Segmentation Using a Region Growing Thresholding

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ABSTRACT

Our research deals with a semi-automatic region-growing segmentation technique. This method only needs one seed inside the region of interest (ROI). We applied it for spinal cord segmentation but it also shows results for parotid glands or even tumors. Moreover, it seems to be a general segmentation method as it could be applied in other computer vision domains then medical imaging.
We use both the thresholding simplicity and the spatial information. The gray-scale and spatial distances from the seed to all the other pixels are computed. By normalizing and subtracting to 1 we obtain the probability for a pixel to belong to the same region as the seed.
We will explain the algorithm and show some preliminary results which are encouraging.

Keywords: Region Growing, Image Segmentation, Parotid Glands, Tumors, Spinal Cord

1. INTRODUCTION

Image segmentation plays a crucial role in medical imaging by facilitating the delineation of regions of interest. Our issue deals with head and neck tumors and risk areas segmentation such as parotid glands ganglionic areas or spinal cord.
Knowledge on precise position or volume of tumors and risk areas is capital for radiotherapy planning. The doses of radiation depend on tumor's volume and the rays must avoid the risk areas. At this moment all the segmentation is done manually. The time needed by a specialist to do a manual segmentation is up to three hours, that is why the need of a tool which saves time is very important.
There are numerous segmentation techniques in medical imaging depending on the region of interest [3]. The most relevant ones for our problem are atlas-guided techniques [5] and region growing segmentation methods [2][3]. Some of them use a semi-automatic approach and still need some operator interaction. Others are fully automatic and the operator has only a verification role. Atlas-guided techniques could work well for the spinal cord segmentation but tumors or parotid glands are quite different from a patient to another. It is very difficult to have a modelization of the parotid glands and even more the tumors. Active contours models [4] as snakes are very efficient only if they are very close to the final solution. Here we study very complex structures as tumors or parotid glands and these models fail to reach the final solution if they are not close enough to this solution.
In this work, we developed a semi-automatic approach based on a region-growing technique in order to segment the spinal cord. As it showed good results [1] we tested it for other organs like the parotid glands (risk areas) and even on tumors with also encouraging results.
After introducing the region growing method, we will present some preliminary results and then make a discussion on future work and improvements.

2. METHOD

2.1. ROI visualization using distances and probability maps

On *Figure 2.1.1* we can see the probability maps: on top-left we have a map based on the spatial Euclidean distance from the initial seed point to all the other pixels. On top-right we have a map based on the gray level value Euclidean distance between the seed and all the other pixels in the image. On bottom-left we have a map based on the gray level mean Euclidean distance from a window centered in the initial seed to all the other windows centered in all the other pixels in the image. Finally we have the same thing on the bottom-right image but using standard deviation instead of the mean.

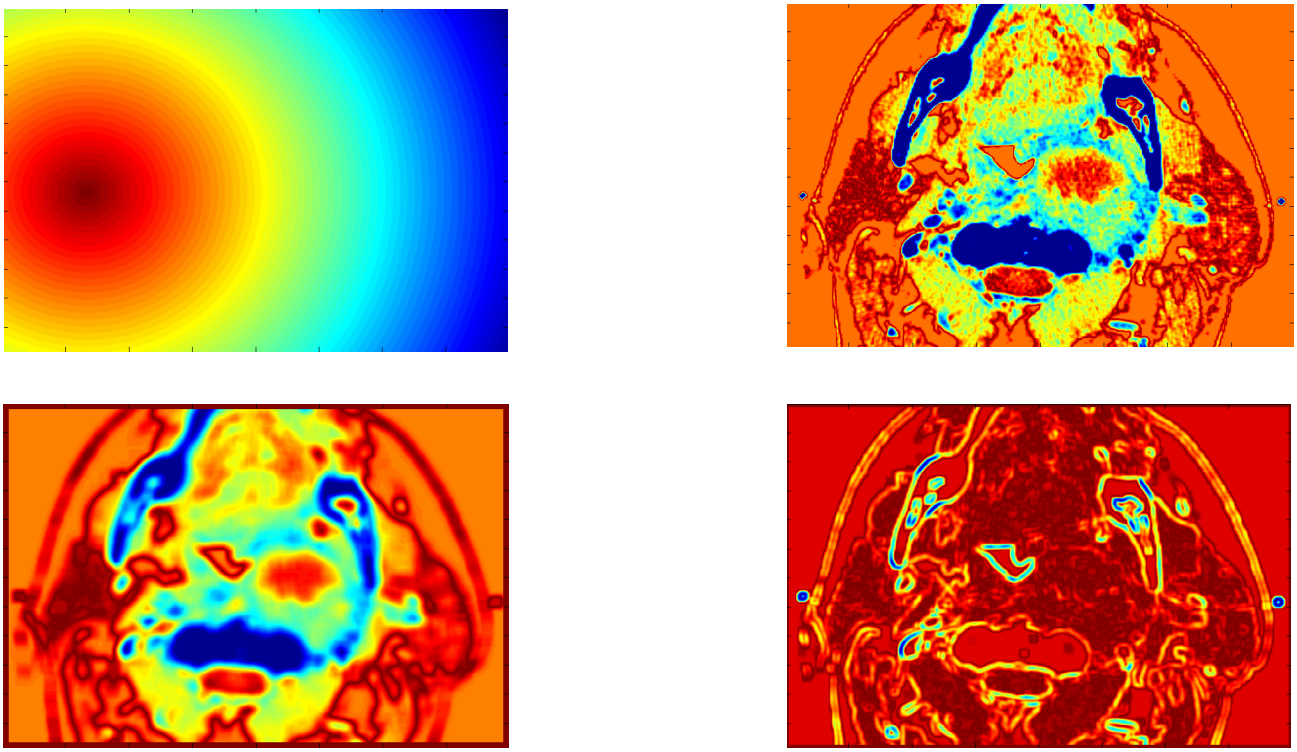

Figure 2.1.1: Probability maps from top-left to bottom-right based on: spatial distance, gray level value, gray level mean and gray level standard deviation.

