Automatic segmentation of focal lesions in the brain, using artificial intelligence methods

Radim Burget, Ondrej Smirg, Milos Kerkovsky, Zdenek Smekal, Andrea Sprlakova-Pukova

Abstract—**Multiple sclerosis is a chronic inflammatory demyelinating disease of the cerebral white matter and spinal cord. This paper describes the first results that were achieved by using an automatic method for the segmentation of affected areas, using data obtained by methods of magnetic resonance imaging (MRI). Methods of artificial intelligence are used to achieve high accuracy in the identification of lesions in the brain.**

Keywords — **Computer Vision, Image Processing, Artificial Intelligence, Magnetic Resonance Imaging, Sclerosis Multiplex.**

I. Introduction

The paper is focused on the issue of automatic tissue segmentation of biomedical image data, which are affected by the multiple sclerosis disease. Image data are obtained using the methods of MRI. MRI is an imaging method that makes use of the fact that protons have their own torque spin. The advantage of MRI is high soft-tissue resolution, which CT (Computer Tomography) does not achieve. Currently most of CT devices have the advantage of better space-geometric resolution. MRI can achieve such a resolution only on technically advanced devices at the cost of longer measurement of individual MRI sequences. A considerable disadvantage of MRI is the time-consuming examination, where for most of the sequences (data acquisition) the patient is required to remain lying quietly. A great advantage of MRI is clearly the absence of ionizing radiation. Specific examination is performed using an MRI device with RF coils that are applied to a certain region of the human body. The field of view can be obtained in the greatest detail possible by setting appropriately the technical parameters. Each measurement is always made up of several acquisitions in different planes, the measurement sequences are always chosen to best display the pathological process under consideration.

Multiple sclerosis is a chronic autoimmune disease in which a disintegration of myelin sheaths is involved. The myelin sheaths act in the brain as an insulating layer for the communication path**s** of neurons. Their disintegration leads to the axons being unable to effectively transmit nerve impulses. When the disease appears, "scarring" in the white matter of the brain can be found. The "scars" arise in the areas of inflammatory deposits (or lesions), where the inflammation has subsided. Based on these white matter lesions in the brain or spinal cord the disease is diagnosed and, depending on the size of these lesions, the development of the disease is monitored and its treatment is selected [9]. Lesions can be measured just by the MRI method, where the T_2-weighted images show up as bright white areas. A disadvantage is that, in the sequences used, other "healthy" areas of the brain - such as liquor - have a high level of signal. For this reason, not only methods based on the identification of high-brightness areas are used but also other methods that identify the diseased areas by their shape. The main contribution of the paper is a newly designed automatic method that relatively precisely identifies the appearance of lesions in MR images. The method is based on a combination of image processing and artificial intelligence methods.

The paper below is subdivided as follows: Chapter II describes the state of the art, Chapter III indicates the way training data and their segmentation are obtained, and Chapter IV gives the evaluation of results.

II. Related work

The methods used to identify lesions can be divided into expert, semi-automatic and automatic methods. The main advantage of the expert method, in which an expert medical specialist performs the identification, is precision and ability to deal with cases that are not standard. Its main disadvantage is the long processing time - estimated time is from approximately 4.8 hours to 9.6 hours per patient [4]. The semi-automatic methods partly solve the time-consuming problem: they can be used to pre-process a set of images during approximately 24.9 minutes per case [4]. The automatic methods are the best methods as regards the required time. A set of images is processed at a significantly higher speed, that is the necessary time per patient is about 1 minute. The quality of identification will depend on the accuracy of the automatic methods. The most common method used for imaging the brain with this disease is the method of magnetic resonance imaging (MRI).

