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A clonal selection based approach to statistical brain voxel classification in magnetic resonance images

Tong Zhang [a], Yong Xia [a,b,c,*], David Dagan Feng [a,d]

[a] Biomedical and Multimedia Information Technology (BMIT) Research Group, School of Information Technologies, The University of Sydney, NSW 2006, Australia
[b] Shaanxi Provincial Key Lab of Speech & Image Information Processing (SAIIP), School of Computer Science, Northwestern Polytechnical University, Xi'an 710072, China
[c] Department of Molecular Imaging, Royal Prince Alfred Hospital, Sydney, NSW 2050, Australia
[d] Med-X Research Institute, Shanghai Jiao Tong University, Shanghai 200030, China

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ABSTRACT

Statistical classification of voxels in brain magnetic resonance (MR) images into major tissue types plays an important role in neuroscience research and clinical practices, in which model estimation is an essential step. Despite their prevalence, traditional techniques, such as the expectation–maximization (EM) algorithm and genetic algorithm (GA), have inherent limitations, and may result in less-accurate classification. In this paper, we introduce the immune-inspired clonal selection algorithm (CSA) to the maximum likelihood estimation of the Gaussian mixture model (GMM), and thus propose the GMM-CSA algorithm for automated voxel classification in brain MR images. This algorithm achieves simultaneous voxel classification and bias field correction in a three-stage iterative process under the CSA framework. At each iteration, a population of admissible model parameters, voxel labels and estimated bias field are updated. To explore the prior anatomical knowledge, we also construct a probabilistic brain atlas for each MR study and incorporate the atlas into the classification process. The GMM-CSA algorithm has been compared to five state-of-the-art brain MR image segmentation approaches on both simulated and clinical data. Our results show that the proposed algorithm is capable of classifying voxels in brain MR images into major tissue types more accurately.

1. Introduction

Accurate delineation of major brain tissues, such as the gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF), in magnetic resonance (MR) images plays a pivotal role in both neuroscience research and clinical practices. The quantification of the volumetric tissue changes, for instance, is an essential step in diagnosing mental diseases and monitoring their progressions. Traditionally, brain tissue delineation relies on manual operation performed by medical professionals, which, however, is time-consuming, expensive and subject to intra-and inter-observer variability. Therefore, automated brain MR image voxel classification is highly in demand and has attracted extensive research attention. As a result, a large number of algorithms have been proposed in the literature [1–13], including those based on the atlas [6–8] and statistical models [9–12].

Atlas-based brain voxel classification algorithms involve a joint registration-comparison process, with the aim of generating an "average" organ representation, i.e. the atlas, from the training image dataset or anatomy, and then mapping the anatomical structure from the atlas to the to-be-classified image through co-registration [8]. Despite its widespread applications, these approaches may have a limited performance due to the normal anatomical variation across patients, inaccuracy of the registration and the atlas itself.

Statistical voxel classification algorithms have rigorous mathematical formulations and have been widely applied to brain MR images. In these algorithms, voxel values are usually assumed to follow a Gaussian mixture model (GMM), which is a weighted sum of finite Gaussian distributions. Each component distribution models the voxel values from one tissue type, and each weight, also known as a mixing parameter, represents the prior probability of voxels belonging to the corresponding tissue type. These algorithms usually consist of two major steps: estimating the optimal model parameters that can maximize the likelihood of the observed image and applying the image data and statistical model to a classifier to generate the class label for each voxel. In the traditional GMM-EM algorithm [9], the GMM model is estimated by using the expectation–maximization (EM) algorithm and the class labels are generated by using the Bayes classifier. The EM algorithm iteratively alternates between an expectation step (E-step), which computes an expectation of the log likelihood with respect to the currently estimated distributions and the observed image, and a maximization step (M-step), which estimates the GMM parameters which maximize the expected log likelihood.

* Corresponding author at: Shaanxi Provincial Key Lab of Speech & Image Information Processing (SAIIP), School of Computer Science, Northwestern Polytechnical University, Xi'an 710072, China.
E-mail address: yxia@nwpu.edu.cn (Y. Xia).

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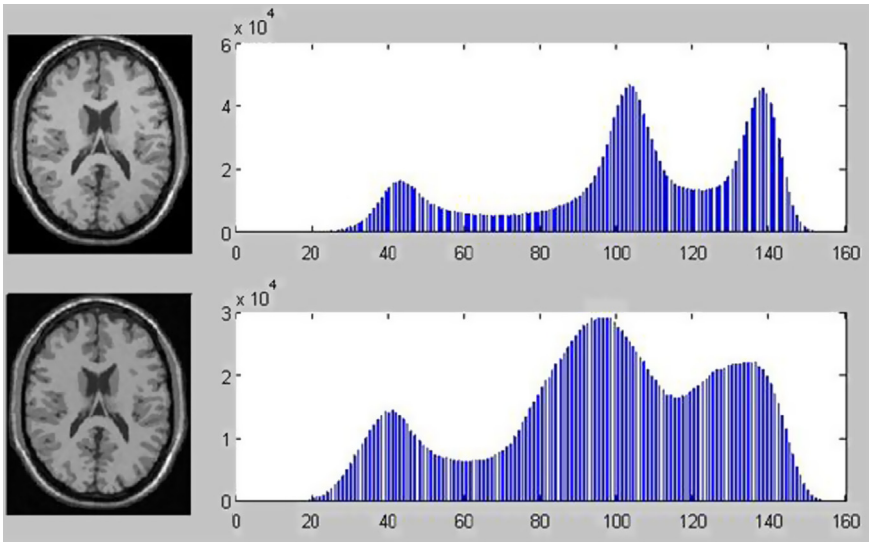

Fig. 1. Simulated T1-weighted brain MR image with 3% noise and (top row) no INU or (bottom row) 40% INU selected from the BrainWeb database [24].

