Adaptive Intensity Windowing for MR Images

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ABSTRACT

Magnetic resonance (MR) images are displayed at low contrast due to the inability of a device to display the complete range of values under a single window. Generic contrast enhancement algorithms cannot be used in MR due to its characteristic variability of voxel values that represent the same object. Consequently, enhancement works better when driven from the viewpoint of application and domain knowledge is used to design the method. In this paper, a method is demonstrated which is dependent on the structure of interest and computes an appropriate window accordingly. The effectiveness of this type of windowing is demonstrated by testing on a cerebellum segmentation task, using a publicly available dataset (IBSR).

Keywords

Contrast enhancement, Automatic intensity windowing

1. INTRODUCTION

MRI is used for in vivo imaging of soft tissues of the body and finds its application in clinical practice for various purposes. Medical images are typically encoded with 12- or 16-bits and hence covers a much higher dynamic range than can be displayed by an 8-bit device. Hence, although an image contains rich information, all of it cannot be displayed at once in a common range of values. A simple solution would be to compress the dynamic range to suit the display, which however, results in a low contrast image which can lead to difficulty in diagnosis by the physician. The wide dynamic range is also a problem for image analysis methods such as segmentation and registration techniques which working on image intensities as subtle variations can get buried in the wide range. A solution to this problem is enhancement of contrast by image processing techniques.

The standard contrast enhancement techniques are mostly global operations. They apply the same transformation to all the pixels in an image. This category consists of logarithmic transformation, power-law transformation, histogram processing techniques. Among these, popular variants are brightness-preserving with maximum entropy histogram equalization (HE), gray-level grouping HE, multi-HE etc. Local histogram equalization methods, as opposed to the global ones, can enhance overall contrast effectively, but have a high computational requirement due to block based processing. These techniques are simple but inadequate for MR images since they achieve global enhancement which is not desirable for specific disease detection. It also results in degraded appearance, amplified noise or introduction of other artifacts.

The MR images are often noisy, with extremal pixel values that vary across images. Different MR sequences produce different contrast for the same tissues. The size and mass distribution of tissues in individual patients can affect the acquired images in different ways. Also, a non-linear transform changes the relative contrast variations among the tissues which can lead to false diagnosis. A linear transform is desired which preserves the relative contrast variations in the data. Such domain knowledge can be exploited in developing an appropriate solution to enhancement instead of a general algorithm for all the sequences.

Previous efforts for windowing clinical data can be broadly classified into three groups. In the first group, the user manually inspects the image quality to find the window width and window level values [5]. The second group comprises of semi-automated techniques which determine the window parameters based on some input given by the user. Based on a threshold set by the user, the bins of the histogram below the threshold are discarded and the window centre is set to be the mean of remaining bins and a suitable window width around the centre is fixed. The third group consists of automated and adaptive methods for determining window parameters [2]. This method makes use of spatial, histogram and spectral information for a linear and a non-linear intensity mapping. The bins of the histogram are grouped and remapped to enhance the contrast. This method aims at global contrast enhancement.

2. METHOD

One of the well known methods for improving the contrast is by windowing. Windowing describes the process of extending a certain range of pixel/voxel values in the image to fill the entire range of the display. Radiologists often manually adjust the window width and centre (known as level) of the MR images to improve the perceptual contrast of the target tissue. Such a manual adjustment requires time and energy. Since the characteristics of the images in a given volume are similar, some clinicians opt to adjust the window once for the most clinically important slices and use it for the entire series. However, when window settings are applied for all the images in the volume the results may not be optimal for all slices and may require additional adjustment for diagnostic use.

Due to the inherent problem in the modality MR images unlike CT ([4]) cannot have standardised windows to enhance the contrast for a given tissue. However, in a global histogram of a volume (after due normalisation), a given structure should have a fixed relation with respect the global structure (brain) across different volumes. This observation can be exploited to *learn* a) the relative position of a target structure's histogram within the global histogram and b)the width of the structure. It is worth noting that any deformation of the structure affects only the height of histogram and not its position.

In this paper, the cerebellum is considered as the structure of interest. A sample histogram of cerebellum $f_c(x)$ overlaid on the global (of entire image) histogram $f_g(x)$ is shown in Figure 1 on a normalised scale. For clarity, f_c is shown with a red line. Let x_1, x_2 be the locations of the first and second peaks, respectively, of $f_g(x)$. Let x_c denote the peak location corresponding to the cerebellum. It is generally observed that the cerebellum occupies a region around x_2. The desired window parameters are the centre x_c and the width l. The exact position of x_c is unknown a priori whereas x_1 and x_2 can be computed from a given $f_g(x)$. Hence, we define a ratio d which can be used to find x_c.

$$d = \frac{(x_c - x_1)}{(x_2 - x_1)} \tag{1}$$

The expected variance σ_c of f_c can be learnt. Hence, we define a second ratio b, to help determine the required window width, as follows

$$b = \frac{\sigma_c}{b_h - b_l} \tag{2}$$

where b_h and b_l are the upper and lower bounds respectively, of f_c. Once d and b are obtained via training, the window parameters x_c and $l = (2 \times b \cdot c)$ can be computed. Here c is a window tuning parameter. The obtained window can be stretched to full scale to obtain a high dynamic image.

