A Fast Method of Separation of the Noisy Background from the Head-Cross Section in the Sequence of MRI Scans

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The paper presents a new method of removing the noisy background from the sequence of magnetic resonance imaging (MRI) scans. The sequence of scans is required in order to monitor a passage of a contrast agent through the brain tissue. The scans contain the noisy head-cross data and also the noisy background data. The latter has to be removed and excluded from a further analysis. It is achieved by applying some basic morphological operations to the previously binarized MRI scans. The results of separating the background from the sequence of scans are presented in the paper. The scans binarization method is described and compared with the widely used Otsu method. The proposed method of the noisy background separation is easily applicable, efficient and does not need any sophi-sticated calculations.

K e y w o r d s: DSC-MRI brain measurements, MRI images binarization, background separation

1. Introduction

MRI techniques are a powerful tool in providing the characterisation of brain tissue perfusion. The term "perfusion" is used for a set of descriptors of the process of oxygen and nutrient delivery to tissues. Perfusion is an important indicator of tissue viability and functioning. Vascular or tissular structures are altered in a pathological tissue when compared to a normal tissue. For example, a faster growth of many

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tumours is accompanied by an increased number of vessels along with the increased permeability and flow. MRI measurements can help one to improve the characterisation of tissue at the risk of disease; as a result an earlier and more efficient diagnosis is possible. Perfusion imaging using MRI measurements is adopted in a wide variety of clinical applications including characterisation of tumours, acute stroke lesions, dementia, Alzheimer's disease and many more [1].

The DSC-MRI technique involves the intravenous injection of a dynamic susceptibility contrast (DSC) agent (Fig. 1) and the sequential measuring (scanning) of the signal during the passage of the bolus from the site of injection, through the circulatory system and the middle cerebral artery (MCA) into the region of interest (*ROI*) in the brain. There is a number of perfusion parameters, calculated on the basis of the raw MRI data and then used for mapping their values, pixel by pixel, over the head cross-section. These parameters are: *CBF* (cerebral blood flow), *CBV* (cerebral blood volume) and *MTT* (mean transit time) [2].



Fig. 1. The schematic diagram of the path taken during the first pass by the injected contrast agent in the DSC-MRI measurement of brain

When mapping of the descriptors is the goal, automatic data processing has to be performed over the whole scan which consists of the background and the head-cross section. Typical MRI scans are shown in Fig. 2 a1), a2) and a3). The dark pathological region (tumour) inside the brain tissue is similar to the background area, and the light disturbances in the background (light dots out of the head-cross) are of similar brightness to plenty of pixels inside the head-cross. Therefore, before the automatic analysis of the MRI scans starts, the preliminary processing of the scans sequence should be performed because the distinction between the background and the head-cross section is needed. The DSC-MRI signals that appear in the head-cross section and in the background (disturbances) may look very similar and it may not be possible to differentiate them without complicated and hard to implement methods of signal processing. During medical diagnosis, which is made on the basis of computed parametric maps, a diagnostician can obviously see which region of the image is a brain cross-section and which is a background, but during the earlier data processing every



pixel from the sequence has to be processed, while processing the pixels that belong to the background is useless, is a waste of time. Brain MRI sequence images may comprise of even dozens percent of the background. Performed tests showed that computation of the higher accuracy [3, 4] parametric maps (CBF, CBV and MTT) may last from a half to a few hours [4]. When the background pixels are excluded from the further data processing, the time of that processing can be proportionally shortened. It inspired our effort to remove the noisy background from the sequence of MRI scans and introduce such the method.

The described algorithm is designed to be used at the very beginning of sequence processing. The specificity of the brain MRI images is that they are (to some extent) predictable with respect to their shape, size and the object placement. The method is not designed to remove the noise from processed images. Our fundamental assumption was to introduce a simple, reliable and easily applicable method of background rejecting on basis of the specificity of brain MRI images. In the whole process of parametric maps computations, we propose to use at first the described procedure and then, to process the sequence using more sophisticated methods with the certainty that every pixel taken into consideration is the pixel that belongs to the brain cross-section region and that no time and power is wasted unnecessarily for the background data processing.

