

# Watershed based Detection of Multiple Sclerosis Lesions in MR Images

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## Abstract

*In this work an automatic method to discover multiple sclerosis (MS) lesions is presented. The technique makes use of an original implementation of the watershed based hierarchical segmentation algorithm applied to Magnetic Resonance (MR) images of the brain. The hierarchical approach is needed because of its merging phase where lesions are isolated from the over-segmented image produced by watersheds. Segmentation is preceded by a dedicated pre-processing stage aimed to eliminate noise and to locate the brain mass. The algorithm has been successfully applied to DICOM images obtained from MR devices using very different field strength and acquisition parameters.*

**Keywords:** *multiple sclerosis, watershed, brain, morphological filters, hierarchical segmentation*

## 1. Introduction

The framework of the present paper is the development of automatic tools acting as a support to the medical diagnosis process for affections that require medical imaging. Such tools should present to the doctor both a qualitative and a quantitative description of the disease and allow him to formulate more detailed diagnoses. Besides, their utilization makes it possible to better follow the evolution of the particular syndrome investigated because comparisons can be easily carried out between successive tests for the same patient. In particular, a novel methodology to the detection of MS lesions in Proton Density (PD) MR brain image is presented, which relies on the application of the hierarchical segmentation approach proposed by Beucher [6] that uses the watershed algorithm [14] followed by a merge process aimed to eliminate over-segmentation, and to isolate the brightest regions, corresponding to lesions pixels. Authors presented, in the past, an algorithm [2] to discover multiple sclerosis brain lesions based on a technique they called "two-channel fuzzy c-means" where both T2-weighted and

PD-weighted slices were used. Next a method which uses only PD-weighted images using the anisotropic diffusion filter [1] has been introduced where the filter coefficients were tuned with the brightness gradient histogram computed from the edge of some manually detected "sample" lesions. In the present work a watershed based segmentation algorithm is used, which has been never used for multiple sclerosis identification and is completely automatic. The use of only PD-weighted data set isn't a limitation because it contains all the information about this neurological stroke so this kind of acquisition is sufficient to identify lesions. In this way medical examination is faster because the doctor can avoid to execute multiple sequences to obtain T1- or T2-weighted images. The system is composed by a pre-processing step which consists of head identification and brain extraction. Each step reduces the amount of data in order to run faster in the following parts of the algorithm. Watershed algorithm is applied to the morphological gradient image of the slice and a hierarchical merging is applied to collapse over-segmented regions. The rest of the paper is arranged as follows. In section 2 some remarks are given about watershed algorithm and its use in medical imaging. Section 3 deals with the preprocessing phase, while section 4 details the hierarchical segmentation process, and in section 5 some experimental results are shown. Finally in section 6 some conclusions are drawn and future work is outlined.

## 2. Theoretical Remarks

Watershed algorithm was introduced by Lantu'ejou and Beucher [7] to segment digital images, while an extension to continuous functions was proposed by Najman [10]. It is a mathematical morphology tool, which considers a grey image as a topographic surface; in particular, with this theory, it is possible to segment an image, assuming that each gray level represents an altitude index. The surface is flooded by water starting from its local minima. Water fills all the catchment basins induced by the surface shape, and some "watersheds" are built along the separation lines between basins in order to prevent water merging. The actual

algorithm is an iterative procedure applied to the image pixels ordered by increasing gray level. For each level  $h$  each catchment basin is enlarged with those pixels with altitude  $h$  which are connected to the basin's pixels or which are inside the basin's "geodesic influence zone". Geodesic influence zone is defined as geometric locus of those points having a "geodesic distance" from a basin that is less than all the other ones. In turn geodesic distance is the minimum length path between two points  $x$  and  $y$  belonging to a simply connected set  $A$  that is totally included in  $A$ . All the pixels belonging to the same basin share a unique label. All the pixels not included in any basin at level  $h$  are to be considered new regional minima at level  $h$ , each having a new label. In fact they cannot be reached without climbing the surface and descending again to level  $h$ . All that points that are exactly half-way between two catchment basins are labelled as watersheds. Vincent and Soille [14] introduced an efficient implementation of the algorithm based on a FIFO queue structure used to perform fast computation of geodesic distances. Watershed transformation has been used to segment aerial photos, iron granulometry, cells images and so on. All these kinds of images present well distinct objects whose pixels have almost the same gray level. In medical imaging this property pertains to images showing large pathological tissues. In [15] Warscotte et al. use the directional watershed transformation applied to a 3D brain MRI data set affected by noise. Paulus et al. [11] apply watershed to time series of thermal images of the skin. They use a modified version of the algorithm proposed by Vincent and Soille with a different method for labelling pixels. Wegner et al. [16] use an iterative method based on graphs to extract the contour of a neoplastic formation located inside the thoracic region. In this work a comparison is made between an interactive version of the approach involving many experts and a completely automatic one. Heirman et al. [9] use watersheds to find line segments which separate two neighboring catchment basins, and a Hopfield neural network to select the best matching line segments to butterfly shape of the spinal cord shown in transversal section. Riddell et al. [12] performed a multi-resolution application of the watershed algorithm to segment noisy PET transmission images. Ghosh et al [8] apply the watershed algorithm to MR images of the knee after a preprocessing which consists of a low pass filtering while Zhu et al. [18] uses a combination of watersheds and active contours. Yim et al. [17] compare methods based on active contours and watershed to identify metastatic liver lesions using CT images. Finally, Sijbers et al. [13] combine the use of anisotropic diffusion filtering and watershed to perform 3D segmentation on a MR volume of a mouse brain. The application presented in this paper is oriented to the identification of small regions as a MS lesion can be. The key idea is that lesions in PD-weighted images have a strong brightness gradient with