These probability maps are computed from the distance maps by simply normalizing and subtracting them to 1. This approach of comparison using a distance from a seed point to all the other pixels according to some features is quite similar to what is done in an unsupervised classifier like the k-means. The difference is that there is only one cluster centroid fixed by the user and the features are only classified with a probability of belonging to the same class that the initial seed or not.
As these probabilities are independent, we can combine them using a multiplication. We obtain images as in the *Figure 2.1.2* on the left image where the parotid gland is very well highlighted.

2.2. The need of a new Gray-Space (GS) map

The problem is that the spatial Euclidean distance as you can see it in *Figure 2.1.1*, top-left image, does not depend either on images dimensions or on structures dimensions… If the parotid gland is smaller, this spatial distance could highlight parts out of the gland for example.

This is the reason why we developed another distance called Gray-Space (GS) map. This distance is based on image topology.

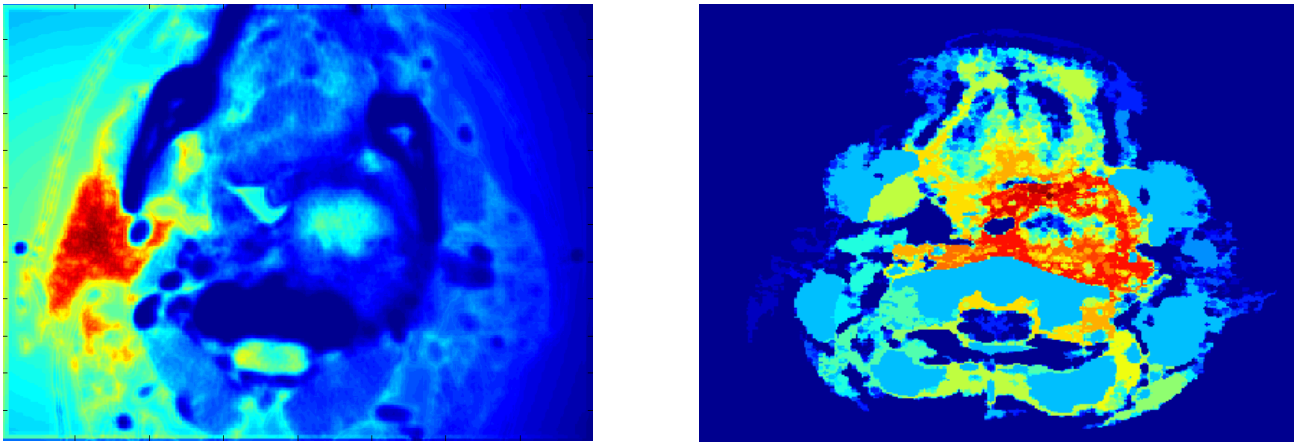

Figure 2.1.2 : Mixing the probability maps on the left and GS map example on the right

The basic algorithm is very simple. We compute the seed gray level : V = I(seed), then look for structures which have the same gray level than the seed overlapping the seed position. At the second iteration, we look for structures having a small gray level difference from the seed : Tmp = AND(I > (V + D), I<(V - D)) and we keep those structures which overlap the seed position. At each iteration we increase the difference D by 1. In this way structures which are closed from a spatial AND intensity point of view to the seed are highlighted with higher values. The more we are far spatially and from an intensity point of view from the seed, the lower is the labeled region score.
We can see this on the right image of *Figure 2.1.2.* The great advantage is that space and intensity are linked as they really are in natural images.
Other refinements can be done as structures with intensity values closed to the seed could be considered not only if they touch the seed but also if they are “not so far”. This parameter can be set using a dilatation on the structures connected to the seed:
The sentence “look for structures having a small gray level difference from the seed and we keep those structures which overlap the seed position” becomes “look for structures having a small gray level difference from the seed and we keep those structures which overlap after dilatation the seed position”.

2.3. From visualization to segmentation

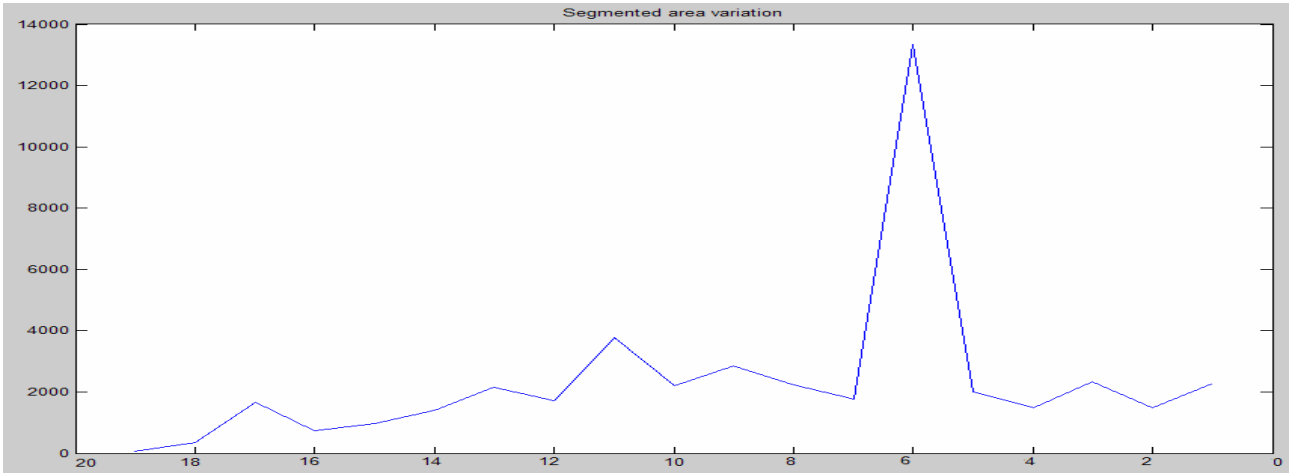

Figure 2.3.1 : Area variation function of the GS map value. Axis Y :n umber of points (area) Axis X: GS map value (up to 20 here)

At the difference of k-means, we only have a good visualization but not segmentation because we have just one seed and no concurrent cluster. A classic approach is to verify that even if the labeled area grows, the homogeneity of the area is constant. We try to see if the statistics of the area are kept during the region growing. When the statistics change too much, it means that we are introducing heterogeneous areas in our region, so we must stop the growing.
In our case we computed the variation of the Euclidean distance between the histograms before and after each growing step. We found this variation to be very similar to the variation of the region area: if we include large areas in our ROI , there is a big area variation, but also, in the same time a big statistic variation.
On the *Figure 2.3.2* we can see a classical histogram after the GS map computation. The ROI is highlighted, so it is placed in the higher intensity range.