3. EXPERIMENTS AND RESULTS

Since contrast enhancement is a subjective operation, its validation should be done from a target application's viewpoint. In this paper, we consider the task to be segmentation of the cerebellum. A level set-based segmentation algorithm described in [3] was used for segmentation. A contour was initialised in the image plane defining an initial contour. The level set function evolution is done according to variational calculus methods.

The data from the Internet Brain Segmentation Repository (IBSR) [1] was used for assessment. The algorithm was trained on 2 brain volumes and testing was done on 20 slices of 5 volumes. The training volumes were used to estimate the parameters d and b. Given a new volume window parameters x_c and l were computed and applied to coronal slices before segmentation was performed. Each slice in the dataset is of size 256x256. Segmentation is performed slice by slice and sample results, before and after the windowing,

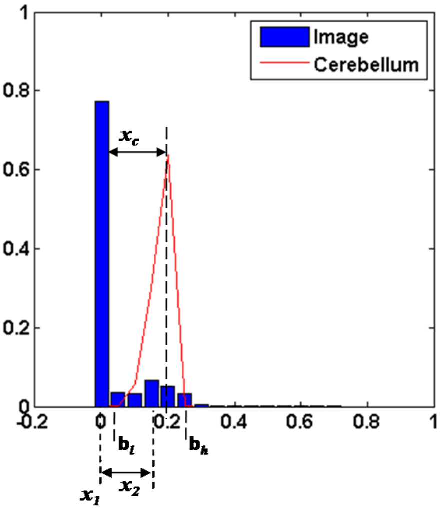

Figure 1: Normalised histograms of image and cerebellum overlaid on each other.

are as shown in Figure 2. The same initialisation was used for fair comparison. A great improvement in segmentation with windowing, can be observed from these results. The boundary around the cerebellum structure is clear and nuanced. To quantitatively verify segmentation the accuracy and validate the results, the segmentation results were compared with the ground truth available in the IBSR dataset using Dice coefficient (DC). Over the 20 slices it was tested on, an average DC of 0.91 ± 0.036 was obtained on windowed images as against 0.50 ± 0.06 on non-windowed images.

4. CONCLUSION

All the operations performed on MRI, like manual diagnosis or automatic analysis algorithms, can benefit from enhanced contrast in the image. MRI, with its characteristic variation of values, needs a customised contrast enhancement method. We have presented an adaptive windowing method and demonstrated its effectiveness both qualitatively and quantitatively in the cerebellum segmentation task. Given some training data, this idea can be extended to other structures as well to obtain the best viewing window for a structure. This method, when coupled with image driven algorithms, contributes to a fair increase in performance of the algorithm.