The method is designed to be used with sequences of MRI images and not with a single MRI image. There are many approaches to denoising of the MRI images presented in the literature, including [5-8], but they are particularly focused on single images, not on the whole sequence of MRI scans. Furthermore, these methods are complicated and time consuming. Even if the amount time needed by these algorithms to process one image could be acceptable, it may be relatively long when processing the whole MRI sequence containing not less than tens of images [1, 2]. In the DSC-MRI measurements, where the diagnostic information is extracted from the signals that represent bolus passing through the brain, noise removal is performed during the further analysis of that data [3, 9, 10]. This approach is justified by a priori knowledge that we have about functioning of the human body and physiological models designed to mimic the body functioning [3, 10, 11]. We can use this knowledge to filtrate the specific data with smaller risk of losing diagnostic information contained, for example using stochastic filtration [9]. That is why we propose the method which only discriminates the background in the sequence, without any influence on the DSC-MRI measurements data of diagnostic importance.

Proposed in the paper method of distinction between the background and the head-cross section utilizes the two basic morphological operations: erosion and dilation, more precisely their compositions i.e. opening and closing. The operators of morphological processing are particularly useful for the analysis of binary images, so the MRI images need to be previously binarized. The original eight-bit 'greys-cale' MRI images have to be converted into one-bit 'binary' images. To discriminate

the greyscale images i.e. to convert them into binary matrices, a method of global thresholding, based on a histogram analysis and processing, is proposed. The main advantages of the proposed algorithm are both its simplicity and speed. The expected results are obtainable with a rational amount of programming work and in a relatively short time.

2. Material and Methods

Magnetic resonance imaging is a brain scanning technique that generates cross-sectional images of a human brain. The scans reveal the distinction between different types of brain tissues (white matter, grey matter, arteries) as well as the distinction between normal and abnormal tissues. A tracer is injected as a bolus signal (see Fig. 1). Then dozens of the MRI scans are executed to show the time dependent changes in the tracer flow. The scans are used as the basis for a direct medical diagnosis or for further computations. Measurements were performed on a GE scanner with the following parameters of the sequence of scans: magnetic field 1.5[T], SE-EPI, 12 layers of size $5 \div 10$ mm, 60 measurement points, $TR = 1250 \div 1610$ ms, $TE = 32 \div 53$ ms. In this paper MRI sequence that consists of 50 images (scans) of resolution 128 by 128 pixels has been used. Three exemplary images (scans number 1, 22 and 50 from the sequence of 50 scans obtained) are shown in Fig. 2. For the final discrimination of the head-cross section from the scan area, all the 50 images are used. The second scan (scan 22 from Fig. 2a) is distinctly different from the two others: it shows the peak of the tracer flow. Used sequence comes from 40-year-old male patient.

3. Binarization

In literature [12–15] some problems with images binarization have already been presented. These problems arise mainly as a consequence of an unpredictable form of an image to be binarized. It concerns, for example, handwriting images [13] and document images [14]. On the contrary, the individual MRI brain images are comparable and predictable. We propose a method of global thresholding, based on a histogram analysis and processing. The method is dedicated, designed and verified, for MRI brain images binarization.

