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Segmentation of Biomedical Imageries Using Data Density Functional Method

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ABSTRACT

This review is about the functional and automatic segmentation methods for biomedical imageries. To improve the desired results, the data density method was incorporated and is very significant in calculating even in pixels. This paper successfully describes combinational technique for solving the segmentation problem of magnetic resonance imaging (MRI) datasets.

Reliable and robust automatic method of image segmentation is still an open problem. To alleviate the undesired consequences from biomedical image segmentation processing, data density functional method made an avenue for measuring the desired connectivity and significance from pixel points within imageries and even within image clusters using the concept of energy functional densities, and then the corresponding clustering morphologies can be visually exhibited in an energy space [1]. By employing any sophisticated probability density estimator, the most probable cluster number and the most probable corresponding cluster boundaries can be extracted simultaneously. Furthermore, as similar as the concept of level set [2,3], the components of the imagery of interest located within similar energy region can be segmented by labeling their corresponding energy values. Eventually, these components will be either merged or segmented by considering their connectivity levels.

Several suspect technical predicaments might degrade the performance or functions of contemporary segmentation methods. For instance, in modern biomedical imaging processes, whatever gray level-typed images, coloring images, or sparse matrix images, each successive digitized image ideally needs to be aligned with previous and subsequent images [4-8]. In the duration of image processing, the images might suffer rotating or stretching when they were processed in measurement and imaging. Meanwhile, the components in the same tissue volume might also have different pixel intensity within films. Thus, the degradation of uniformity and contrast of the pixel intensity would limit the performance of the segmentations.

In other hands, labeling of the pixels is also a considerable problem [5,7,9-19]. For instance, the snaking neurons in a Brainbow system [1] stitch confusedly intertwining patterns, thus the chrominance within an imaging voxel would be possibly contaminated by adjacent components. Severe color crosstalk tends to undesirably penalize spurious branches and premature terminations when the image resolution is compromised [1,6,13,20]. Saturated luminous intensity within the voxels can probably cause not only topological errors on neural clustering but also the bogus neural connectivity. The ambiguous regions within the pixels due to the mentioned problems would cause the difficulty of image clustering and then the inaccuracy segmentation.

The merit of employing the data density functional method might elegantly solve the mentioned predicaments. By mapping the image pixel intensity into a specific energy space, the degradation of uniformity and contrast of the pixel intensity might be efficiently alleviated by introducing the action of connectivity from potential energy functional density. Meanwhile, the image pixels having color contamination and intensity saturation would be regularized by introducing the kinetic energy functional density. In a nutshell, by employing the data density functional method associated with the intrinsic properties of connectivity and significance within biomedical pixel points, the paper proposes a method of segmentation for biomedical imageries of interest. The data density functional method, based on the mathematical framework of quantum chemistry, has a sophisticated and pragmatic characteristic to easily connect

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to the theoretical framework of contemporary methods in the field of machine learning. Thus, the relevant techniques from machine learning methods can be used to reinforce the performance of the data density functional method.

In the paper, we successfully used the proposed combinational technique for solving the segmentation problem of magnetic resonance imaging (MRI) datasets. The connectivity and significance of the employed MRI dataset were respectively estimated by means of the corresponding data functional densities [1]:

$$u[\rho] = \sum_{n=1}^{W \times H} M_n / |\mathbf{r}' - \mathbf{r}'_n|_{\mathbf{r}' \neq \mathbf{r}'_n}, \qquad (1)$$

and

$$[\rho] = \pi^2 \rho \qquad (2)$$

Where, W and H are respectively the width and height of an image, $\mathbf{r}'$ and $\mathbf{r}'$ are respectively the positions of the nth pieel and the observation point and M_n is the corresponding normalized intensity. Then, the input pixel intensity was:

$$\rho(\mathbf{r}') = \sum_{n=1}^{W \times H} M_n \times \delta(\mathbf{r}' - \mathbf{r}'_n) \qquad (3)$$

Eventually, the employed MRI dataset was segmented by considering the connectivity levels of components:

$$\mathcal{L}[\rho] = \gamma^2 t[\rho] - \gamma u[\rho] \qquad (4)$$

$$\gamma = \frac{1}{2} \frac{\langle u[\rho] \rangle}{\langle t[\rho] \rangle}. \qquad (5)$$

The consequence is shown in **Figure 1**, wherein the mean value of the $\mathcal{L}[\rho]$ was used to be a threshold to segment the skull and tumor from the normal tissues. Main parts of the image as shown in **Figure 1a**, such as skull and tissues, were totally segmented as well as the other parts of brain tumors.

