

Computer assisted segmentation, quantification and visualization of an infarcted myocardium from MRI images

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Abstract *Since myocardium diseases are one of the main mortality causes in industrial countries, a lot of studies are devoted to the evaluation of the consequences of myocardium infarcts. In this paper, we present a precise method to evaluate the percentage of infarcted muscle versus sane muscle volumes, based on direct measures from MRI images. The method is implemented in a semi-automatic software tool for medical staff and helps to accelerate and enhance (in terms of precision) the infarct evaluation process. Medical experts assessed the quality of the results and the ease of use of the tool.*

1 Introduction

Since myocardium diseases are one of the main mortality causes in industrial countries, a lot of studies are devoted to the evaluation of the consequences of myocardium infarcts. Nevertheless, few medical studies on consequences of infarcts are interested in direct consequences on the muscle. The majority of research teams studies indirect consequences in order to quantify the importance of infarcts. For example, the evaluation of the ejection fraction, the pressure at the beginning of the aorta, are good metrics to evaluate the importance of infarcts. In the work presented here, the main idea is to study the muscle directly, by segmenting 3D magnetic resonance images.

The purpose of this article is to present a new method for the analysis of MRI of Left Ventricle (LV) after infarcts. The presented method and an associated software are the result of a project that has been initiated by the cardiology department of the H. Mondor Hospital (Créteil, France). The study is aimed at measuring the volumes of sane and infarcted muscle of the LV after infarcts. More precisely, a new approach of segmentation techniques was necessary in order to propose a semi-automatic tool for segmentation: existing methods (see e.g. [11, 3, 1, 6]) allow to easily segment images of the LV, only in absence

of infarct; whereas the images that we study are generally impossible to segment with a completely automatic process and some knowledge about the shape of the LV is used by medical experts for segmenting objects of interest.

To this aim, we developed a software tool which is both ergonomic and fast during the segmentation process, and which gives the choice to the medical expert to validate or modify the result of automatic computations. The presented method permits to segment a set of MRI slices and compute volume of sane muscle, infarcted muscle and blood cavity, in approximately 20 minutes with a precision of 5% on the volume evaluation. The speed of the proposed process and its precision were validated by comparing our results to manual segmentations and volume computations, and to real volume measurements of LV muscle on 3 pigs obtained through meticulous dissections and weightings. The medical experts assessed the quality of the results and the ease of use of the tool.

2 Overview of the image processing chain

The data are grey-scale MRI of the myocardium, which typically consist in 10 short-axis slices of the left ventricle (LV). These slices are parallel to each other and each slice is the image of a certain thickness of tissue (typically 6 mm). The image processing chain that we propose may be divided into three main subparts (see Fig. 1):

- 1: ROI (Region Of Interest) selection and epi, endocardic walls marking;
- 2: Slice-by-slice interactive segmentation;
- 3: 3D reconstruction, smoothing, and volume estimation.