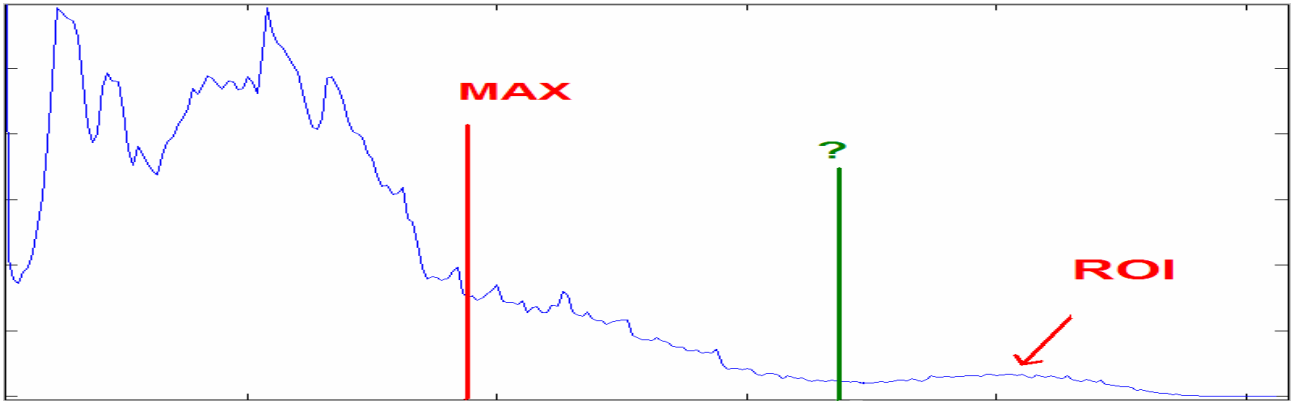

Figure 2.3.2 : Our visualization technique histogram

Here is our thresholding process :
First we find the maximum area variation in *Figure 2.3.1* which means that from this intensity to 0 we are sure that this is not the ROI.
Second we cut the histogram on *Figure 2.3.2* from MAX to 0. Than, we have to find the threshold from MAX to the highest intensity which separates the uncertainty area from the ROI. This is simply done using the well-known Otsu thresholding method. This is a parameter free thresholding technique which maximizes the inter-class variance. It is interesting to observe that the Otsu method is more accurate in cutting into two classes than a k-means for example, because the k-means just measures distances between data and classes' centroids but Otsu also take care to get compact clusters using the inter-class variance.

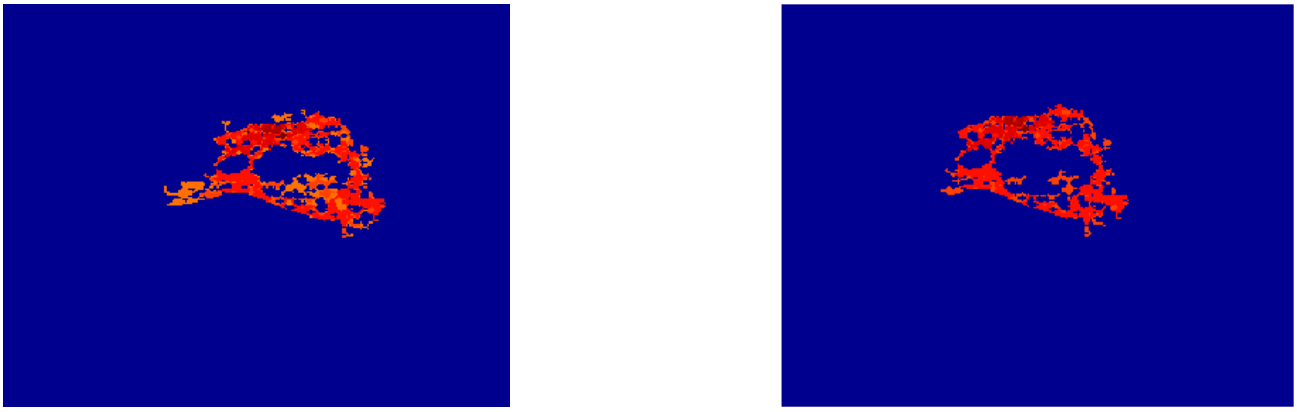

Figure 2.3.3 :Left : after thresholding with MAX, Right : after refining using the Otsu method

On *Figure 2.1.2* at right we have the GS map, than a thresholding eliminating all gray levels below MAX (Figure 2.3.3, left) and finally the refining step using the Otsu algorithm (Figure 2.3.3 right).

3. RESULTS

3.1. A general method

Even if the initial purpose of this method was medical images segmentation, it works quite well with all structures which are homogenous according to a criterion. The first part of the segmentation is the research of the homogeneity criterion. In *Figure 3.1.1* we can see the Matlab rice image. In order to segment the rice, we decide to click once on the background. As we can see after having computed the probability maps of the gray level value, mean and standard deviation, we see that the values and the mean of the gray levels are not very homogenous because of a varying initial image illumination. But if we look to the gray levels standard deviation probability map, we can see the it is quite homogenous.