When comparing the quality of semi-automatic and automatic segmentation methods, the expert processing, which is realized by manual marking, is usually considered as default ideal state. The other methods are then compared

Radim Burget, Department of Telecommunications, Brno University of Technology, Purkynova 118, 612 00 Brno, Czech Republic. E-mail: burgetrm@feec.vutbr.cz

Ondrej Smirg, Department of Telecommunications, Brno University of Technology, Purkynova 118, 612 00 Brno, Czech Republic. E-mail: smirg@feec.vutbr.cz

Milos Kerkovsky, Department of Radio-diagnostics, Faculty of Medicine, Masaryk University and Faculty Hospital Brno, Czech Republic. E-mail: mkerkovsky@fnbrno.cz

Zdenek Smekal, Department of Telecommunications, Brno University of Technology, Purkynova 118, 612 00 Brno, Czech Republic. E-mail: smekal@feec.vutbr.cz

Andrea Sprlakova-Pukova, Department of Radio-diagnostics, Faculty of Medicine, Masaryk University and Faculty Hospital Brno, Czech Republic. E-mail: asprlakova@fnbrno.cz

using the Dice Similarity Index (DSI), which takes values from zero to one [8]. The higher this index, the closer to the ideal case the method under study is. The calculation of DSI can be done as follows:

$$D_{\text{DSI}} = \frac{2\,(A \cap B)}{A + B} \ , \qquad (1)$$

where DSI for two sets of points A and B is calculated as twice the intersection between the two sets over the total number of points. Set A is obtained via manual marking of medical data by medical experts, and set B is obtained as results of semi-automatic or automatic methods.

Well-known methods of segmentation are compared in references [5], [6] and [7]. However, the references say that the fully automated methods are not reliable; it is always necessary for medical experts to check the results obtained.

III. TRAINING DATA

A. Scanning device

Data analysis is performed on MR images taken from a Philips tomograph. A new sequence called VISTA (Volume ISotropic T2W Acquisition) is used, with whose help a 3D matrix with a resolution of 1.0 mm x 1.0 mm x 1.0 mm can be obtained, and up to 160 slices of the head can be made, with achieved times $T_{\text{R}}/T_{\text{E}}$ = 2500/900 ms. The sequence is intended solely to display the head with the focus on the brain. Using the sequence we can get these 160 slices with a high signal-to-noise ratio. The images are useful for automatic data processing, because of the high contrast of tissues, and therefore these areas can be segmented very well. Moreover, they provide a higher number of slices compared with the conventional sequences used, where the number of slices is about 13. Figure 1 shows the same slice obtained using the VISTA and T_1-weighted sequences. Figure 2 shows a brain slice with marked lesions.
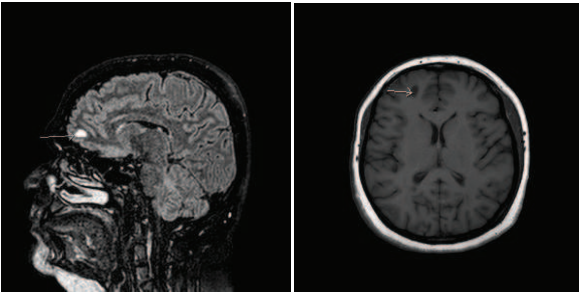

Fig. 1.   Slice obtained by the VISTA sequence (left) and by the conventional sequence weighted by time T_1 (right).

The VISTA sequence is useful for measurements in the brain areas, and therefore it is also used for the diagnosis of multiple sclerosis.

B. Marking the training and test data

For training and testing the results of VISTA-sequence measurement for 3 patients were available, 160 slices were measured by each sequence, 480 images were obtained altogether. The method was trained on 10 images and tested on 20 images. The selection of all samples was inappropriate, since the adjacent sections are usually very similar, and have no significant benefits for the training itself. For this reason,

various medical findings were selected, and one representative was always chosen from them.
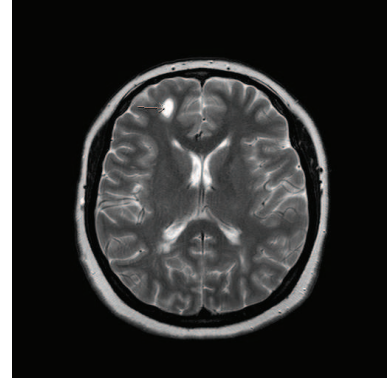

Fig. 2.   Brain slice with marked lesions (T_2) [9].