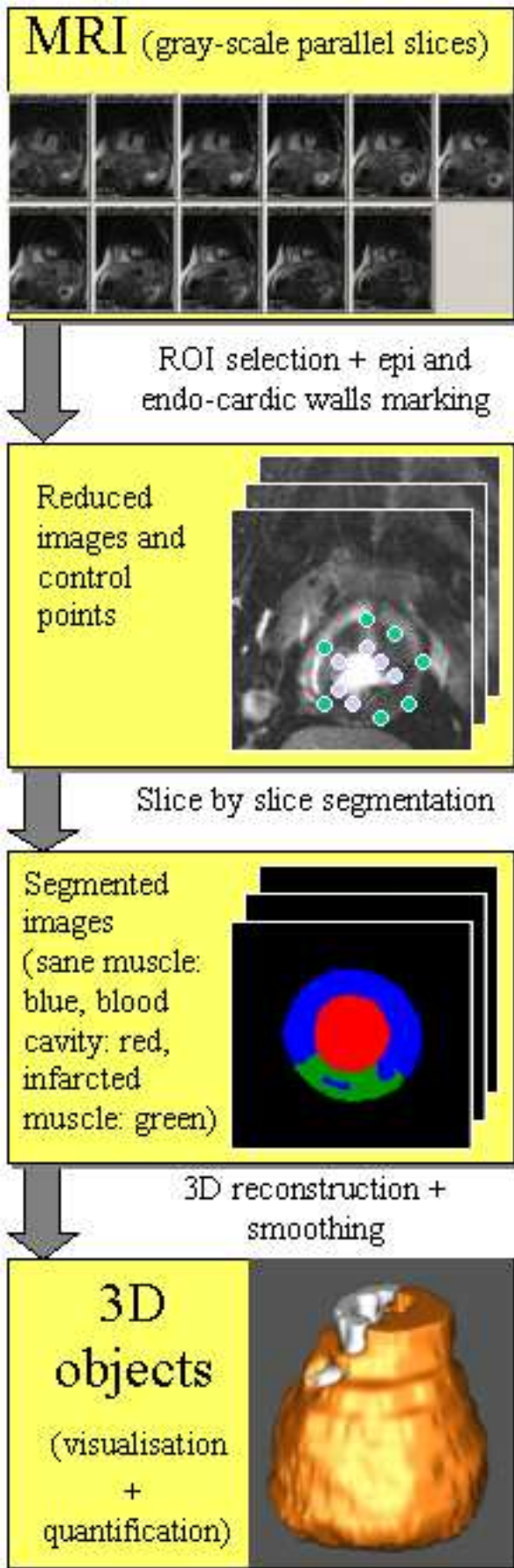


Fig. 1: Overview of the processing chain.

Step 1. The input of step 1 is a series of grey-scale images of 200×256 pixels. These images are centered on the LV but also contain other structures which are outside the scope of the study (the right ventricle, for example). By means of a system of markers manually but grossly placed we compute:

- a rectangle (smaller than the original size of images) common for all slices and centered on the LV;
- two ellipses that minimize a global distance to the markers defined by the user.

For each slice, the two ellipses approximate the contours of the endocardic and epicardic walls. This information will be used by the segmentation algorithm (next step).

Step 2. The input of step 2 (interactive segmentation) is a group of grey-scale images in which 3 different objects have to be recognized. The final result of the segmentation process is a group of new images in which pixels are marked with identifiers that correspond to the objects of interest. This segmentation process is made semi-automatically, slice per slice, thanks to an algorithm based on the watershed approach, which will be described in detail in the next section.

Step 3. From the set of 2D segmented slices produced by step 2, we have to compute a 3D model of the three objects of interest, both for visualisation and volume calculation purposes. Thanks to a discrete 3D smoothing algorithm [4], we compute interpolated slices between the original ones. This method allows to compute a geometrical model which is homogeneous in each dimension, despite the difference between the pixel resolution in each slice and the interslice distance (typically, the pixel size is 1.3×1.3 mm, while the interslice distance is 6 mm). We compute a 3D model of each part of the LV: infarcted muscle, sane muscle and blood cavity, using a topologically sound variant of the marching cubes method [7]. These models are represented by closed surfaces composed of triangles (mesh representation). They can thus be visualised through standard rendering tools, that use a mesh representation of 3D objects. From these models, the volumes of different tissues may be computed.

3 Computer assisted segmentation tool

The segmentation of an image consists in a partition of the image space into different regions which are homogeneous in terms of pixel intensity. The watershed approach to segmentation is made of two steps: the computation of the module of the gradient image, and the detection of the main crest lines of the gradient (see Fig. 2) thanks to the watershed transform.

Gradient. The gradient transformation allows to detect the discontinuities in an image, in terms of

pixel intensity. Here, we use the Canny-Deriche gradient operator [5] and we combine results computed for different scale parameters in order to have good responses for both sharp and smooth contours.

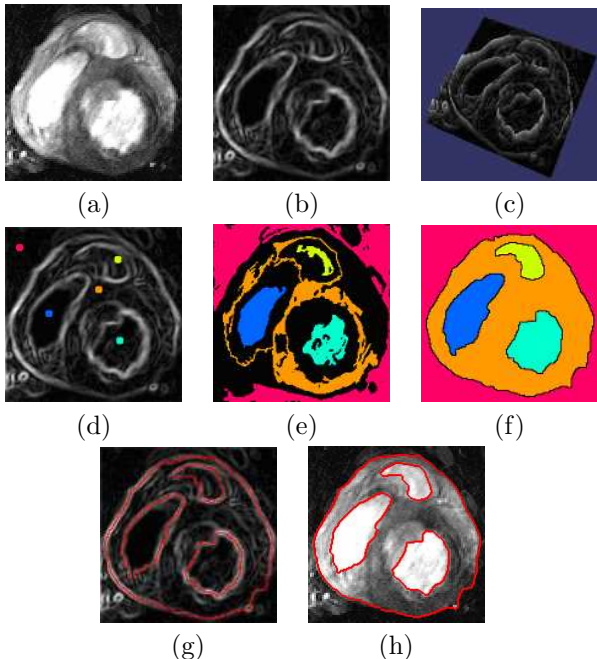


Fig. 2: (a): original image, (b): gradient image, (c): topographical view of b, (d): minima marking, (e): marker propagation (flooding simulation), (f): end of the propagation, (g): watershed lines superimposed to b, (h): watershed lines superimposed to a.