Three exemplary, out of 50, histograms of greyscale MRI images are shown in Fig. 2 b1), b2) and b3). Vertical parts (lines) of the histograms are omitted for aesthetical reason. The histogram of an image is a graph using 256 vertical values to represent the brightness levels b_l from 0 to 255. The darkest pixels relate to the brightness level $b_l = 0$, while the lightest relate to $b_l = 255$ and n_p is the number of pixels in the image of a particular brightness level. All histograms have two peaks. The left and larger peak represents the background dark pixels and the dark pixels situated inside the head-cross section. The right, smaller and more spread peak represents mainly the pixels of intermediate darkness from the head-cross section. The histogram, which has two noticeable peaks, is known as bimodal one [15]. The obtained bimodal histograms are then binarized with the use of a specially designed algorithm. Thus, the binarization steps are as follows:

1. The histograms are smoothed by the 2nd order low-pass Butterworth filter with the cut off pulsation equal to $\omega = 0.1$ [rd/s]. The Butterworth filter produces the flattest pass band response. It starts out extremely flat at the zero frequency and bends over near the cut off frequency f_n . Although the Butterworth filter has not an excellent phase characteristic, in the considered range of pulsation its time delay can be assumed to be constant. The performed tests using various MRI images showed that the selected cut off pulsation and order of the Butterworth filter occurred to be sufficiently good for smoothing the histograms. The smoothed histogram is much more convenient for further analysis, especially when there is a problem with an appropriate assigning of maximum and minimum of the histogram and of their derivatives. For filtering the Matlab procedure *butter*(N, ω_n) was used. The procedure enables us to design an N order low pass Butterworth filter, with the cut off pulsation ω_n . The procedure returns the filter coefficients in length N+1 vectors **B** (numerator) and A (denominator). The smoothed histogram from Fig. 2 b1) (N = 2, $\omega_n = 0.1$) is shown in Fig. 3. The second (lower) peak of the smoothed histogram will be used to determine the binarization threshold.

2. The filtered histogram is then differentiated. The minimum of the derivative curve (located on the left) is used for further fixing of the threshold position.

3. The threshold is positioned in half between the value of the right peak of the smoothed histogram and the value of the left minimum of the derivative curve. The threshold location is shown in Fig. 3.



Fig. 3. The location of threshold in the proposed binarization method. The solid line represents the smoothed histogram $n_p(b_l)$ and the dashed line represents the derivative curve dn_p/db_l

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The described procedure was applied to the subsequent 50 scans (images) and each scan has been binarized with the use of different, adequate threshold levels. As Figure 2 shows, there are such scans in the sequence that differ significantly from the others. The binarization of such images, using the same threshold level, may produce an incorrectly binarized image.

The result of binarization of an exemplary image (scan 1/50) using the method described in the paper is shown in Fig. 4 a). In Figure 4 b) the result of binarization of the same scan, by means of Otsu method of automatic thresholding is shown.

The Otsu method of automatic thresholding remains one of the most referenced thresholding methods [12, 16, 17, 18]; therefore it was used for comparison with the results obtained by means of the algorithm presented in the paper. The Otsu method selects the binarization threshold on basis of the weighted sum minimization of the within-class variances of the foreground and background pixels [12, 17].

Figure 4 shows that there is no considerable difference between results of the Otsu method (b) and the new method (a). The primary advantages of the proposed binarization algorithm are both the simplicity of the methods adopted and the effortlessness of their implementation. Tests performed with various MRI images show that the Otsu method results in a slightly lower threshold level and a consequently bigger number of white pixels in the image. The obtained blackout level $l_{b-a} = (n_b/n_a) \cdot 100\%$, where n_b is the number of black pixels and n_a is the number of all pixels in the image, was $l_{b-a}^{Otsu} = 73.9\%$ and $l_{b-a}^{New} = 75.1\%$. The binarization algorithm proposed in the paper is relatively simple and easy to implement. It takes effect in a fast algorithm performance. The numerous tests performed showed that the algorithm proposed in the paper is, depending on the image properties, 28-31%faster than the Otsu algorithm. The processing time is meaningful because usually a big number of MRI images are processed. There exist some known modifications of the classic Otsu algorithm, which can be faster [16, 17], but we have chosen the classic method as the most frequently cited reference method. It was not our aim to propose a universal thresholding method but to introduce a reliable method for specific application, the method which shows a comparable or better performance then the classic one.