To obtain information from physicians, a program for marking the areas was designed. The program enables marking up to 3 different types of tissue and sending them safely and automatically to remote data storage for analysis. Based on these data, the existence of lesions can be statistically evaluated. Figure 3 shows an example of image marked by the labelling program, which serves as a pattern for training.
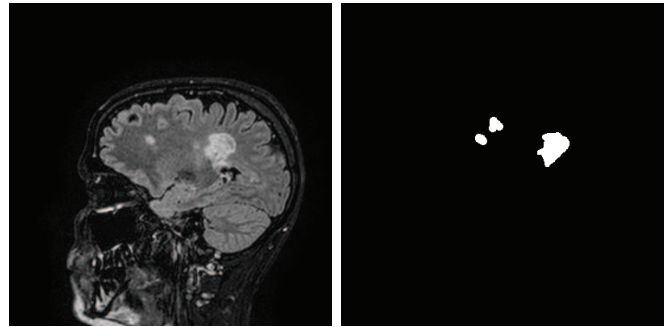

Fig. 3.   Input data: an original image (left) and a mask with marked areas with lesions (right).

The marking program was proposed in the JAVA environment and its core is formed by a system for the segmentation of images, developed by the American National Institute for Health and referred to as ImageJ. ImageJ is distributed with public-domain license. The actual algorithm was programed in the RapidMiner environment, which also works on the JAVA platform. The RapidMiner environment was extended by image processing to be compatible with the ImageJ software tool.

IV. PROPOSED MODEL

The proposed segmentation procedure is divided into three parts: first, the field of view is selected where the disease may occur, i.e. the brain while the other undesirable components, such as the jaw, eyes, etc. are removed from the image. Consequently, the segmentation of the remaining images is performed and segments are only selected that meet the conditions for marking the lesion.

A. Selection of brain regions from MR data

The block diagram in Fig. 4 shows how to select the field of view and eliminate all the other artefacts. The original image is first segmented using the method of statistical region

merging [2]. It is a region-based detection method based on the similarity of pixels around every point. Similarity is usually evaluated according to image brightness and statistical properties of pixels. The method proceeds from the bottom upwards, i.e. from one pixel to the whole segment. First, the so-called seed pixels are spread in the image by a suitable algorithm. The segment arises by iteratively connecting pixels and the already created segments into larger areas. The combined field is then applied to the original image. The number of independent random variables Q was set to 32 and the smallest possible image size was set to 10% of the original image [2]. In order to avoid too sharp transitions, the Gaussian blur with a core of 3.5 was applied to the mask.
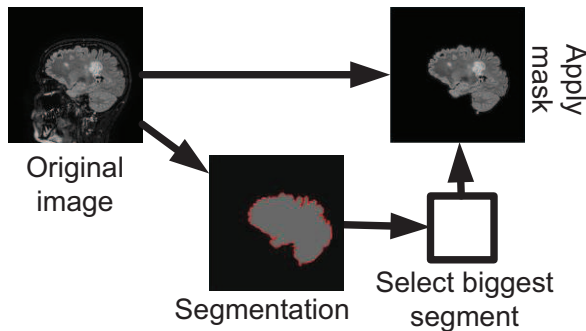

Fig. 4. Block diagram of how to select the field of view and eliminate interfering artefacts from the image.