The watershed transform is a classical segmentation technique that was developed in the framework of mathematical morphology [2]. Its principle is based on the simulation of a flooding process on a topographical relief. In most cases, the watershed transformation is not computed directly on an original image, but on its gradient (see Fig. 2b), since the “basins” of the gradient correspond to the homogenous regions of the original image, and the “crest lines” correspond to the contours of these regions (the gradient image is considered as a relief where each pixel has an altitude equal to its intensity (Fig. 2c)). The process begins by marking some of the local minima of the relief (Fig. 2d, this step is called marker selection and will be explained in a forthcoming paragraph). Then a progressive flooding of the image is simulated (Fig. 2e). When the waters coming from two different markers would meet, a watershed line pixel is created. At the end of this process, the watershed lines separate the different marked regions (Fig. 2f) and correspond to the contours of the objects in the original image (Fig. 2h).

Adding a geometric model of the LV walls. In general, MRI images of infarcted myocardium cannot be fully automatically segmented. The main reason is that some contours of objects are not visible in

terms of grey-scale information. Indeed, due to the imaging technique and to the rapid movement of the heart, some different tissues may appear with the same grey-scale average in the image.

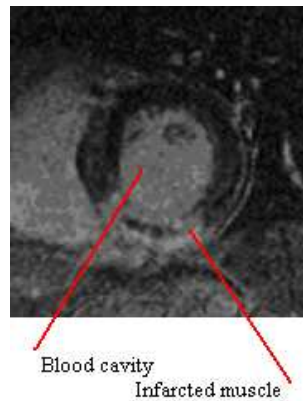


Fig. 3: Image with non-visible boundary between blood cavity and infarcted muscle.

In particular, blood and infarcted muscle have very similar intensities (Fig. 3). For solving this problem, we make the hypothesis (commonly accepted) that the LV internal and external walls have a shape that can be approximated by an ellipse. In our approach we combine in a simple manner the grey-scale information present in the image and a geometric model of LV walls. To do this, two ellipses which pass at the shortest possible distance of the LV walls are computed. This is made by means of manual placement of control points (minimum 6) all around the walls. The ellipse is then computed to minimise the distance from these control points (Fig. 4). The optimisation method used is from Fitzgibbon et al. [9]

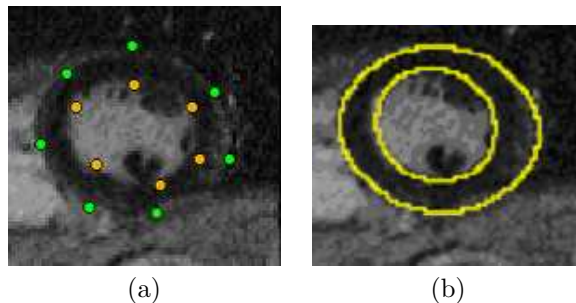


Fig. 4: (a): manual placement of control points, (b): automatic computation of optimal ellipse.

Then, the gradient image and the elliptic LV walls model are combined in a simple manner. We apply a Gaussian filter on the ellipses image for defining, not an ellipse of unit thickness but an influence zone of the geometric model on the grey-scale information. Then an linear combination of the two images is performed (Fig. 5). A parameter α (relative importance of geometric model) is inserted in the formula: $c = \alpha.a + (1 - \alpha).b$

This simple idea gives very interesting results (see Fig. 6) and solves a difficult segmentation problem.

