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An intelligent modified fuzzy *c*-means based algorithm for bias estimation and segmentation of brain MRI

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Abstract

The segmentation of magnetic resonance images (MRI) is a challenging problem that has received an enormous amount of attention lately. Many researchers have applied various techniques however fuzzy *c*-means (FCM) based algorithms have produced better results compared to other methods. In this paper, we present a modified FCM algorithm for bias (also called intensity in-homogeneities) estimation and segmentation of MRI. Normally, the intensity in-homogeneities are attributed to imperfections in the radio-frequency coils or to the problems associated with the image acquisition. Our algorithm is formulated by modifying the objective function of the standard FCM and it has the advantage that it can be applied at an early stage in an automated data analysis before a tissue model is available. The proposed method can deal with the intensity in-homogeneities and Gaussian noise effectively. We have conducted extensive experimental and have compared our results with other reported methods. The results using simulated images and real MRI data show that our method provides better results compared to standard FCM-based algorithms and other modified FCM-based techniques.

Keywords: Medical image processing; MRI; FCM; Segmentation

1. Introduction

There are many kinds of image processing techniques used as diagnostic imaging modalities and amongst them the most popular is MRI (Bushong, 1996). The advantages of MRI are its high spatial resolution and soft-tissue contrast and that is why

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MRI is widely used in many medical applications (Chaozhe and Jiang, 2003). A typical MRI analysis of a patient involves vast amounts of data, thus it is time consuming as manual segmentation is normally done for many slices of images. Therefore, there is a need for computer analysis of MRI such as precise delineation of tumors and reliable, reproducible segmentation of images. In segmenting MRI data, we have mainly three considerable difficulties: noise, partial volume effects (where more than one tissue is inside a pixel volume) and intensity in-homogeneity. The bias field (intensity in-homogeneity) is induced by the radio-frequency coil in MRI and is a major problem in computer-based analysis of MRI data. Although MRI images may appear visually uniform, such in-homogeneities can cause serious misclassifications when intensity-based segmentation techniques are used (Ahmed et al., 2002). Ideally, for any given set of MRI, the intensity values of the voxels of any given tissue class should be constant, or, in view of the partial volume effect, it should correspond to a Gaussian distribution. With small standard deviation and differentiation between white and gray matter in the brain, it should be easy to segment it since these tissue exhibit distinct signal intensities. However, in practice, spatial intensity in-homogeneities can be as much as 30% of image amplitudes and thus causes the distribution of signal intensities associated with these tissue classes to overlap significantly (Ahmed et al., 2002; Chaozhe and Jiang, 2003). Therefore, the correction of spatial intensity in-homogeneity has been regarded as a necessary requirement for robust automated segmentation of MRI.

In the last decade, a number of algorithms have been proposed for the intensity in-homogeneity correction (Bushong, 1996; Axel et al., 1987; Listerud et al., 1989; Wicks et al., 1993; Tincher et al., 1993; Lai and Fang, 1998; Moyher et al., 1995; Meyer et al., 1995). Early methods for bias field estimation and correction used prior acquisition of a phantom image to empirically measure the bias field in-homogeneity (Axel et al., 1987; Listerud et al., 1989). Wicks et al. (1993) proposed methods based on the signal produced by a uniform phantom to correct MRI of any orientation problems. Furthermore, Tincher et al. (1993) modeled in-homogeneity function by a second-order polynomial and fitted it to a uniform phantom-scanned MRI. However, all such approaches based on a prior phantom acquisition have the drawback that the geometry relationship of the coils and the image data is normally not available (Ahmed et al., 2002; Chaozhe and Jiang, 2003). They also require the same acquisition parameters for the phantom scan and the patient. In addition, these approaches assume that the intensity corruption effects are the same for different patients, which is not valid in general (Lai and Fang, 1998; Moyher et al., 1995).

Meyer et al. (1995) presented an edge-based segmentation scheme to find uniform regions in the image followed by a polynomial surface fit for those regions. The result of their correction is, however, very dependant on the quality of the segmentation step. Dawant et al. (1993) developed a two-step approach for estimation of bias field. In this approach first ''reference points'' are selected for at least one tissue class (they used white matter) throughout the image, then a thin-plate spline is ''least-squared'' and fitted to the reference point data. They suggest the coefficient of variations as a measure for the degree of restoration. The selection of reference points is either done manually, or by a tissue classification algorithm after a partial classification. They found that the expert selection of reference points can give better results than automatic selection; and also it is prone to errors when points are mislabeled (Ahmed et al., 2002). The homomorphic filtering approach to remove the multiplicative effect of in-homogeneity has also been commonly used due to its easy and efficient implementation (Johnston et al., 1996; Brinkmann et al., 1998). This method assumes that the frequency spectrum of the bias field and the image structures are well separated, but this assumption is generally not valid for MRI (Tincher et al., 1993; Dawant et al., 1993).

Wells et al. (1996) developed a statistical approach based on the expectation–maximization (EM) algorithm to estimate the bias field and the tissue classification. Guillemaud and Brady (1997) improved this approach by introducing an extra class called ''others'' with a non-Gaussian probability distribution. This new extra class is