Fig. 4. The scan number 1/50 from the processed DSC-MRI sequence after the binarization described in the paper (a) and after the binarization using Otsu method (b)

After binarization we received the images with basically distinguishable regions of the head-cross section and the background, but there are, as previously, some white pixels in the background and many black pixels in the head-cross section. We still need an image binary matrix, where "1" represents the pixel of the head-cross section and "0" represents the discriminated background pixels. To achieve the aim we suggest that the basic morphological operations of dilation, erosion, opening and closing should be adopted.

4. Morphological Processing

The field of mathematical morphology includes a wide range of image processing operators. The two most basic operations of mathematical morphology are dilation and erosion. These operators take two pieces of data as input: an image to be processed and a reference shape, known as structuring element, which is a matrix used for defining a neighbourhood shape and size. It is usually much smaller than the image being processed and has a simple shape, often one of the predefined ones like square, disk, diamond or cross. The central pixel of the structuring element identifies the pixel of interest, which is the one being processed and other pixels in the structuring element with values of 1 define the neighbourhood and they are taken into consideration in morphological processing. The structuring element can be of any size and may have an arbitrary shape and it determines the precise details of the effect of the operator on the processed image so, by choosing the shape and size of the element, we control the morphological operations sensitivity with respect to specific shapes appearing in the considered image. The structuring element *S* is swept over the binary image *B*. The pixel $B_{x,y}$, in each position (*x*, *y*), is subjected to some specific operations, which are stated below.

The *erosion* of the binary image *B* by the structuring element *S* is defined as follows:

$$B \otimes S = \left\{ x, y : S_{x, y} \subseteq B \right\}.$$
⁽¹⁾

The basic effect of the erosion operation on a binary image is eroding away the boundaries of the foreground region. Thus the areas of foreground pixels shrink in size, and the holes within those areas become larger [18, 19].

The *dilation* of the binary image *B* by the structuring element *S* is defined by the formula:

$$B \oplus S = \left\{ x, y : S_{x,y} \cap B \neq \emptyset \right\}.$$
⁽²⁾

The basic effect of the dilation on a binary image is enlarging gradually the boundaries of the foreground region. Thus the area of foreground pixels grows in size, while the holes within those regions become smaller [18, 19].

The operations of *closing* and *opening* are the combinations of erosion and dilation, both using the same structuring element. Morphological opening is erosion followed by dilation, while morphological closing is dilation followed by erosion. The application of closing and opening eliminates undesirable features of erosion and dilation which are decreasing (in the case of erosion) and/or increasing (in the case of dilation) areas of processed figures. Main features of opening and closing are:

- neither of the operations changes shape or size of big figures with smoothed edges,
- opening removes small objects and details from an image, and it can uncouple objects with thin connections,
- closing fills in waists and gaps inside a processed figure, and it can join objects that are close to each other as well [18, 19].

Figure 4 shows that in a binarized image there are some white pixels outside the head-cross section that represent the remaining background, and also some fragments of the scull contour that can be seen in non-binarized images in Fig. 2 as grey halos around the head cross-section. To remove the leftover pixels the opening operation was used. The effect of opening depends on an adequate choice of a large enough structuring element and on its shape. In that case, the requirement is fulfilled for the N_4 basic element:

$$N_4 = \begin{bmatrix} 0 & 1 & 0 \\ 1 & 1 & 1 \\ 0 & 1 & 0 \end{bmatrix}.$$
 (3)

As the result of performed opening operation all the leftover pixels are removed from the background.

After the background noise becomes eliminated, the next step of image processing is performed: the head outline needs to be marked off. It has been done with the use of the morphological closing operation, with the bigger than before structuring element.

In that case a disk-shaped structuring element, with the radius of 7 pixels, was used. It allowed us to fill in (with white pixels) all the black regions inside the headcross section.