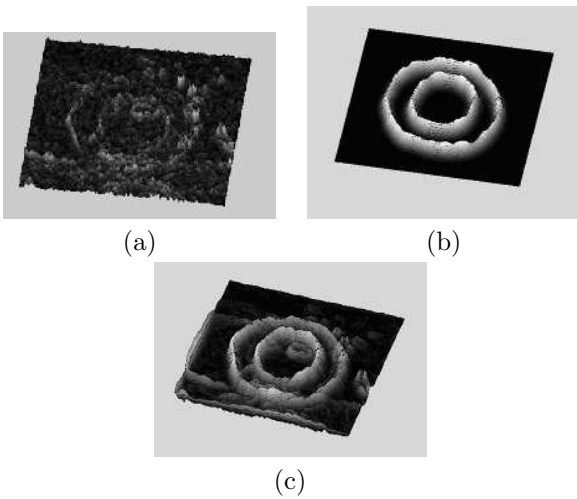


Fig. 5: Topographical representations of (a): gradient, (b): filtered ellipses, (c): weighted average of a and b.

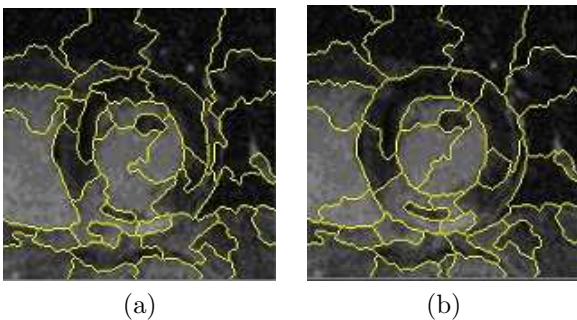


Fig. 6: Results without (a) and with (b) elliptical models.

Marker selection. We use a marker selection technique based on connected operators [10]. This method automatically selects the m principal basins of the image, where m is a parameter of the algorithm, according to a criterion which is also a parameter of this algorithm. The criterion of basin selection can be the surface of the basin, its depth, or its volume.

Watershed simplification. When a partition of the image is made, each region has to be identified since three different objects may be present on a slice. We propose a simplification process which allows the user to give a label to each region, depending if the region is the blood cavity, the same muscle or the infarcted muscle. A partition of the image and a labelling of each region may be considered as a final segmentation of the image. Typically, we are in the situation illustrated by Fig. 7a. At this step, a simplification of the partition is possible, since boundaries between two regions with the same label are not significant. For the same reason, boundaries between two regions that are not labelled (background regions) have to be deleted. We propose a merging process in 2 steps:

1. the labels are propagated to the whole regions, respecting their contours;

2. for each contour pixel which has only neighbours labeled with the same identifier, delete the pixel from the contour set and mark it with the common identifier.

The result of this process is presented Fig. 7b.

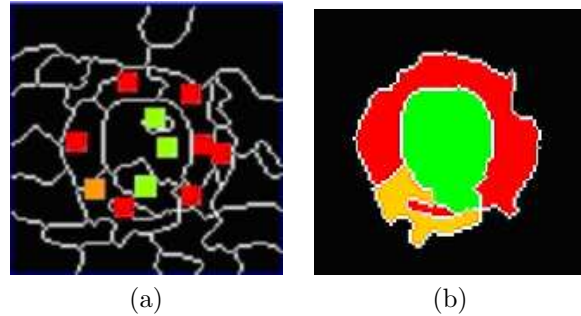


Fig. 7: (a): region labeling, (b): simplification of the partition.

Combination of these previous techniques for a semi-automatic segmentation tool. To summarize, with watershed and minima selection, a user is allowed to segment an image in m significant (for a chosen criterion) regions. In a certain region of the segmentation, it is possible for a boundary to be misplaced. Another possible case is when the user wants more details in a given region. For these two cases, it is interesting to have the possibility to re-segment a given region and to combine the 2 segmentations that are made at different scales. In our tool, we propose to compute the watershed algorithm firstly on the whole image and then recursively on whatever region delimited by the previous segmentation.

This recursive process, associated with the simplification algorithm allows to find whatever desired contour for a given object as illustrated in Fig. 8. The principle of the whole segmentation process is summarized in Fig. 9.

In order to visualize easily both the original image and the current segmentation, we have implemented the segmentation method in a grid with a doubled resolution (see Annex).

Nevertheless, one may argue that a manual segmentation is perhaps faster than our method. In fact, the contours that our algorithm proposes to the user are significant in terms of grey-scale and so the segmentation obtained with our tool is generally more precise than a manual segmentation. Moreover, when images are contrasted, the automatic selection of markers and the watershed transform give good results, and the method requires very few interaction with the user. Another advantage of this approach is to allow the user to choose the precision degree of segmentation he needs.