5. REFERENCES

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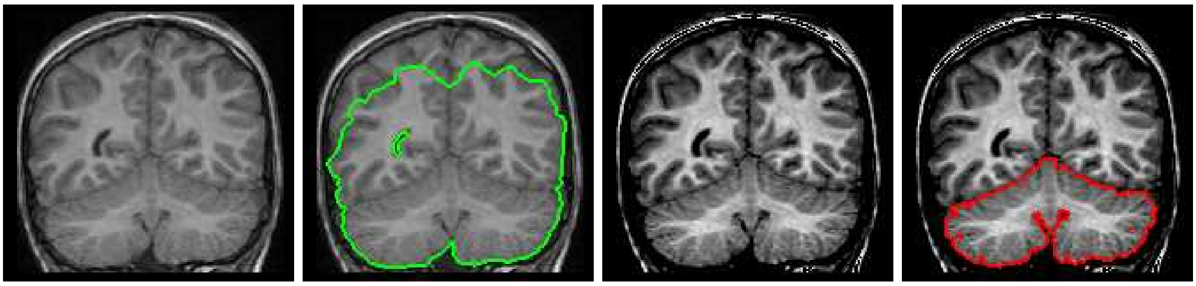
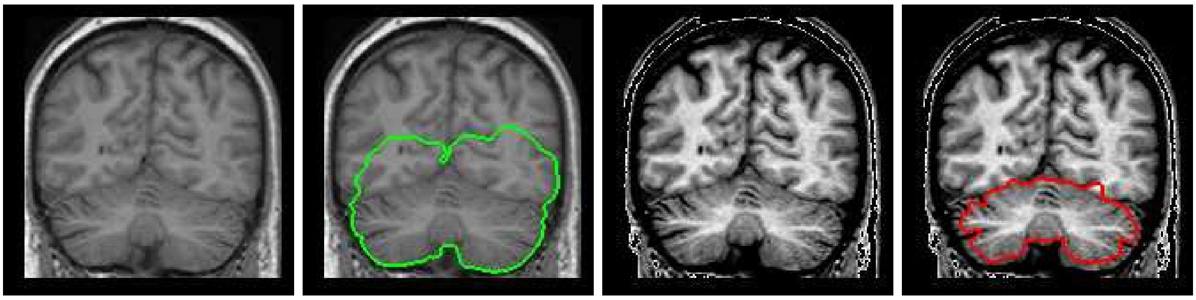
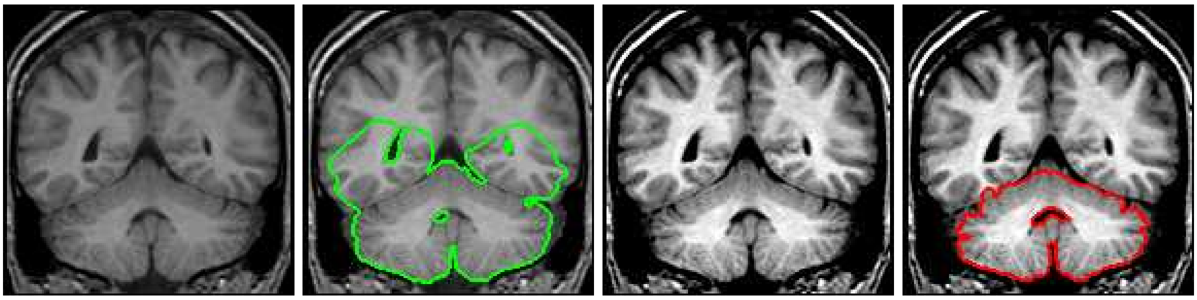


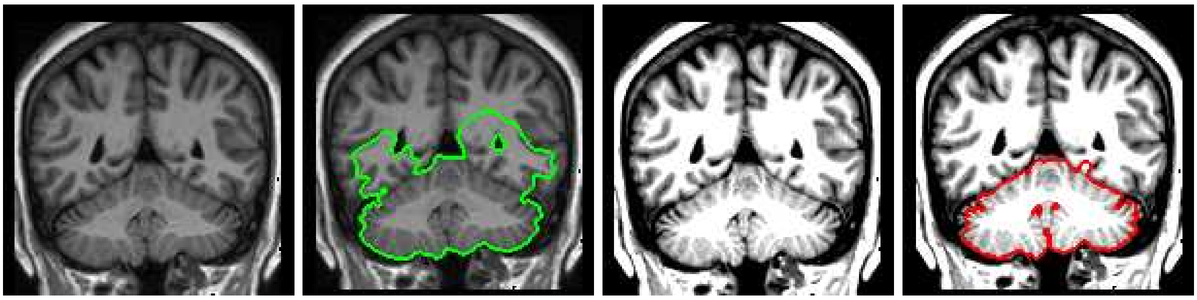
(a) I_1 (b) Segmented I_1 (c) I_{W1} (d) Segmented I_{W1}



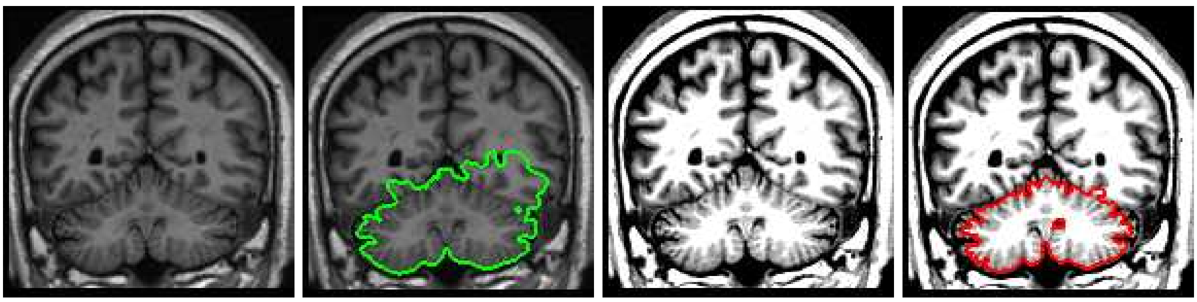
(e) I_2 (f) Segmented I_2 (g) I_{W2} (h) Segmented I_{W2}



(i) I_3 (j) Segmented I_3 (k) I_{W3} (l) Segmented I_{W3}



(m) I_4 (n) Segmented I_4 (o) I_{W4} (p) Segmented I_{W4}



(q) I_5 (r) Segmented I_5 (s) I_{W5} (t) Segmented I_{W5}

Figure 2: Segmentation results. I: Original; I_W : windowed. Green/Red contours are derived from segmentation.