respect to surrounding pixels, and a uniform gray level. A zonal technique like watershed is well suited to devise them, despite their size.

### 3. Pre-processing

The watershed algorithm must be applied only to the brain tissues without skin, bone and fat; so an original algorithm has been developed to extract encephalic mass without damaging the actual brain contour. The algorithm deals correctly with those parts, like eyes, which are strongly connected to the brain. Really, we don't need to identify exactly the brain contour, but only deleting extra-encephalic tissues. Even if a few cortex pixels are cut off, it's no matter because the lesions are deeply inside the brain. The method we present is very fast and simple to implement and works fine over all our data set. This method consists of two parts: background suppression and morphological brain identification.

#### 3.1. Background Suppression

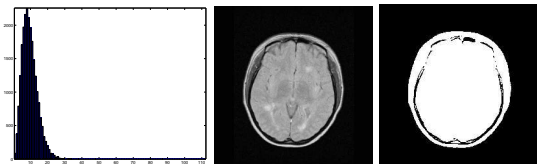
Brummer [3] has shown that the background noise in a PD-weighted image has a Rayleigh probability density function:

$$p(x) = \frac{x}{\sigma^2} \cdot e^{-\frac{x}{2\sigma^2}} \quad (1)$$

where  $\sigma$  is the standard deviation of white noise. Given a sample data vector  $\mathbf{x}$ , the maximum likelihood estimator of this parameter is:

$$\sigma = \sqrt{\frac{1}{2N} \sum_{i=1}^N [x(i)]^2} \quad (2)$$

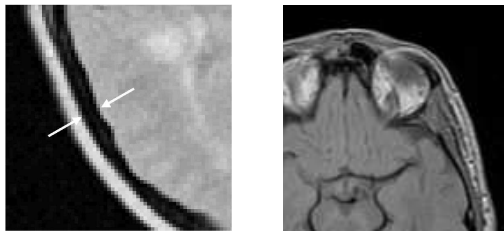
If a threshold starting from  $\sigma^2$  is performed, the binary image will contains only the head with some holes due to threshold operation. Performing a filling of this regions a mask of the head will be obtained in this simple way.



**Figure 1. From left to right: background histogram; original image; image after thresholding**

### 3.2. Brain Identification

The reason for this phase of the algorithm is that the skin has high intensity pixels which are identified by the watershed algorithm with a lesion-like grey level. As you can see from fig.2a, the encephalic mass is separated from external tissues by the skull which appears with low gray level. At first sight, it can be easy to separate the brain from the other tissues but it is not always true. For example, in fig.2b you can see that the eyes are directly attached to the encephalic mass. This fact doesn't allow to apply directly a threshold so we need an algorithm which permits to enlarge the skull region in order to separate external tissues which are attached to the brain. A fundamental paper on brain extraction is [5] where an approach based on "contour snake" opened the way to other algorithms like Brain Extraction Tool (BET) [4] where an active and deformable model is used for the same goal. These methods are sophisticated with high degree of precision; unfortunately these performances are obtained paying an heavy computation time.



