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Introduction

This report details our approach to the problem of identifying melanomas in skin images. A comparative study between different preprocessing techniques has been carried out, and a parameter-testing methodology for fine-tuning has been applied. A set of clustering and thresholding segmentation methods have been studied to finally perform refinement adjustments in a post-processing phase. Additionally, a parallelized version of the evaluation function has been implemented to speed up the described processes.

Attached as a demonstration of implementation, the files are organized as follows

- *segmentation_*.ipynb* ➜ Jupyter Notebook containing the images and final parametrized functions
- *segmentaton.py* ➜ Equivalent to the Jupyter Notebook (for imports)
- *fast.py* ➜ Parallelized version of the solution used for parameter tuning and filtering.

Pre-processing: motivation and techniques.

Image pre-processing techniques were first used to limit the search for anomalies [1]. However, our situation presents some extra needs. To increase the quality of the images, both for sharpening the edges and improving the difference in brightness between background and foreground, **contrast enhancement** is our first step. Nonlinear contrast enhancement techniques are commonly used in the medical field [2], so a **logarithmic** exposure adjustment method has been selected.

Although the thin blood vessels and the cutaneous lines are smoothed using filters, the presence of short hair in this kind of analysis has been proven an impediment to the performance of the segmentation phase [3]. We have found interesting papers on **hair removal** techniques [4], and after several implementations of filter combinations, we have tried a function developed by Vatsal Parsaniya [5]. The algorithm performs a **black-hat filtering** to find the hair contours and a grayscale space is passed as argument. The black-hat transform is defined as the difference between the closing and the input image, and works well with this kind of feature extraction [6]. The function creates a kernel and applies the filter using the OpenCV library for Python. Then, it performs a **binary threshold** to intensify the hair contours. This is needed for the final step, where the inpainting of the original image is performed depending on the mask [7]. After doing multiple tests, we have found that the optimal **kernel size** for this hair removal algorithm is **3**.

As stated previously, skin irregularities may present as unwanted artifacts when segmenting. The ideal approach should be blurring them while keeping the important edges. To address this, we have tested the most common filters skin cancer researchers apply to optimize images, i.e. **median filter**, adaptive filter and **Gaussian smoothing** filter [8, 9]. Additionally, we have tried the mean filter; we found that the **geometric mean** filter achieves a level of smoothing very similar to that of the arithmetic mean filter. However, it tends to lose less detail in the process, so it fits in our case.

Initially, our testing was carried out on the grayscale images. However, it has been verified that in this type of skin images, presence of non-uniform background illumination and shadow artifacts often leads to false detection [10]. As RGB presents certain limitations in high-level processing, other color space representations have been proposed [11]. Since the difference in saturation between the skin and the melanoma is acceptable, and barely influenced by the illuminance artifacts, we decided to convert the image to **HSV** and work with the **saturation channel**.

Segmentation: approach and methods.

Research on the main image segmentation algorithms has been carried out [12], and we can group them into region-based, thresholding methods, edge-based and clustering. Following the references of the following paper [13], we have decided to delve into thresholding and clustering, rather than superpixel. This also allows us to complete extra work for this assignment, expanding our options beyond k-means.

Thresholding approach.

With this approach, thresholding functions create a binary or multi-color image based on a threshold value on the pixel intensities. For this case, we have studied the standard categories [14], and we have decided to try global thresholding techniques, which work better for our scenario. The downside of this type of thresholding is that we would obtain disappointing results on poorly illuminated images, but we assume that this is not the case given the medical nature of the images.

The code provided proposes an **Otsu threshold**, which belongs to the traditional thresholds. As we will discuss in the results section below, its performance is good. We have decided to seek to improve its result with iterative selection methods, and we have concluded that the **ISODATA** (Iterative Self-Organizing Data Analysis Technique) method appears to be one of the best [15]. Here, obtained thresholds are intensities that divide the image into two pixel groups, where the threshold intensity is midway between their mean intensities.

In addition, other thresholding methods have been parameter tuned, but we have not found a combination of method and pre-processing adjustments that surpassed the quality obtained with the best setup of the ISODATA method. These are the *yen*, *mean*, *triangle*, *li* and *adaptive thresholding methods*. In order not to elaborate unnecessarily in this section, we will not comment on them, although we will compare the results later.