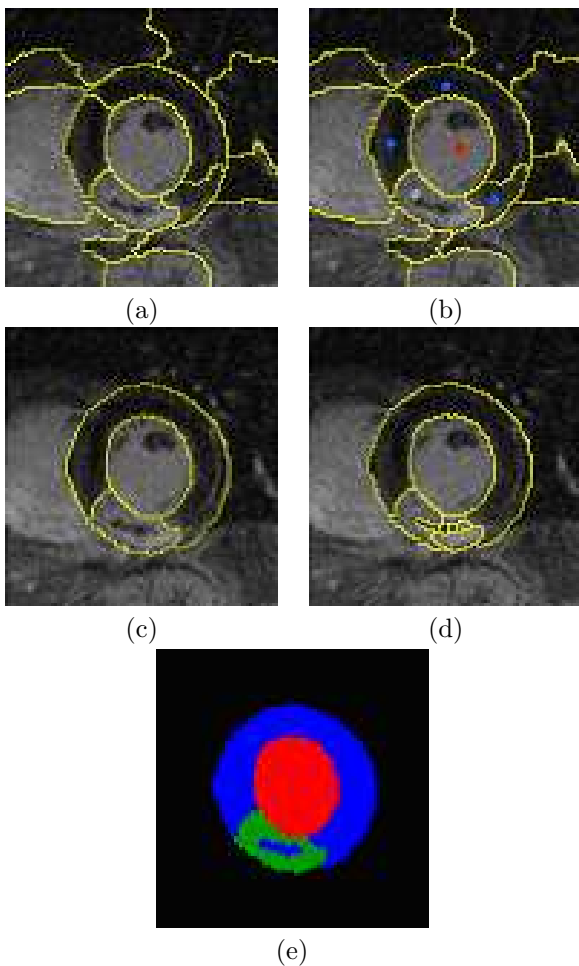


Fig. 8: Successive steps for recursive segmentation: (a): first automatic segmentation, (b): region labeling, (c): simplification, (d): regional segmentation at a different scale, (e): final result after labeling and simplification.

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Annex: New simple implementation of inter-pixel watershed transform

Motivations. Through a very simple implementation, we propose here the computation of an inter-pixel watershed from the classical implementation of Meyer[8]. Meyer proposes two types of watershed segmentation. The first one divides the image in regions which are in contact with each other (each pixel is marked with an identifier corresponding to each detected region), whereas the other one produces contour lines which separate the regions. The drawback of the second algorithm is an imprecision due to the arbitrary placement of a contour on an internal or external frontier of an object (see Fig. 10a,b). This imprecision on boundaries is small (1 pixel) but may have importance on certain applications (for our application, a misplacement of 1 pixel on each boundary line during the segmentation process creates an error of 10% on the volume calculation). So, we give an implementation of a watershed line that is not arbitrarily placed on pixels but only on inter-pixels. Moreover, during the segmentation process, the user may want to have on the same screen the original image in grey-scale and the current partition of the image (to control the placement of frontiers). The easiest manner to do this is the superimposition of the two images. With a classical segmentation in region, this visualisation is not possible except through manipulation of layers with transparency properties, which makes the precise localization of frontiers difficult. Our solution, which consists in working on a double-resolution image, makes it possible to visualize both the original image and the computed

contours, and provides the same precision as a segmentation without contours.

Principle. To combine the advantages of a segmentation without contours (precision) and those of a segmentation with contours (visualization), we propose here to work in a grid with a doubled resolution (for each dimension) and to use the Meyer’s implementation of the watershed algorithm with boundaries. Between two vertically, horizontally or diagonally adjacent pixels of the original grid, we add a new element called an inter-pixel element. In this new space, the problem is reduced to compute a classic watershed with boundaries and to force the contours to pass only on inter-pixel elements. Then, the segmentation without contours is easily obtained by selecting only the elements that correspond to pixels of the original grid.

Illustration. The problems and solution cited above are illustrated in Fig. 10. Applying the Meyer’s

watershed with contours algorithm to Fig. 10(a) may cause a problem of misplacement of the watershed line (b), due to the arbitrary placement of the contour of a region on pixels belonging either to the internal or to external frontier of this region. Moreover, we can see that the dark region that is one-pixel thick at the left of the image is not well segmented, since the 2 dark pixels on the left are assigned to the white region. In (c) we illustrate a possible visualisation of the result of watershed computation in regions, in superimposition of the original image. With this technique, it is not easy to clearly see both the original and the resulting partition. Finally, in (d) the classical computation of watershed line with contours is made in the over-sampled grid, forcing the line to pass exclusively on inter-pixels. In (d) the watershed line is correctly placed and the visualisation of the segmentation is ergonomic.

