Brain Tumor Detection Using Scale Invariant Feature Transform

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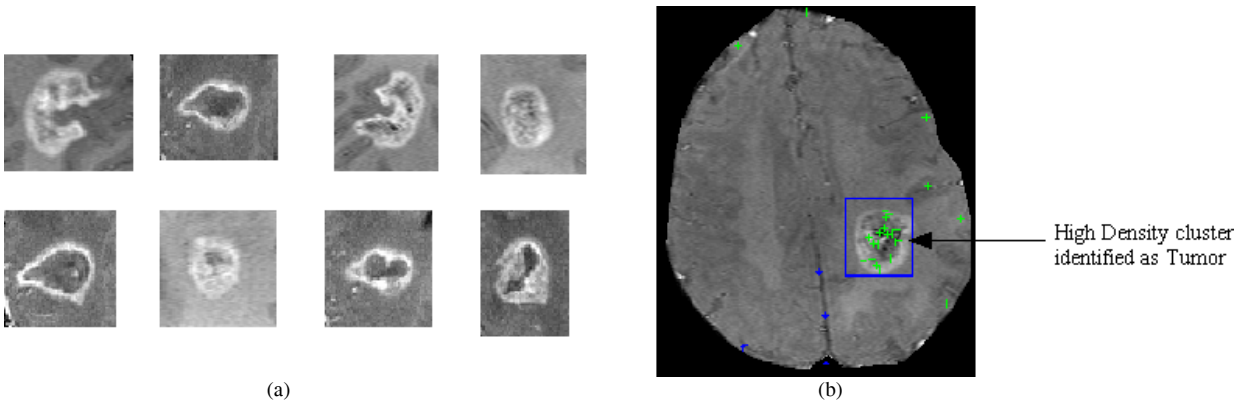
Introduction: A brain tumor is any intracranial mass created by an abnormal and uncontrolled growth of cells either normally found in the brain itself (primary tumors), or spread from cancers primarily located in other organs (metastatic tumors). Computer vision techniques, coupled with non-invasive, high-resolution imaging modalities such as Magnetic Resonance Imaging (MRI), play a central role in the detection and diagnosis of brain tumors [1]. In this work, we propose a novel tumor detection scheme using Scale Invariant Feature Transform (SIFT) in MRI. SIFT has been proved as an effective method to extract keypoints from images which are invariant to translation, scale, rotation, affine transform, change in illumination, change in 3D viewpoint, etc., and is used extensively in object recognition applications such as face recognition and object-based image retrieval [2,3]. Based on SIFT features, our method can automatically identify tumors through keypoint matching between a test image and previously collected training images.

Methods and Materials: Conventional model matching methods (segmentation + classification) for brain structure labeling [4,5] are not suitable for lesion categorizing since tumors are irregular and diverse in nature. In this work, we develop a robust tumor detection algorithm based on SIFT. As the first step, SIFT algorithm is applied on a set of training images representing the typical tumor cases. For a typical 512X512 T1 post-contrast image, around 500 keypoints are detected by SIFT. Only the keypoints that are detected from the tumor region are added to the training dataset while the rest are discarded. As SIFT feature vector is calculated from the neighborhood around a keypoint at different scales, the localized structure of the tumor is precisely recorded by SIFT. Given a test image, the second step is to find the best candidate match for each keypoint in the image by identifying its nearest neighbor in the set of keypoints obtained from training images. The nearest neighbor is defined as the keypoint with the minimum Euclidean distance for the invariant descriptor vector. Notice that many keypoints from a test image will not have any correct match in the training set because they arise from background clutter or other brain structures. Those keypoints will be removed based on a predefined matching threshold. A more effective measure is to compare the distance of the closest neighbor to that of the second-closest neighbor. This measure gives more stable results as we add one more constraint to the nearest neighbor that it should have closest neighbor significantly closer than the closest incorrect match to achieve reliable matching. The computational efficiency of matching process is greatly improved by computing the inverse cosines of scalar products between keypoints extracted from the test image and keypoints stored in the training dataset, and then sorting them. Once matched keypoints are detected for the test image, it is necessary to remove the outliers before recognition because some of the matches may come from other parts of the image other than tumors. Fortunately, we observed that most of the matches come from the tumor. In this case, it is intuitive to remove the outliers through clustering analysis. Specifically, we used standard K-means algorithm with squared Euclidean distance measure for spatial clustering. The seed points for the K-means are selected uniformly at random. The value of k is selected in a way that the initial seed points can cover the whole image. After clustering, the group with the maximum number of keypoints is identified as the most probable tumor region.

Experimental Setup and Results: For our experiments, we considered Post Contrast T1 Magnitude images. We created a training set of SIFT keypoints from 30 tumor images. In each image, every tumor region is described by about 50 keypoints, while each keypoint is represented by a 128 element feature vector, which captures the gradient magnitude and orientation of the neighborhood of the keypoint, invariant to various transformations such as translation, rotation, scale, affine transform, etc. Test images are selected from Post Contrast T1 images with tumors but are different from the training dataset. Our experiment results show that the proposed method is highly effective and robust for tumor detection under various conditions. Fig. 1 shows an example. Fig. 1a shows some tumor images from our training dataset. Fig. 1b shows a test image with matched keypoints (green "+"). The rectangle is the tumor region detected by our algorithm based on the cluster of keypoints with the highest density.



(a) (b)

Figure 1: an example of Tumor Detection by SIFT

Conclusion: SIFT is used to extract keypoints from MR images and tumor detection is performed by keypoint selection and matching. Experiments on Post contrast T1 Magnitude images show the effectiveness of our approach.

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