B. Segmentation of brain regions

When the disturbing parts of the image have been removed, the granular image segmentation can be performed. Several methods were used for the segmentation: the Markers Watershed-controlled method, the K-mean clustering method, the above-mentioned region-based method, and the level set function method. The Markers-controlled Watershed method considers the image as a "terrain" where the bright parts are the "mountains" and the dark parts represent the "lowlands". Using a suitable algorithm, local extremes are searched for, and so-called "dams" are formed in this region. "Pouring water" begins to flow to designated places, and the given areas are flooded. The segmented parts of the image are defined by flooded areas. The method is very effective for images that do not contain noise, and is used a lot for the segmentation of MR brain images. However, the method does not take into account the shape of objects and is controlled by mere brightness values. This can cause an incorrect segmentation of objects that have similar luminance values but differ mainly in shape.

The second method is the K-mean clustering method, which is based on determining the centre of a group of pixels of similar properties. In our case image brightness is again chosen as the leading property. One of the main parameters of the method is the number of groups into which individual pixel areas are divided (the number of "colours" into which the image will be divided). Another parameter which is looked for is the centre of these groups. The main drawback of this method is the intuitive setting of layers into which the image should be split. The number of levels cannot be determined automatically, and even the choice of group centres affects the results of this method. Therefore it is

necessary to find an optimum setting for each object, which is sometimes quite difficult.

The region-based segmentation methods are based on detecting pixel similarity with respect to some appropriately chosen property. The brightness or statistical properties surrounding the point can be chosen as the property. The method proceeds from the bottom upwards, i.e. from one pixel to the whole segment. First, seed pixels in the image are spread by a suitable algorithm. The segment arises by iteratively connecting pixels and the already created segments into larger areas.

The fourth segmentation method is the method using the level set function. The method is based on the numerical solution of discretized partial differential equations. The steady-state solution is a curve that encloses the object in the image on the basis of visual information. Recently, these approaches have increasingly been used, especially for the segmentation of medical images. The basis can be seen in the level set equation (Stanley Osher) [12]:

$$\frac{\partial \phi}{\partial t} + F|\nabla \phi| = 0 \, , \qquad (2)$$

where $\phi(t,x,y)$ is the level set function which develops in time t according to speed function F. We determine the resulting curve as the cut of multi-dimensional level set function for zero level. The resultant curve is expressed by the relation:

$$C(t) = \{(x, y) \mid \phi(t, x, y) = 0\} \quad . \qquad (3)$$

Although the segmentation method using the level-set function is very efficient, the method is unfortunately sensitive to the setting of the parameters of the level set function, mainly to the setting of the boundaries of convergence. The setting of boundaries is very important for finding the segmented area. Moreover, this method ignores the spatial distribution of objects, and therefore can exhibit segmentation also in those parts which are not related to the desired tissue. A parameter setting was used with which the segmentation does not divide the image into very small parts and, at the same time, does not neglect smaller segments that represent medical findings. As result of this process, an average of 14.8 segments per frame is generated, where a positive finding is in 14% of the segments on average.

C. Selection of segments containing lesions

In the third step, only segments that represent a lesion in the brain are selected from all the segments. For this purpose, 28 different statistical parameters of each segment have been calculated that describe their properties. Using artificial intelligence tools, models have been created that distinguish which segment contains medical findings related to multiple sclerosis, and which segment does not.

To select the best classifier, the following algorithms were tested: the Random Forest algorithm, Support Vector Machines (SVM) algorithm, k-Nearest Neighbours algorithm, Naive Bayes Networks algorithm, One R algorithm, and Artificial Neural Network algorithm. The best algorithm was selected based on the recommendation in reference [3]. The accuracy of the classification of each lesion is shown in Table. I.

TABLE I

Algorithm	Accuracy
RandomForest-Weka	0.973
SVM	0.966
k-Nearest Neighbors	0.966
Naive Bayes	0.932
One R	0.885
Neural Network	0.959

D. Visualization of marked areas of lesions

Finally, the segments selected are highlighted in the original image. This is indicated in red colour. The results are shown in Fig. 5.