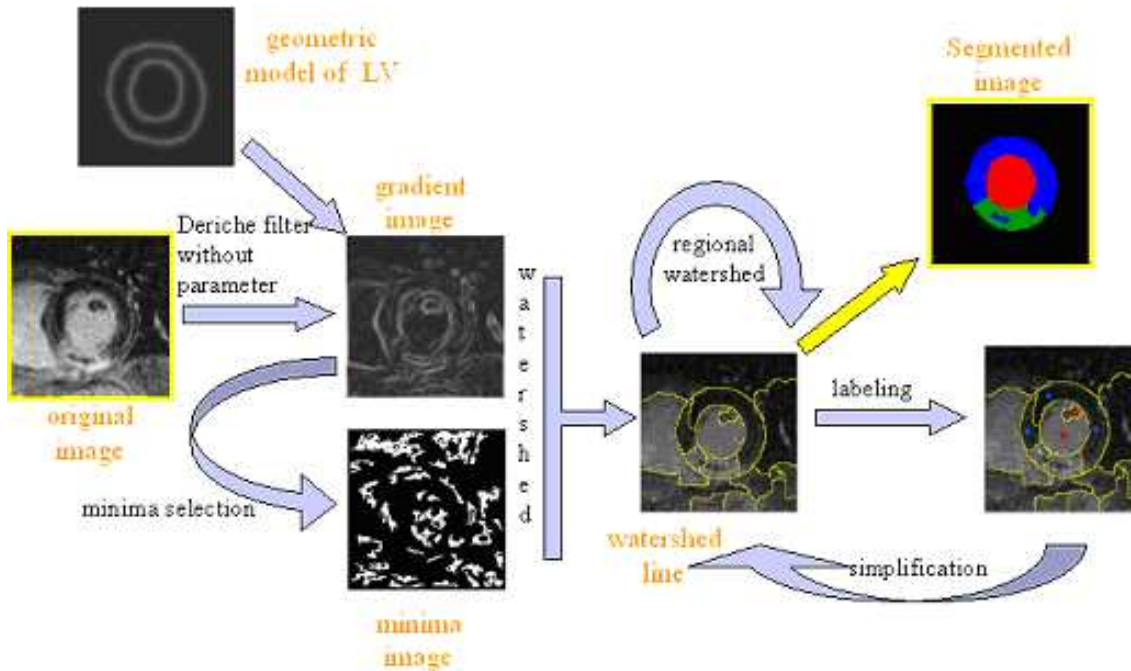


Fig. 9: Summary of the segmentation process.

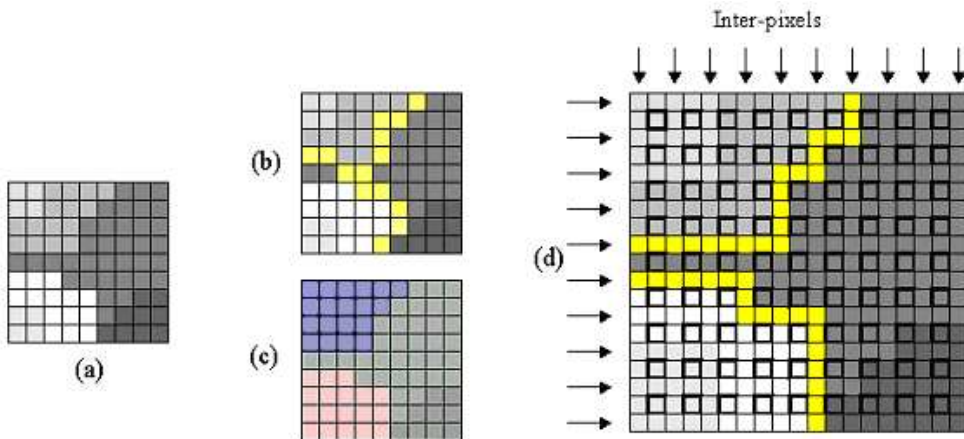


Fig. 10: (a): original image, (b): misplacement of watershed contours, (c): correct placement with no contours, (d): solution for both correct placement and visualization using inter-pixel elements.