Clustering approach.

Clustering is a method to perform image, pixel-wise segmentation, where we try to cluster pixels that are nearby. In this approach we have used a **K-Means**. As we need to differentiate two regions in the image we have used K=2 for the number of clusters. By selecting the best centroids, a mask prediction of the melanoma region is computed. As we will demonstrate in the results section below, clustering and thresholding methods produce very similar results.

We have made the decision to emphasize the testing of thresholding methods rather than clustering algorithms, balancing the possible upside in efficiency with the downside in increased complexity and computational cost. In making this decision we have considered the research done on other clustering methods, such as *fuzzy c-means*, *Mean Shift Clustering* and *DBScan*.
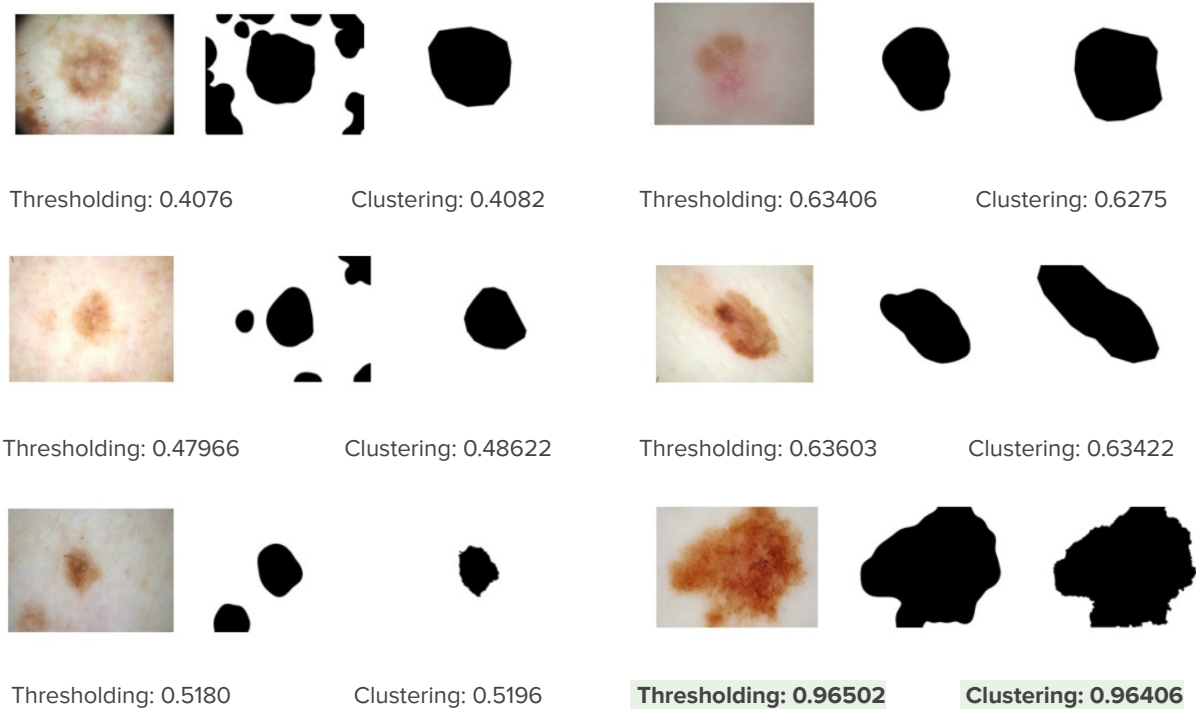
Post-processing techniques

The result of the above procedure is a set of masks with fairly good accuracy, but irregularities have been found when compared to the ground-truth examples provided. One of the most obvious problems was the presence of small spots, or holes, inside masks whose outer contour was well delimited. To solve it, we needed to merge the whole area inside the optimal contour within the same region. A fill holes operation is implemented for this purpose.