The skull in **Figure 1c**, normal tissues in **Figure 1e** and the tumor in **Figures 1b and 1d** were successfully segmented using the data density functional method. The MRI dataset was sourced from the open data [21]. The **Figure 1e** also had shown a limitation of the proposed combinational method. As shown by the arrows, the residual edges from tumor and skull are respectively still mixed with the brain tissue.
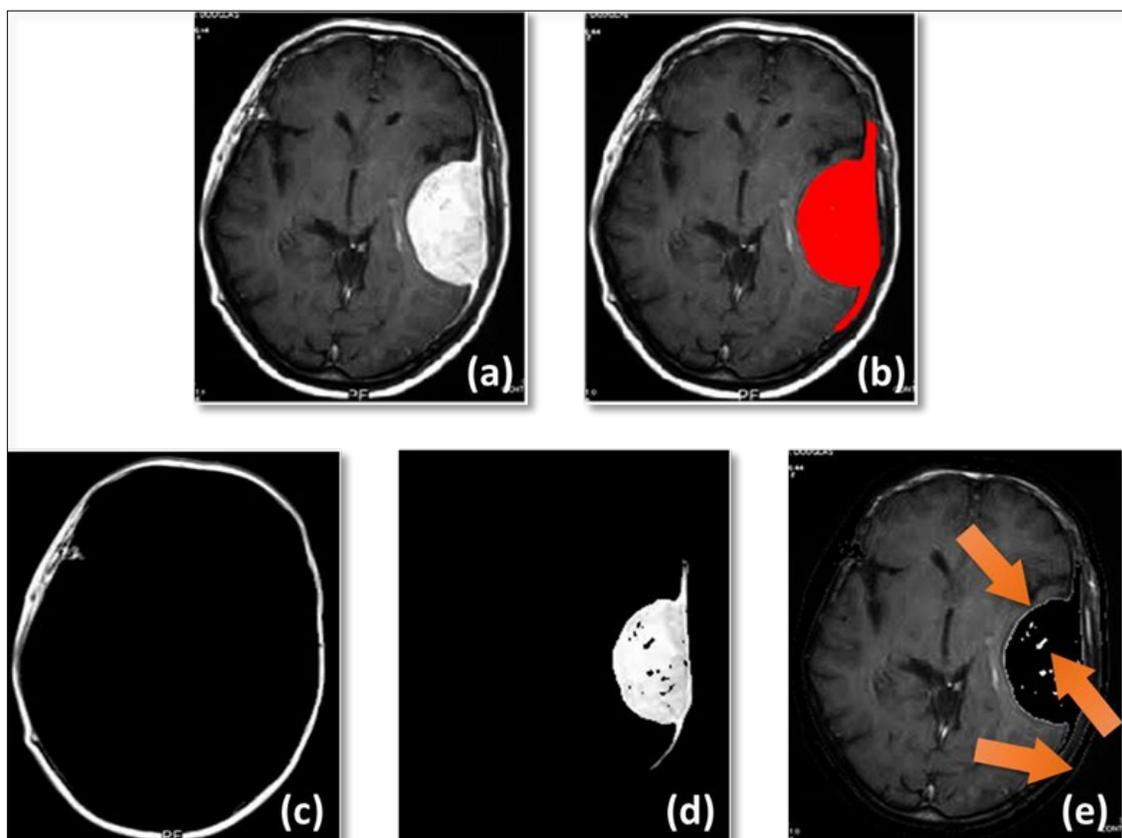
Figure 1. The segmentation results of a MRI dataset [21] using the proposed combinational method. The dimension of the original MRI data (a) is 205*246 in pixel space, then the result of tumor recognition is shown in (b). (c) and (d) respectively show the segmentation results of skull and tumor. (e) reveals the technical limitation of the proposed method that the residual edges from the other components still can be identified.

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