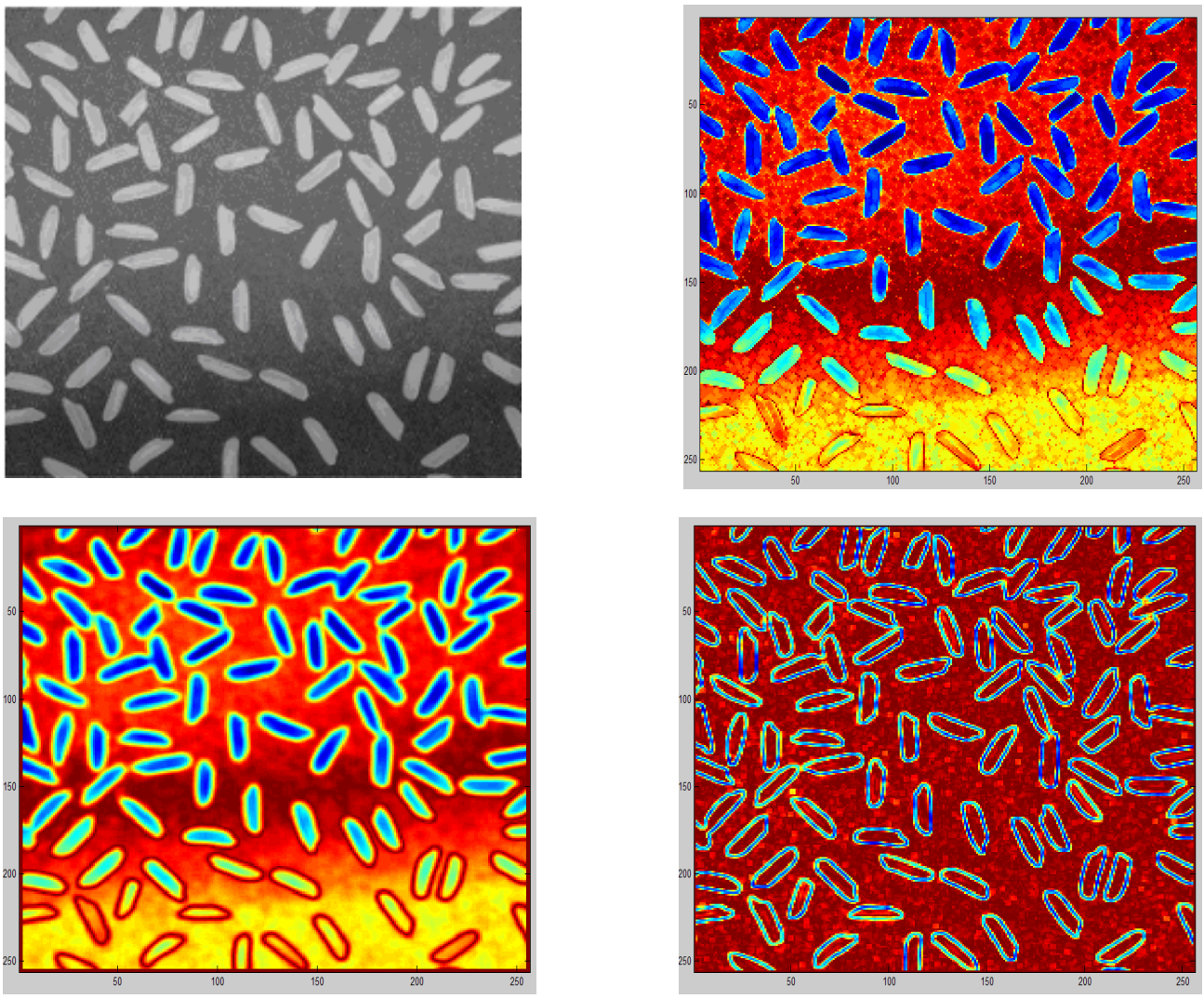

Figure 3.1.1: The original rice image is on the top-left part. On the top-right part there is the gray level probability map after a click in the background. On the bottom-left image there is the probability map using the gray level mean and finally in the bottom-right image the probability map using the standard deviation.

This is due to the fact that the background texture is homogenous and the low frequency illumination noise has no effect on the high frequency texture of the background.

We will now use only the standard deviation probability map in order to compute the GS map. As you can see on the left image of *Figure 3.1.2,* we obtain zeros inside the rice. There is still a problem on the peripherals where the rice contour is broken but for internal rice , this one has no chance to be of the same class than the background.

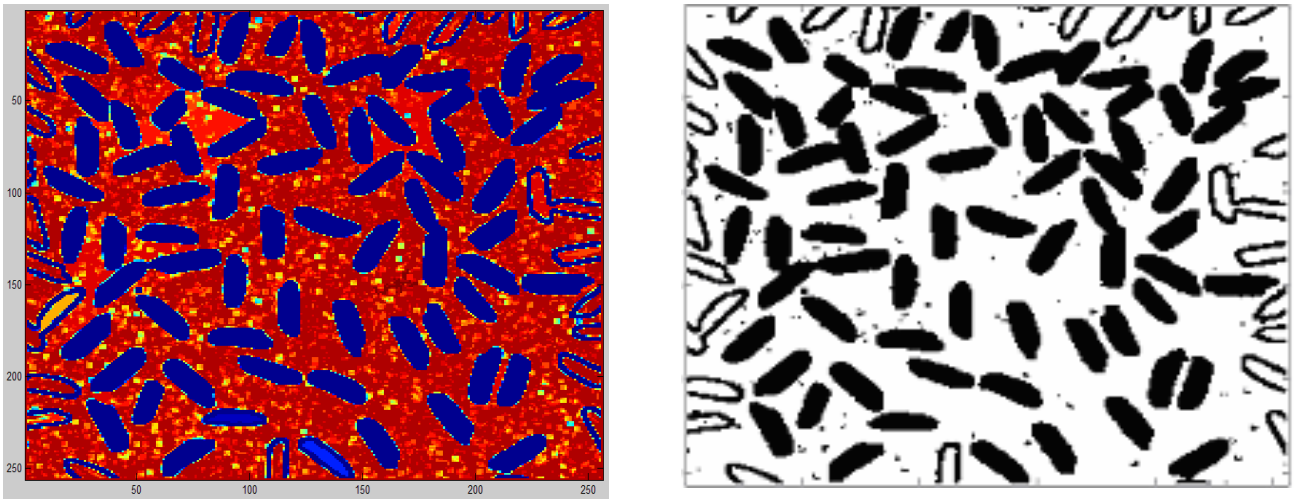

Figure 3.1.2: The GS map of the standard deviation probability map is computed on the left image, than on the right we have the segmentation