Size of used structuring elements depends on the resolution of processed image. All the exemplary MRI images, shown in the paper, are of 128 by 128 pixel resolution. For images of higher resolution, the structuring element should be proportionally larger, preserving described shapes of elements, the shape of cross for opening and the shape of disk for closing. This assumption was verified by doubling and trebling the resolution of processed sequence and enlarging the used structuring elements proportionally. The received results proved its rightness. Binary masks received as the final effect (see Paragraph 5) of the algorithm application to the enlarged sequences have comparable shapes to the ones received while processing images with smaller resolution.

The final result of computations is a binary matrix (see Fig. 5) of the same resolution as the original image. White pixels represent the head-cross region and black pixels represent the background. Figure 5 shows that there are different boundaries of the head-cross region for different images. To obtain the final head-cross section, common for all the images, the same mask for all the scans has to be computed.



Fig. 5. Binary masks obtained for the processed scan number 1/50 (a) and the scan number 22/50 (b). The boundaries of the head-cross sections for the two different scans are different

5. Final Choice of the Head-cross Section

The result of MRI measurements is a sequence of scans differing from each other to some extent. Consequently, the results of binarization algorithm implemented to individual scans are also different. The aim is to obtain one final binary matrix from all the received ones. It is done by comparing all the previously received matrices and the selection of the pixels that appear in the same position with the occurrence at a particular (chosen) incidence level.

When too low incidence level is used (10% in that case), it results in obtaining too large mask. As a result, a thin black contour around the head-cross region appears. Using too high incidence level (90% in that case) causes that too small mask is found. Consequently, in some places around the head-cross region certain pixels may be missing. These effects are shown in Fig. 6.

In the paper the incidence level of 65% was used. The final mask obtained and then used for every scan to discriminate the background is shown in Fig. 7a). The head cross-sections of the three exemplary scans, separated with the final mask from Fig. 7a), are presented in Fig. 7b), c) and d).

The algorithm classifies 4754 pixels as the head cross-section pixels and 11630 pixels as the background pixels. It means that the presented method allowed to exclude 70.98% pixels from any further useless data processing.

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Fig. 6. The scan number 40/50 discriminated with too low (a), too high (b) and proper (c) incidence levels with enlarged fragments of these images showing described undesirable effects more precisely



Fig. 7. The final binary matrix (mask) used for every scan in the processed DSC-MRI sequence to separate the background (a) and head-cross sections of the three exemplary scans from the sequence separated with the that mask (b, c and d). The discriminated background is indicated with an inverse intensity map

6. Conclusions

The paper presents a new method of removing the noisy background from the sequence of MRI brain images. The whole image consists of both the head-cross section, which is essential for further analysis in medical diagnosis, and the noisy background, which is insignificant. The quality and speed of automatic analysis of the MRI images performance, in order to acquire a parametric map, requires getting rid of the undesired background and selecting the head-cross section. The number and size of the processed MRI images are large. Therefore, this is reasonable and desirable to make an effort to search for an adequate, efficient and fast method of images processing. Basing on some specific properties of MRI images, we proposed such a procedure and an algorithm of computation.

An advantage of the proposed algorithm is its simplicity, which was achieved due to the uncomplicated binarization algorithm and then basic morphological operations. Generally, problems in image processing appear as a result of an unpredictable shape of images to be binarized. The brain MRI images are a specific type of images, which are similar in contour and nature. Therefore using a complicated algorithm is not reasonable. Instead, very good results can be obtained with the simple and efficient algorithm presented in the paper.

Embedding the described method in the whole process of computations of parametric maps severely reduces the time of computation. Furthermore, it gives us certainty that no noise pixels from the outside of the region of interest could be mistakenly taken into consideration for calculation of the image descriptors used in medical diagnosis. The method can also have other applications in further image processing, for instance: segmentation, shape recognition etc., and the received binary mask can be used to discriminate the background and to select the head-cross region, at a very early stage of processing.