While we are satisfied with our approach to pre-processing, we have noticed that the masks are sometimes contaminated by small artifacts. These minor flaws derive mainly from elements of the skin and hair fragments after inpainting. A morphological closure is needed. The dilation operator can be effectively used to fill holes of unmarked vertices at the boundary of the features. Another operation is needed to reverse the effect of the dilation and recover the original shape, so we need shrinking. This is achieved with an erosion operator that cuts off undesired branches. The mask is first grown and shrinked afterwards, filling holes in the inner region of the feature, and filling bays along the boundary. In this way we achieve the desired morphological closure, which we could define as $close^n := erode^n \circ dilation^n$. [16]

Evaluation and discussion of results

As mentioned in the extra work section of the assignment, we have implemented a function that allows us to automatically obtain the 5 worst results. These are the results obtained with the train set. In the following comparisons, ordered from worst to best, we show first the original image, then our result and finally the ground-truth mask provided. The Jaccard indexes for each are also displayed. Additionally, we have shown the best result for both approaches.

| Thresholding: 0.4076 | Clustering: 0.4082 | Thresholding: 0.63406 | Clustering: 0.6275 |

| Thresholding: 0.47966 | Clustering: 0.48622 | Thresholding: 0.63603 | Clustering: 0.63422 |

| Thresholding: 0.5180 | Clustering: 0.5196 | **Thresholding: 0.96502** | **Clustering: 0.96406** |

The results obtained by thresholding with ISODATA and k-means are practically identical. Therefore, we only show the comparison of the best of them for the 5 worst results. This leads us to think that the quality of our method lies more in the pre- and post-processing than in the choice of segmentation. The Mean Jaccard Score obtained for **thresholding** is approximately **0.8277**, and with **clustering 0.8272**: almost identical. However, if we approach it from an efficiency perspective, we have found that **thresholding** is, on average, **10% faster** than clustering.

Finally, a quick look at some examples that have made us opt for the ISODATA method previously explained in the thresholding segmentation stage.

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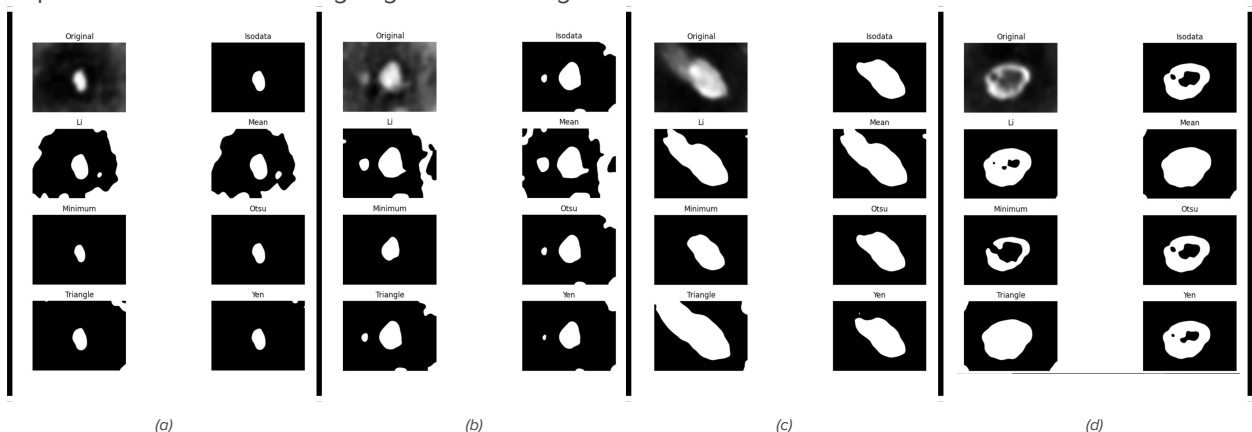
We can observe in (a) and (d) how the ISODATA performs extremely well, accompanied by the Otsu. However, in (c) we find an area with less intensity, which misleads this method, while others such as Li, Triangle or Mean, which do not usually perform optimally, excel in this situation. In case (d), it is clear what we commented in the post-processing section: the outer contour is very accurate, but we must apply a fill holes operator to fix it. With this visual approach, and obtaining the mean Jaccard index for each method, we have determined that ISODATA is the best option to implement in the thresholding segmentation.

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