Due to the remarkable consistency shown in brain structures across individuals, the knowledge of brain anatomy can be an effective heuristic prior available for this classification task. To incorporate such prior knowledge into the classification process, atlas-based and statistical approaches have been combined to form a uniformed framework in several approaches [10,12]. Although these modifications have substantially improved the voxel classification accuracy, most of them still rely on the EM-based model estimation, which is intrinsically a greedy approach that may converge to a local maximum of the observed data likelihood function. Hence, the performance of these algorithms depends highly on initializations [14]. An intuitive solution to overcome this drawback is to replace the EM algorithm with global optimization techniques in model estimation. A typical example is the GA-EM algorithm [11], in which the genetic algorithm (GA), a population-based global optimization technique, is used to achieve the maximum likelihood estimation of statistical model.

As a traditional evolutionary algorithm, GA has the drawback of slow convergence and lack of the local search ability. Recently, optimization algorithms inspired by the immune system has drawn increasing attentions as a potential source of more effective evolutionary algorithms [15]. These algorithms mimic the behavior of living organisms in protecting themselves against antigens, and hence have the potential to achieve both local and global optima. Among them, the clonal selection algorithm (CSA) has shown superior performance comparing to several other bionic algorithms [15] and traditional optimizing mechanisms in a variety of applications [16,17]. CSA is designed to simulate the affinity maturation process based on the clonal selection theory, which claims that only those cells that recognize the antigens will be selected to proliferate, and the proliferated cells will improve their affinity to the antigens through an affinity maturation process [15,18,19].

Naturally, more accurate brain voxel classification can be expected when using CSA to replace traditional deterministic (such as EM) and evolutionary (such as GA) algorithms in the statistical model estimation. In this paper,[1] we propose the GMM-CSA algorithm for automated brain voxel classification in MR images. We include adaptive bias field estimation and correction in the iterative model estimation and voxel classification process, so that these operations can benefit each other to yield better results. We also use a set of training data to construct a probabilistic brain atlas for each study and employ this atlas to facilitate voxel classification with the aim of achieving more stable performance. We have compared the proposed GMM-CSA algorithm to the EMS algorithm [10], GA-EM algorithm [11], Genetic VEM (GVEM) algorithm [12] and two state-of-the-art brain MR image segmentation routines in the widely used statistical parametric mapping (SPM) package [21] and FMRIB Software library (FSL) [22] on both simulated and real brain MR images.

2. Bias field estimation

The inherent challenge faced by brain voxel classification is the bias field, also referred to as the intensity inhomogeneity or intensity non-uniformity (INU), existed in MR images. The bias field arises from the imperfections of the image acquisition process and manifests itself as a smooth intensity variation across the image [23]. A simulated brain MR slice with 3% noise and the corresponding bias filed corrupted version [24] are compared in Fig. 1. It shows that, due to the existence of 40% INU, the intensity of the same tissue varies with the spatial locations and the overlaps among three modes in the histogram increase significantly. Thus, the bias field may cause a lot of difficulties in MR image analysis and should be estimated and corrected [25–30].

Let an observed 3D brain MR image be denoted by $\boldsymbol{X}=\{x_i; i=1,2,\ldots,N\}$, where x_i represents the intensity value at voxel i and N is the number of voxels. Generally, the unknown bias field $\boldsymbol{B}=\{b_i; i=1,2,\ldots,N\}$ can be modeled as a multiplicative component of $\boldsymbol{X}$, as follows:

$$\boldsymbol{X}=\boldsymbol{B}\cdot\boldsymbol{X}0+\aleph \tag{1}$$

where $\boldsymbol{X0}$ is the ideal image without bias field, and $\aleph\sim N(0,\sigma_n^2)$ is the additive Gaussian white noise. The bias field $\boldsymbol{B}$ varies very slowly in the image, and hence is usually assumed to be a smooth function defined within the entire image domain. We adopt orthogonal polynomials $\{\boldsymbol{W}_j : j=1,2,\ldots,N_{OP}\}$ as basis functions to approximate the bias field [31]

$$\boldsymbol{B}=\sum_{j=1}^{N_{OP}}\varphi_j\boldsymbol{W}_j \tag{2}$$

where $\varphi=\{\varphi_j : j=1,2,\ldots,N_{OP}\}$ denote the real-valued combination coefficients, $N_{OP}=(D+1)(D+2)/2$ is the number of polynomials, and D is the degree of polynomials. Theoretically, such an approximation can achieve up to arbitrary accuracy [32].

[1] The preliminary version of this paper was presented in IScIDE 2011 [20].