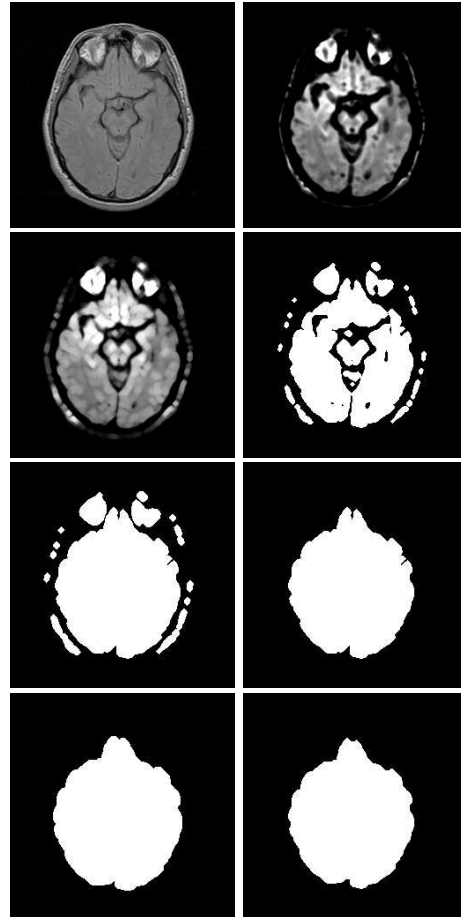
**Figure 2. a) arrows show skull region; b) eyes are attached to encephalic mass**

We prefer for our work a method which sacrifice a little of precision to obtain a very fast brain extraction. A method based on morphological filters applied on the entire volume is shown in Brummer, but we present an algorithm to extract the brain using one slice a time. In this way you doesn't need the entire volume but you can perform our algorithm using only one slice. The algorithm starts from the image obtained in the background suppression phase, and it is detailed in the following algorithm.

1. repeat 2 times
  - (a) apply an erosion with a 3x3 cross structuring element
  - (b) apply a square transform to the image pixels
  - (c) use a 3x3 blurring filter to reduce erosion artifacts
2. apply 2 times a dilation using a 3x3 cross structuring element
3. perform a two clusters fuzzy c-means segmentation [2] on the PD image; pixels are selected using the binary mask obtained in the previous section, to avoid background pixels
4. extract the cluster whose centroid is the highest one with respect to the dynamic range of the image grey levels
5. apply a binary transform to the image, setting to 1 each pixel whose membership to the cluster is higher than the other one

6. fill the holes and dilate using 3x3 cross structuring element
7. select the biggest 4-neighbor connected component
8. Dilate using 5x5 cross structuring element and fill the holes
9. erode using 5x5 cross structuring element

After binary transform a dilation is necessary because the cerebrospinal fluid has low intensity gray level in some PD-weighted images so encephalic lobes may be split by the fuzzy c-means algorithm. For the same reason we perform a dilation after the last erosion filter because the fluid is also present in the peripheral zone of the brain.



**Figure 3. First row: original, step1 - Second row: step2, step5 - Third row: step6, step7 - Fourth row: step8, step9**

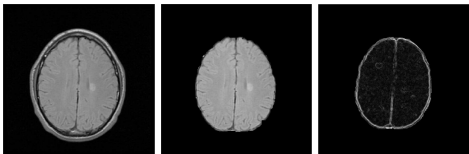
### 4. Hierarchical Segmentation

Watershed is applied to the topographic surface obtained from a morphological gradient image. We use the morphological gradient filter in order to enhance edge points which will be labelled as watersheds. As a consequence, low

variation regions inside these contours will be our catchment basins. Lesions are the most suitable candidates to be detected as single regions by the watershed algorithm. The definition of morphological gradient is based on two operators of mathematical morphology: erosion and dilation; in fact, if the image is represented by a function  $f : N \cup \{0\} \times N \cup \{0\} \rightarrow N \cup \{0\}$ , and if we consider a structuring element  $B$  (for example a 3x3 square) then the morphological gradient is given by:

$$g(f) = (f \oplus B) - (f \ominus B) \quad (3)$$

where  $\oplus$  and  $\ominus$ , are respectively the dilation and erosion. The next figure shows the effect of the morphological gradient to a PD-weighted MR image using a 3x3 square structuring element. Direct application of watershed suffers from



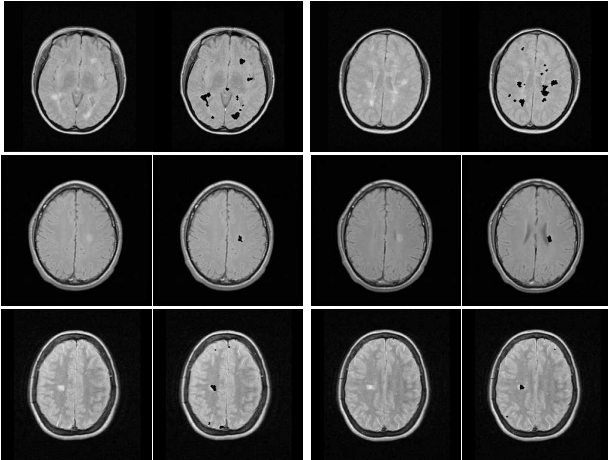
**Figure 4. From left to right: PD-weighted MR image; brain image; morphological gradient image**