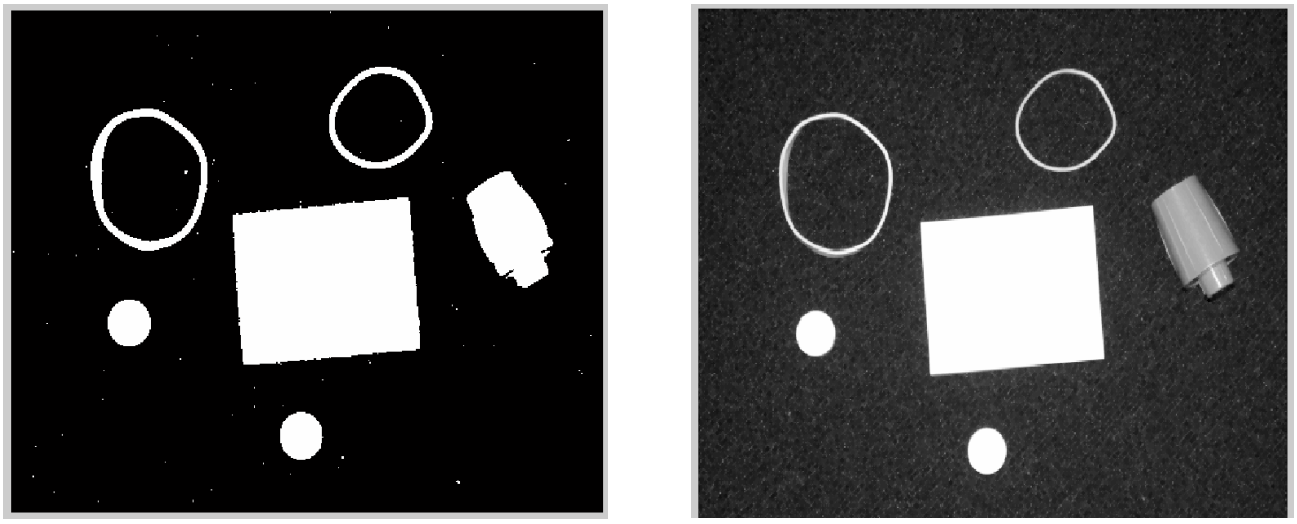

Figure 3.1.3: Another original Matlab image segmented using the background

The same technique was used in *Figure 3.1.3* were one click in the background was enough to segment all the objects. The following figures contain images where the three criterions are used together. You can see on the *Figure 3.1.6* that a non-uniform illumination on the vegetable is considered as another class and it is bad segmented here. The initial seed was placed on the centered vegetable.

Figure 3.1.4: A segmentation using gray levels value, mean and standard deviation

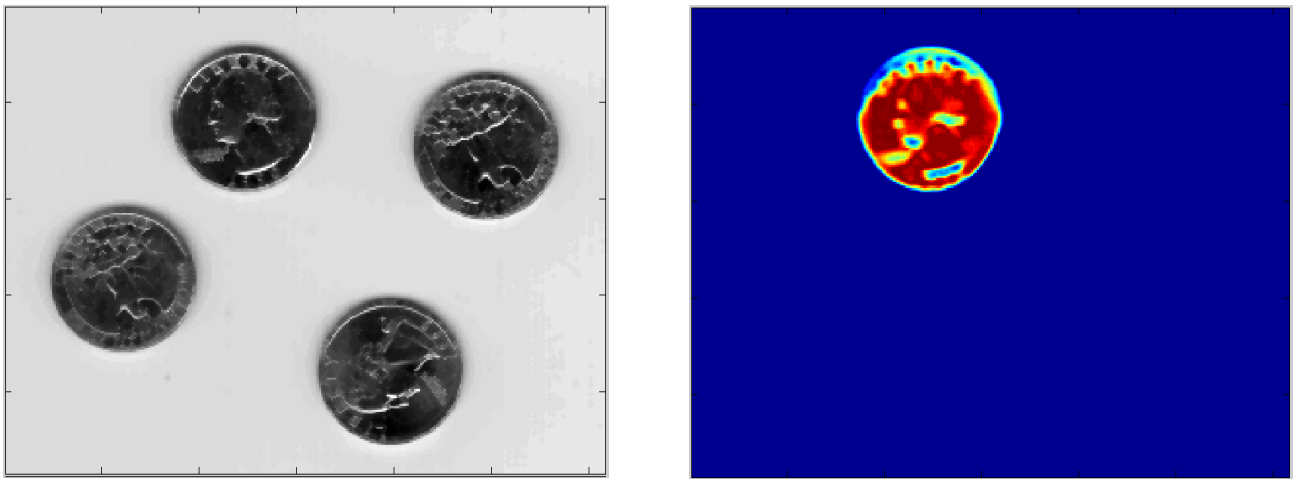

Figure 3.1.5: GS map of a coin on the right and the initial image on the left.

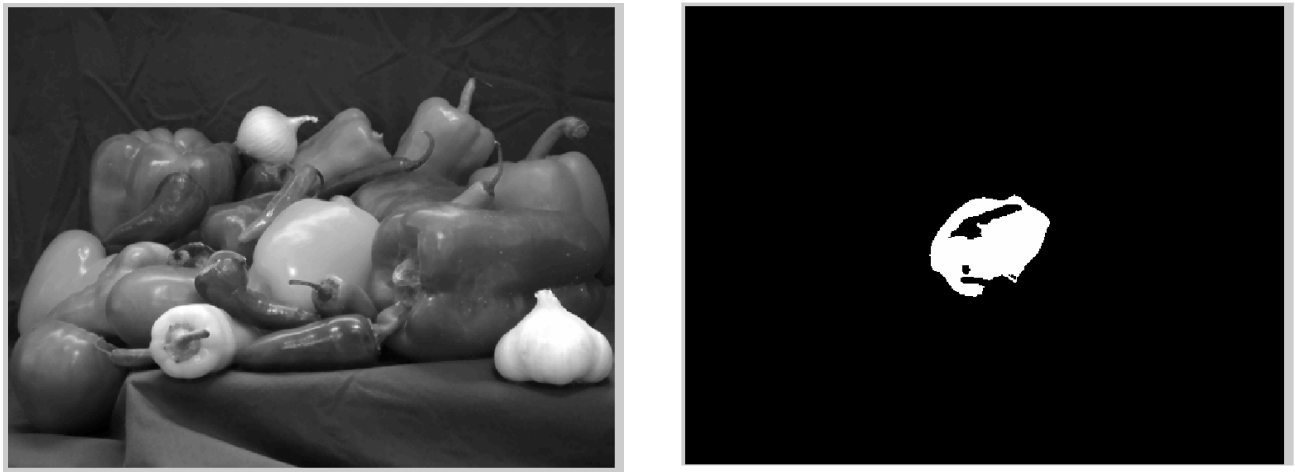

Figure 3.1.6: Vegetable segmentation

3.2. The Spinal Cord

The spinal cord segmentation can be done easily because it is quite homogenous. As you can see on the *Figure 3.2.1,* it is possible to use directly the initial image to compute the GS map. The results are quite accurate and does not need much refinement.

