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Parallel genetic-based algorithm on multiple embedded graphic processing units for brain magnetic resonance imaging segmentation[☆]

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ABSTRACT

Medical imaging has played an important role in helping physicians to make clinical diagnoses. Magnetic resonance imaging technology has been used to image the anatomy of the brain. Typically, image segmentation is utilized to observe the brain's anatomical structures and its changes, and to identify pathological regions. In this paper, we propose an efficient parallel fuzzy c-means clustering algorithm for segmenting images on multiple embedded graphic processing unit systems, NVIDIA TK1. The experimental results demonstrate that the maximum speedups of the proposed algorithm on 15 TK1s greater than 12 times and 7 times than that of fuzzy c-means algorithm with single ARM and Intel Xeon CPUs, respectively. These experimental results show that the proposed algorithm can significantly address the complexity and challenges of the brain magnetic resonance imaging segmentation problem.

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1. Introduction

In recent decades, the rapid growth of noninvasive medical imaging technologies has increased our ability to analyze the anatomy and function of the brain. These medical images help physicians to make better clinic diagnoses. Current types of medical imaging technologies include X-rays, ultrasound, computed tomography scanning (CTs), and magnetic resonance imaging (MRIs). All these technologies are utilized routinely to identify irregularities in the human body. MRI is often used to detect abnormalities in the brain and to explore brain anatomy. Brain MRIs produce a large amount of high quality image data. However, these brain MRI datasets are large and complex, and clinicians must manually extract important information from them. This process is tedious and complex, and the manual analysis of brain MRI data can be time-consuming and prone to human error. Therefore, a computational method for processing brain MRIs could greatly improve disease diagnosis and testing. Recently, a variety of computational methods, including MR image segmentation and visualization, has been widely used to assist physicians in qualitative diagnosis.

Today, brain MRI segmentation [1] is used as an essential process in many clinical applications because it can improve the accuracy of diagnosis. Usually, clinical diagnosis relies on the accurate segmentation of anatomical regions. For example,

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MRI segmentation is routinely used to measure and visualize different anatomical structures, lesions, tissues, and tumors in the brain. Various segmentation techniques with varying degrees of accuracy and complexity have been proposed for different applications.

A brain MR image can be classified into three regions: white matter (WM), gray matter (GM), and cerebrospinal fluid spaces (CSF). In the segmentation process, a brain MRI is clustered into a series of non-overlapping homogeneous regions [2], which are then classified into two clusters of white and black regions. White clusters represent WM, and black clusters represent the other two regions. Based on these clusters, physicians can examine these regions and make accurate diagnoses [2,3]. In addition, physicians can determine the presence of abnormalities by the reconstructed images of these clusters.

Brain MR image segmentation is generally a complex task because the acquired images are often corrupted with various imaging artifacts. Due to the diversity of MR images, there is no single suitable method for all image types [4]. Of the available methods, some use a gray-level histogram to segment images, and others use probabilistic or fuzzy set theoretical approaches to enhance the segmentation result. The fuzzy clustering algorithm [5] has been successfully applied in medical imaging. The main idea of clustering methods is to partition an image into clusters of pixels/voxels with similar intensities. For MR image segmentation, the most commonly used clustering methods are k-means clustering (KM) [6], moving k-means (MKM), fuzzy c-means clustering (FCM) [7], and the expectation-maximization (EM) methods [8]. The FCM method demonstrates superior segmentation performance compared to that of other clustering algorithms. Some extended FCM approaches adopt the feature information of neighboring pixels to enhance the accuracy of the FCM [9,10]. Although FCM is a useful method for segmentation, it is sensitive to the initialization of the center of the clusters. The genetic-algorithm-based FCM (GAFCM) [11], proposed to solve this problem, combines genetic and fuzzy c-means clustering algorithms. However, all these clustering algorithms are computation intensive, so parallel computing methods have become an important consideration.

Recently, general-purpose computing on graphics processing units (GPGPU) has been applied to solve computation-intensive problems. GPGPU devices consist of hundreds of cores and it can simultaneously launch thousands of threads to execute a single instruction. In 1996, NVIDIA Corp. released a single-instruction multiple-thread (SIMT) architecture, which generates multiple threads that simultaneously execute the same instructions. GPGPU programming models, such as Open Computing Language (OpenCL) [12] and compute unified device architecture (CUDA) [13], have made high performance computing available to MRI segmentation applications. Rumpf and Strzodka [14] proposed the first parallel segmentation method using computing level set segmentation as a sequence of image blending graphics operators on graphics processing units (GPU). Cates et al. [15] proposed the parallel curvature regularization method, which segments a 3D image on a GPU to produce smooth isosurfaces. Jenog et al. [16] proposed a multiphase level set segmentation approach, implemented on CUDA, for reconstructing complex neural processes. Stoev and Straßer proposed parallel watershed and region growing algorithms on GPU [17,18] that use pixel/voxel information to identify target regions without having requiring any statistical information for the target regions. In contrast, Narayanaswamy et al. [19] proposed a statistical method that uses an adaptive region growing process on GPU to cluster confocal microscope images. Walters et al. [20] proposed a Markov random fields segmentation method on GPU to process liver images. De et al. [21] proposed a self-organizing map network approach on GPU for segmenting brain MRI images. In our previous work [22], we presented a parallel FCM algorithm based on an NVIDIA embedded GPU system, the NVIDIA Jetson TK1, to successfully accelerate the computation speed of FCM for segmenting brain MRIs.

In this paper, we propose a novel parallel FCM method that uses a genetic algorithm on multiple NVIDIA embedded GPU systems. The main idea is to partition the genetic population into many subpopulations. Every thread on the GPU executes the FCM process iteratively, based on the size of the subpopulations. A main node collects all the FCM objective values of the subpopulations and performs genetic operations to generate new populations. These steps are executed iteratively until the minimum objective value is reached. The proposed algorithm is implemented by integrating the message-passing interface (MPI) with CUDA. Our experimental results show that the proposed algorithm can significantly improve the performance of the GPU-based FCM algorithm.

The remainder of this paper is organized as follows. In Section 2, we discuss the FCM algorithm, the GPU-based FCM algorithm, and the GPU-based genetic FCM algorithm on multiple GPUs. We present our experimental results in Section 3, and in Section 4, we draw our final conclusions and suggest some directions for future work.

2. Algorithm

We propose an efficient parallel FCM algorithm based on multiple GPUs via a genetic algorithm. As such, our proposed algorithm integrates two algorithms, a GPU-based FCM and a genetic algorithm. The GPU-based FCM algorithm is performed in each GPU, and is implemented using the MPI and CUDA. We describe our proposed algorithm below.

2.1. Fuzzy c-means clustering

The FCM clustering algorithm [7] is one of the most commonly used clustering algorithms for segmenting brain MR images. The concept of clustering involves the grouping of data in one data set into numerous clusters. The FCM algorithm groups the data into numerous clusters, and every data member in the data set belongs to a cluster, depending on the minimization of an objective function. Our data set comprises images, and the data members are the pixels/voxels. Let $X = (x_1, x_2, \dots, x_n)$ denote an MR image with n pixels/voxels, where x_i represents the gray value of the i th pixel/voxel. The

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