over-segmentation because the brain structures induce in the image a continuous changing in the gray levels values. Also lesions can be split if they are too small because they have more than one pixel selected as regional minimum. We implemented a hierarchical segmentation approach inspired to the work of Beucher, that makes use of a merge process allowing to group adjacent catchment basins if their gray level is "similar", that is the absolute value of the difference between their gray level is less than a threshold. Merging is composed by three steps: mosaic image determination, computation of the Region Adjacency Graph (RAG) and grouping of similar basins. The mosaic image is obtained adding a label to each catchment basin which is the gray level that the original image has in the correspondent minimum point. Each uniform region can be considered as a dowel of a mosaic. RAG is computed from the mosaic image. Every node represents a region of the mosaic image, and there exists an arc between two nodes if they are adjacent. Every arc is labelled with a cost representing the dissimilarity between the two regions. In particular, the dissimilarity function that has been applied is  $\zeta(i, j) = |\nu(i) - \nu(j)|$  where  $\nu(i)$  is the  $i$ -th region gray level. Starting from the graph the adjacency matrix can be obtained where the rows are the starting nodes, the columns are the arrival nodes and the generic element located in  $(i, j)$  contains the cost  $\zeta(i, j)$  for the arc connecting nodes  $i$  and

$j$ . The cost between two nodes is set to  $\infty$  if they aren't adjacent. The matrix is symmetric because the graph is a-directional, and all the main diagonal elements are null. The adjacency matrix is used for the actual merging. This process relies on the idea that we have to group all the regions with low gray level in order to isolate lesions that are greatly dissimilar from the surrounding tissues. Starting with the catchment basins with the lowest gray value, only the adjacent region with minimum cost between all those having a dissimilarity less than  $\theta$  must be merged. The value of  $\theta$  is selected on the basis of the strength of the magnetic field used in the MRI device. Low field devices are noisier than high field ones and can have severe dis-homogeneities in their Field of View (FOV) so a more relaxed threshold has to be used to group the basins. Merging of two regions results in the elimination of the corresponding couples of rows and columns from the adjacency matrix. Each new region has to be labelled with the lowest value of the original ones. The graph and the adjacency matrix must be recomputed considering the new merged region and a new deleting step can be performed. The process terminates when no more regions can be merged. As a consequence, a lesion split in several high brightness basins will be recognized as a unique element because they cannot be merged with any contiguous region.

## 5. Experimental Results

The algorithm has been applied to a large data set coming from different machines. DICOM files have been extracted from a GE 0.5T device (Spin Echo sequence, slice thickness 6mm,  $t_r = 2500ms$ ,  $t_e = 40ms$ , FOV 256x256 pixels) a GE Signa 1.5T device (Spin Echo sequence, slice thickness 4mm,  $t_r = 1800ms$ ,  $t_e = 15ms$ , FOV 256x256 pixels) and an open coil Hitachi AIRIS-II 0.3T device (Fast Spin Echo sequence, slice thickness: 5mm,  $t_r = 4600ms$ ,  $t_e = 20ms$ , FOV 256x256 pixels). Images exhibit very different gray levels dynamic ranges due to the variability in the acquisition times, and to the different noise amount. Despite these variations, all the lesions have been carefully and automatically detected after an initial tuning phase to select the best value for the aggregation threshold  $\theta$  when merging regions in the mosaic images. The  $\theta$  value can be considered as a device-dependent parameter, and its evaluation has to be performed only once, when all the acquisition parameters have been set. Figure ?? shows some segmentation examples. All the system has been developed on a MATLAB R.13 version 6.5 platform running on a AMD Athlon 2GHz processor equipped with MS Windows XP. Execution times of the whole process as MATLAB un-optimized code are about 90s per image.



**Figure 5. From top to bottom: two segmentation outputs (left and right) for a 0.5T, 1.5T and 0.25T open coil scan**

## 6. Conclusions

A novel technique to segment MS lesions in MR brain images has been presented, that is based on an original preprocessing aimed to suppress background noise, and non interesting tissues, and an original implementation of the watershed based hierarchical segmentation proposed by Beucher where a new merging scheme for mosaic images has been proposed. The presented medical imaging application is a completely new one: in fact, other watershed implementations in the literature have been devoted to segment large regions, and not to isolate subtle lesions. Future work will be oriented to extend the algorithm to deal with 3D volumes, and to devise a unique criterion to choose the value of  $\theta$ . As an example, this value could be set according to a statistic analysis of the brightness gradient distribution across the edges of some sample lesions extracted manually with the help of an expert.

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