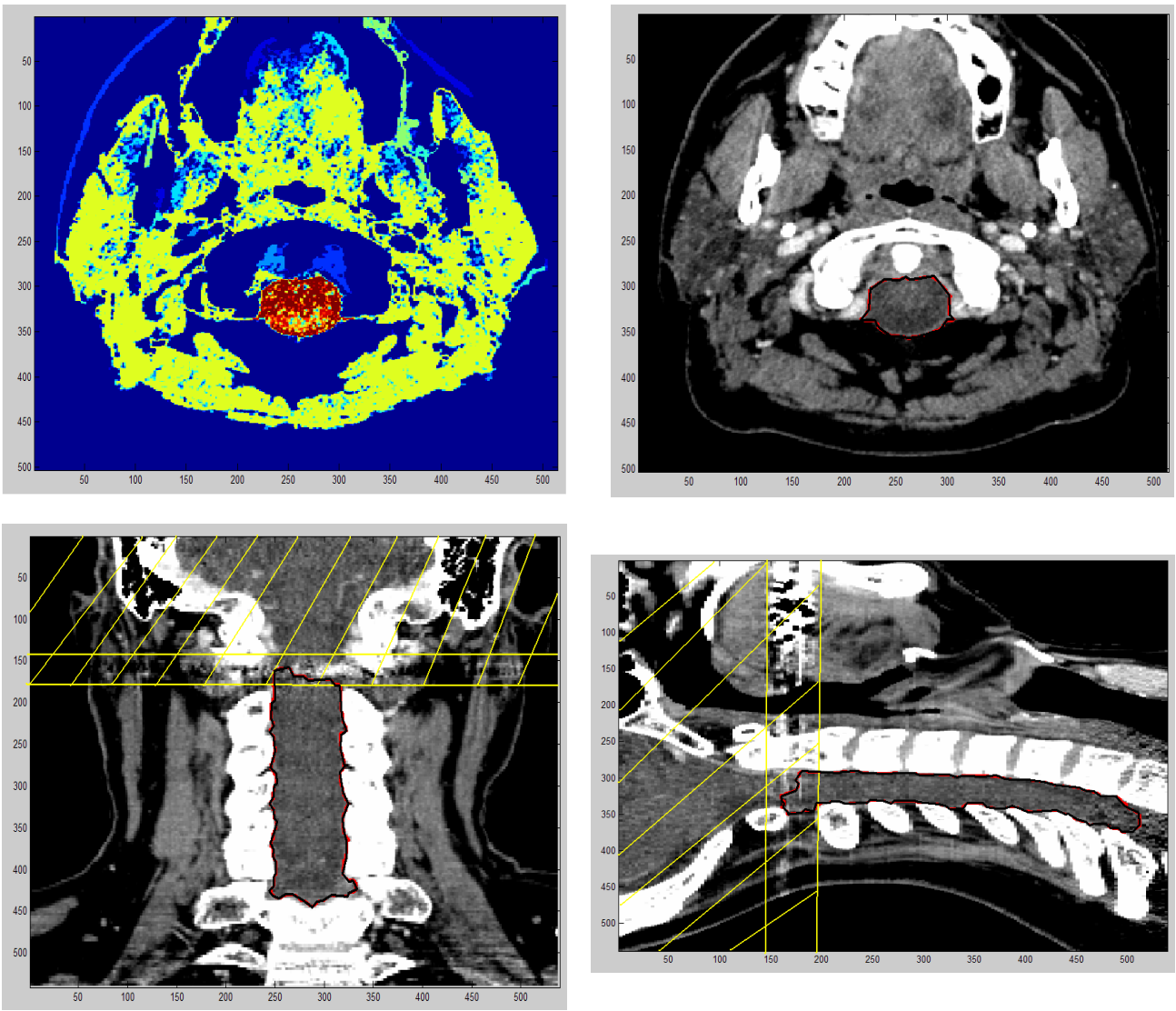

Figure 3.2.1: Spinal Cord segmentation. On the top-left side, this is the GS map when we click inside the spinal cord. On the top-right image we have the superposition on of the segmentation on the initial CT-Scan. On the bottom-left and right images we have the segmentation results on a coronal and sagittal view of the neck.

3.3. Tumor segmentation

After a short study of the homogeneity criterion, it appears that textural features as the standard deviation are not very relevant, because the tumors are very heterogeneous structures which often have a texture closed to muscles. We also use directly the initial image to compute the GS map.

