figure 3: Final image highlighting the perimeter.

2.3 Results

All the moles' photos have been processed in this way. In the end, the perimeter of the mole is compared with the perimeter of the circle with the same area, as already mentioned in previous section. All the ratio are reported in the table below (1).

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 1: Tables reporting the perimeter of the mole, the perimeter of the circle with the same area and the ration between the two.

The mean values are reported in the table below (**??**):

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: Average and Standard Deviation for each category of moles

For a more intuitive result the histogram below (4) shows that, the low risk moles have ratio lover than, while the medium risk moles and melanoma ones have higher ratio value.

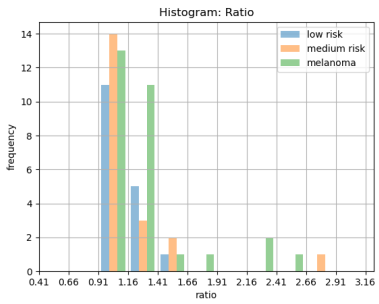


Figure 4: Histogram reporting the recurrence of ratio values for low and medium risk moles and melanoma.

3 Conclusions

As we can see from the results we have obtained, analyzing only the border of a mole isn't sufficient to make a 'correct classification' like: 'it's melanoma' or not. In fact, as said at the beginning, the features of a mole we should analyze to understand its evolution are summarized in the acronym ABCDE: A asymmetry; B border; C color; D diameter; E evolution. So, it's impossible to diagnose a melanoma from a mole only analyzing the perimeter. Despite this, the algorithm we have used works well and gives us a correct result. In fact, as we can see from final results, the ratios from 'melanoma' images are, on average, higher than the ones from 'low risk' moles, similarly for the ones from 'medium risk' moles.