V. CONCLUSION

The paper deals with an automatic method for segmenting multiple sclerosis lesions in cerebral white matter, which is measured on an MR tomograph. The VISTA sequence (Philips) was used to obtain individual slices. The sequence exhibits both higher precision (higher number of slices) and higher signal-to-noise ratio compared with the results of sequences used up to now.

In the area of semi-automatic and automatic diagnosis of multiple sclerosis many algorithms have been proposed that focus primarily on the luminance characteristics of lesions in MR images. References [10] and [11] describe automatic and semi-automatic methods that segment lesions with an average efficiency of 85%. Our method uses the VISTA sequences, which allow increasing the scanning accuracy and the number of slices scanned. In addition, a marking program has been proposed that allows obtaining a quality database showing marked diseased areas of patients. This accurate marking is performed by medical experts, and it increases the accuracy of the automatic segmentation method for monitored areas. Based on such prepared data, the proposed method can construct a probabilistic model that captures the essential characteristics of the segmented object. The accuracy of the method depends on the number of images from which the probability model is generated. The more images exist, the higher accuracy and reliability of this model are obtained. Therefore, in future work we intend to focus on extending the marked training set and on setting the optimal default parameters of the segmentation method.

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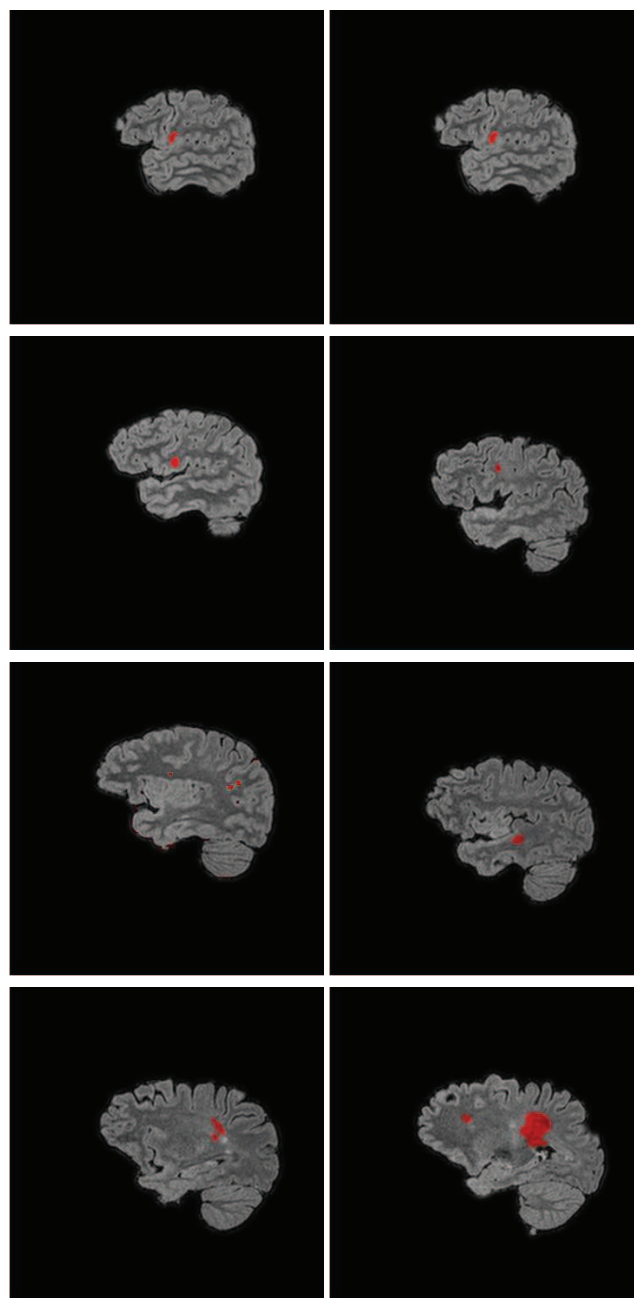
Fig. 5. Resultant designation of lesions to identify the location of brain affliction.