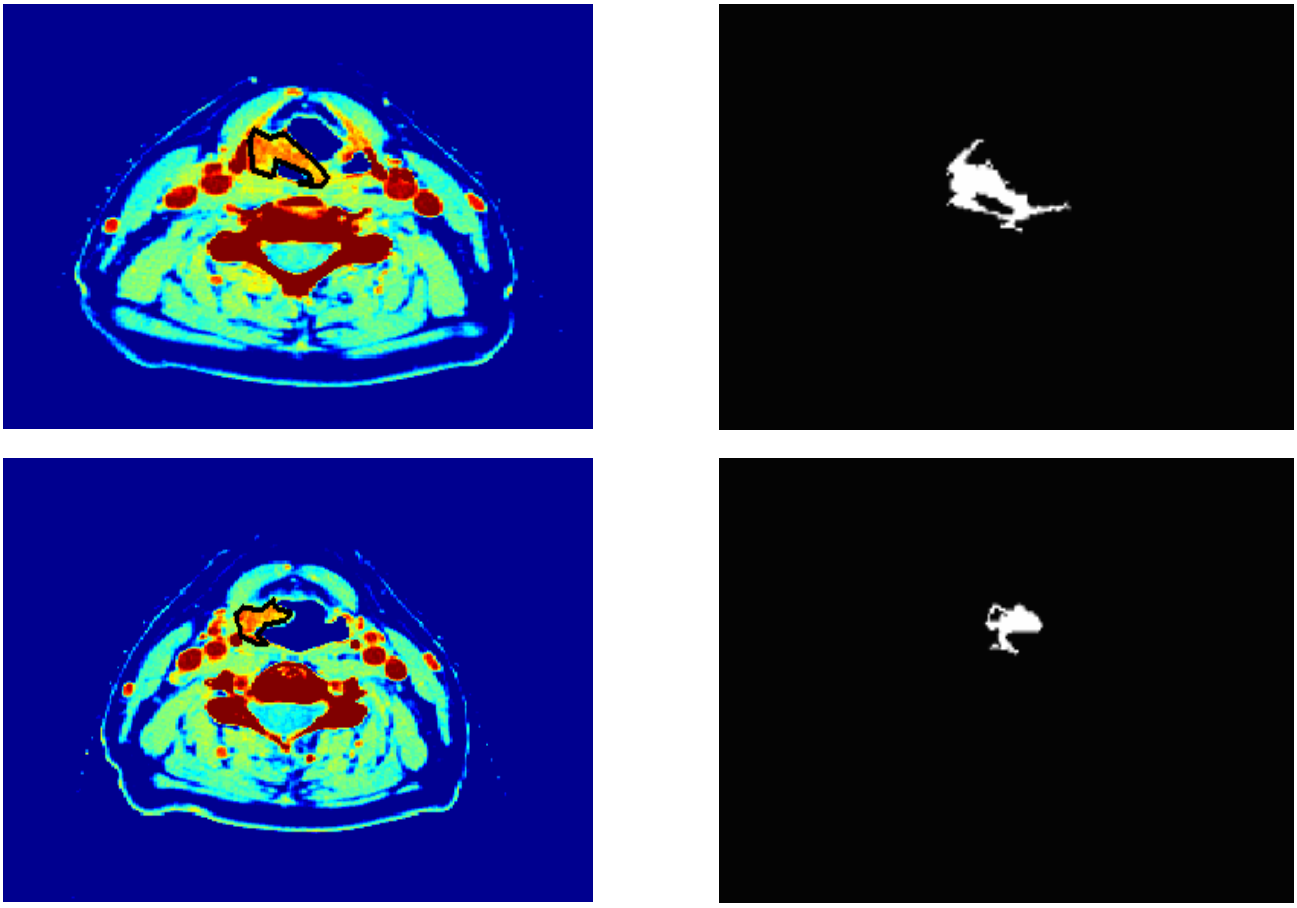

Figure 3.3.1: On the left row, two CT-scan images with the tumor segmentation in black and the final segmentation

On *Figure 3.3.1* we can see a quite good segmentation because it is a homogenous tumor. In reality some tumors are heterogeneous, mainly if they contain necrotic cells which have a different gray level from the active areas. In this case it is impossible for a region growing technique using only one seed to segment the entire structure. Here we concentrate ourselves on the active area which is the most dangerous area in a tumor and which has to be well targeted in a radiotherapy planning as we can see in *Figure 3.3.2*.

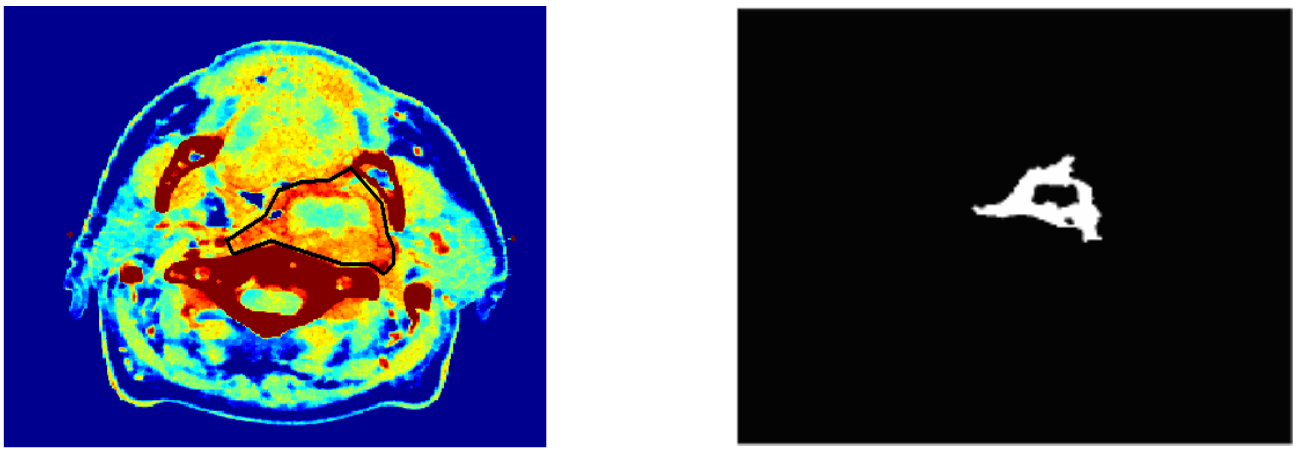

Figure 3.3.2: A heterogeneous tumor manually segmented on the left and segmented using GS maps on the right

3.4. Parotid glands segmentation

The parotid glands are more homogenous from a textural point of view, so the standard deviation probability map will be very useful here. We use all probability maps (values, mean and standard deviation) in order to compute the GS map.