References

- Rumiński J., Kalicka R., Bobek-Billewicz B.: Parametric imaging in brain studies with the use of MRI and PET. (in Polish) Wydawnictwo Gdańskie, Gdańsk 2006.
- 2. Sorensen G.A., Reimer P.: Cerebral MR Perfusion Imaging.Georg Thieme Verlag, Stuttgart, 2000.
- Kalicka R, Pietrenko-Dabrowska A.: Parametric Modeling of DSC-MRI Data with Stochastic Filtration and Optimal Input Design Versus Non-Parametric Modeling, Ann. Biomed. Eng., 2007, March, 3, 453–464.
- Kalicka R., A. Pietrenko-Dąbrowska A., Lipiński S., Nowicki R.: Brain perfusion imaging with the use of parametric modelling basing on DSC-MRI data. Proc. 1st Intern. Conf. Inform. Technol., Gdańsk 2008.
- Awate P.S., Whitaker R.T.: Feature-preserving MRI denoising: A nonparametric empirical Bayes approach. IEEE Trans. Med. Imag., 2007, 29, 9, 1242–1255.
- Behzadi Y., Restom K., Liau J., Liu T.T.: A component based noise correction method (CompCor) for BOLD and perfusion based fMRI. Neuro Image, 2007, 37, 90–101.
- Lysaker M., Lundervold A., Tai X.: Noise removal using fourth-order partial differential equation with applications to medical magnetic resonance images in space and time. IEEE Trans. Image Proc., 2003, 12, 1579–1590.
- Pizurica A., Wink A.M., Vansteenkiste E., Philips W., Roerdink J. B.T.M: A review of wavelet denoising in MRI and ultrasound brain imaging. Curr. Med. Imag. Rev. 2006, 2, 2, 247–260.
- Kalicka R., Lipiński S.: Valuation of usefulness of Kalman filtration to improve noise properties of DSC-MRI brain research data. (in Polish) Pomiary Automatyka Kontrola 2008, 3, 118–121.
- Salluzzi M., Frayne R., Smith M.R.: Is correction necessary when clinically determining quantitative cerebral perfusion parameters from multi-slice dynamic susceptibility contrast MR studies? Physics in Medicine and Biology 2006, 51, 407–424.
- Smith M.R., Lu H., Frayne R.: Signal-to-noise ratio effects in quantitative cerebral perfusion using dynamic susceptibility contrast agents. Magn. Reson. Med. 2003, 49, 122–128.
- 12. Sezgin M., Sankur B.: Survey over image thresholding techniques and quantitative performance evaluation. J. Electr. Imag. 2004, 13, 1, 146–165.
- 13. Solihin Y., Leedham C.G.: The multi-stage approach to grey-scale image thresholding for specific applications. Internet site address: http://www.ece.ncsu.edu/arpers/.
- Wu S., Amin A.: Automatic thresholding of gray-level using multi-stage approach. Proc. Seventh Intern. Conf. Doc. Anal. Rec. 2003, 1, 493–497.

- Antoine Ch., Lloyd M., Antoine J.: A robust thresholding algorithm for halftone dots. J. Pulp Paper Sc. 2001, 27, 8.
- Lin K. Ch.: On improvement of the computation speed of Otsu's image thresholding, J. Elec. Imag. 2005, 14, 2.
- Xianpeng L., Feng Z., Yingming H., Jinjun O.: Integral Image Based Fast Algorithm for Two-Dimensional Otsu Thresholding. Congr. Image Signal Proc. 2008, 3, 677–681.
- 18. Shapiro L., Stockman G.: Computer vision, Upper Saddle River, Prentice Hall 2001.
- 19. Tadeusiewicz R., Korohoda P.: Computer analysis and image processing. (in Polish) Wydawnictwo Fundacji Postępu Telekomunikacji, Kraków, 1997.