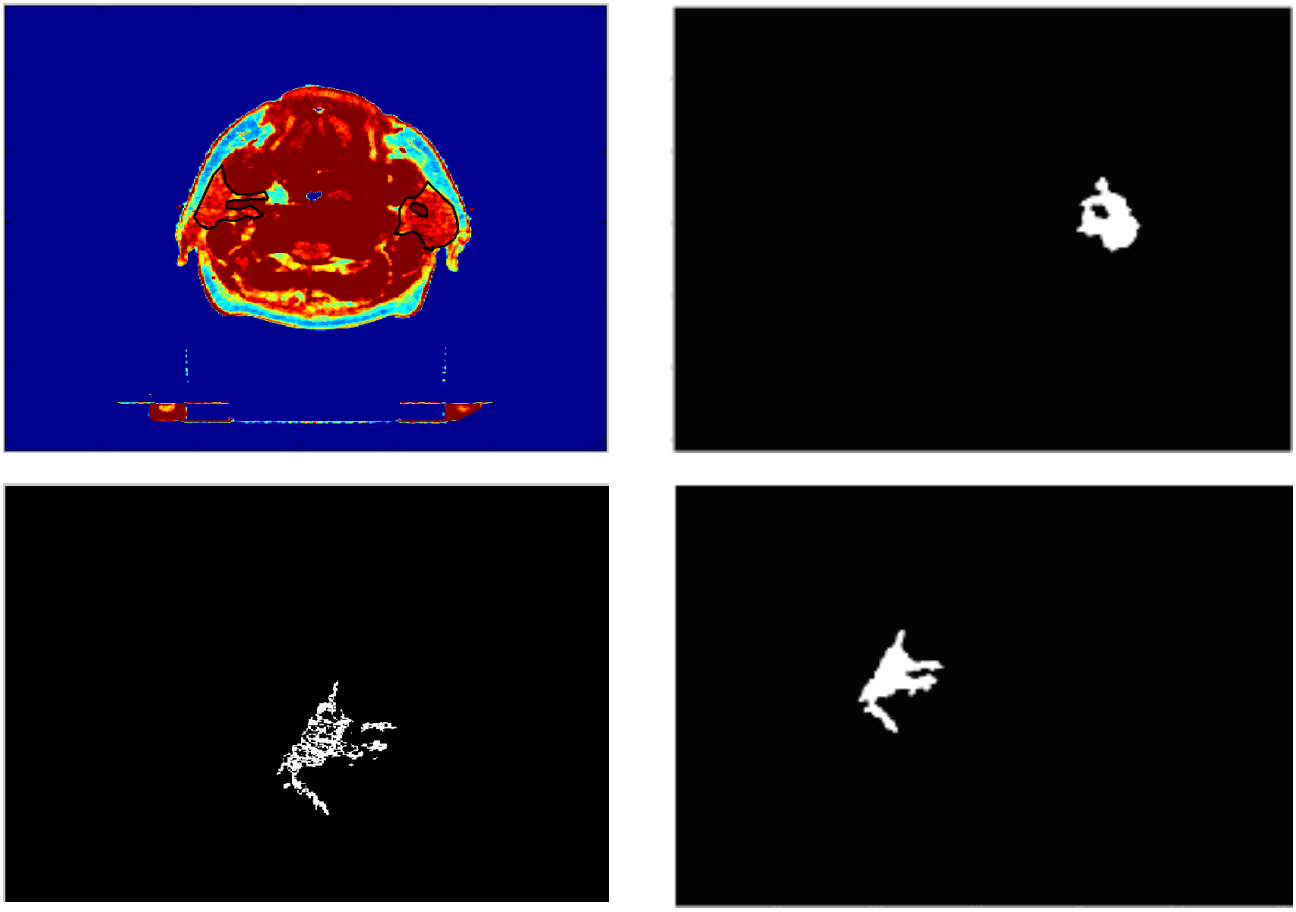

Figure 3.3.2: On the top-left the CT-Scan image and the parotid glands manually segmented in black. On bottom left we have the direct result of the left parotid gland segmentation. On the right column we have the results after post-processing of the right parotid gland (top-right) and left parotid gland (bottom-right)

The parotid glands have also some gray level heterogeneities even if this phenomenon is less important than in some tumors. Their structure is sometimes very complex as you can see here on the left parotid glands. As for tumors the result is not perfect and there is sometimes noise like the thin bottom part of the left gland here on this difficult example. Nevertheless, even if the result is not perfect, it is encouraging. We had no time until now to do serious tests on a dozen of patients, but all preliminary tests are satisfying. Moreover, this is a novel approach and we already see many possible improvements.

4. DISCUSSION AND CONCLUSION

4.1. Reproducibility

The reproducibility is one of the problems of all semi-automatic methods. A mean value is here computed on a window centered on the seed in order to minimize the initial seed position variability. Nevertheless this method is still dependent on the initial seed position. Moreover, as we saw in the previous section, for heterogeneous areas as tumors, the different regions (active cells, necrosis) must be segmented separately and then added to obtain the entire structure segmentation. In the future we will use more than one click per tumor. We could for example ask to the operator to draw a triangular shape inside the structure and automatically choose some seeds from this shape. Moreover, this shape should contain more spatial information which could reduce the variability of this method. The same problem must be faced with the parotid glands which are sometimes a little heterogeneous. For the spinal cord one seed should be enough because the structure is quite homogenous and easy to segment.
This method is a general one but the homogeneity criterion depends on the kind of image we have to segment. It is very important to use the good criterion in order to achieve an accurate segmentation. A preliminary test is required in order to choose the image or probability map on which the GS will be computed.

4.2. Computational complexity

For instance, the probability maps are implemented in C and in 3D. It takes 30 seconds (Pentium IV, 500 Mo RAM) to compute all the probability maps on a volume of 612 x 612 x 5 voxels. The GS map is only implemented in 2D in Matlab but it is only computed locally so it is very efficient. The computation time depends on the parameters.

4.3. Conclusion

We presented here a new growing thresholding method based on probability maps and a new Gray-Space map which takes into account the image topology and its intensity levels. This method seems to be enough general to be applied to medical or other computer vision domains and it is quite fast. A future work will consist in the 3D generalization of the GS map which will help a lot in noisy elimination. As the algorithm is very simple, this generalization will be easy.
More extensive tests on medical images will be done.
Finally, until now, the results are a good approximation of the organs' segmentation. These results could be a perfect initialization of some active contours based methods which are very effective if they are closed to the final solution.

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