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Brain MRI image segmentation based on learning local variational Gaussian mixture models

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ABSTRACT

Measuring the distribution of major brain tissues, including the gray matter, white matter and cerebrospinal fluid (CSF), using magnetic resonance imaging (MRI) has attracted extensive research efforts. Many brain MRI image segmentation methods in the literature are based on the Gaussian mixture model (GMM), which however is not strictly followed due to the intrinsic complex nature of MRI data and may lead to less accurate results. In this paper, we introduce the variational Bayes inference to brain MRI image segmentation, and thus propose a novel segmentation algorithm based on learning a cohort of local variational Gaussian mixture (LVGM) models. By assuming all Gaussian parameters to be random variables, the LVGM model has more flexibility than GMM in characterizing the complexity of brain voxel distributions. To alleviate the impact of bias field, we train each LVGM model on a sampled small data volume and linearly combine the trained models to classify each brain voxel. We also construct a co-registered probabilistic brain atlas for each MRI image to incorporate the prior knowledge about brain anatomy into the segmentation process. The proposed LVGM learning algorithm has been evaluated against five state-of-the-art brain MRI image segmentation methods on both synthetic and clinical data. Our results suggest that the LVGM algorithm can segment brain MRI images more effectively and provide more precise distribution of major brain tissues.

1. Introduction

Precisely measuring the distribution of major brain tissues, including the gray matter, white matter and cerebrospinal fluid (CSF), is an essential step in both clinical practices and neuroscience research [1]. Magnetic resonance imaging (MRI) can provide high spatial resolution of anatomical details and unique contrast between soft tissues, and hence is suitable for this task [2]. The enormous brain MRI images produced globally, however, are currently analysed almost entirely through visual inspection on a slice-by-slice basis. This requires a high degree of skills and concentration, and is time-consuming, expensive and prone to operator bias. Therefore, automated delineation of major brain tissues using MRI that would enable doctors and researchers to bypass the above-mentioned issues has attracted extensive attentions over the past decade. As a result, a large number of brain MRI image segmentation algorithms have been proposed in the literature [3–5]. Among them, those based on brain atlases and statistical models are the most popular ones.

1.1. Related work

Conventional approaches to brain MRI image segmentation are atlas-based joint registration-comparison [6–8]. A brain atlas is composed of serial sections along different anatomical planes of the human brain, where each relevant brain structure is assigned a number of coordinates to define its volume [9]. Usually, atlas-based approaches first register a brain atlas with the brain MRI image to be segmented and then map major brain structures from the atlas to the image. Although straightforward and easy to implement, such approaches are often less accurate due to the inevitable registration inaccuracy and normal anatomical variations across subjects.

Statistical brain MRI image segmentation can be traced back to the work done by Cline at al. [10]. Most statistical approaches nowadays are based on the Gaussian mixture model (GMM), in which the gray level distribution of brain voxels from one tissue type is assumed to be Gaussian and the prior probability of belonging to that tissue gives the mixing weight of the Gaussian component [11–17]. Once the statistical parameters in GMM are estimated according to the maximum likelihood (ML) principle by maximizing the likelihood of the observed MRI image, the class label of each voxel can be predicted by applying the voxel value to

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a naive Bayes classifier [18–20]. Wells et al. [12] applied the expectation-maximization (EM) algorithm [21] to GMM parameters estimation, and thus developed the GMM-EM framework. Leemput et al. [11] proposed an explicit parametric model to estimate voxel labels and used a brain atlas to represent the prior knowledge. Besides the EM algorithm, evolutionary techniques, such as the genetic algorithm (GA) [22], have also been applied to GMM parameter estimation [23]. Tohka et al. [24] proposed a real coded GA with new permutation operator specifically designed for GMM parameter estimation. In spite of their abundance applications, GMM-based statistical approaches usually have limited accuracy, which can be largely ascribe to the following three major causes.

First, classifying brain voxels into tissues of interest is essentially different from other pattern classification problems in that the prior probability of a voxel belonging to each tissue is largely determined by its location. However, GMM lacks the mechanism to use such prior anatomical knowledge for brain MRI image segmentation. To remedy this, Greenspan et al. [25] incorporated the spatial constraints into the GMM through employing a large number of Gaussian components to represent each tissue. Nguyen and Wu [26] proposed a fast and robust spatially constrained Gaussian mixture model and directly applied the EM algorithm to model optimization. Nikou et al. [27] adopted the Markov random field (MRF) model to characterize the spatial smoothness and included it in the process of maximizing the posterior probability of voxel labels given the observed MRI data. Zhang et al. [28] employed the hidden MRF (HMRF) model to explore the spatial information embedded in MRI images.

Second, the bias field, also referred to as the intensity non-uniformity (INU), renders a challenging task for brain MRI image segmentation [29]. It arises from the imperfections in the radio-frequency coils or problems associated with the acquisition sequences, and usually results in a shading effect across the image [30,31]. Generally, the bias field is assumed to be a multiplicative component of the observed brain MRI image and varies slowly in the entire image domain [32]. Therefore, it is safe to assume that the bias field can be ignored within a small image patch. Based on this assumption, kernel techniques have been used to construct local statistical models, each of which characterizes the MRI data in the neighborhood of a voxel, instead of the entire image [33–36]. Chen et al. [34] replaced the original Euclidean distance with a kernel-induced distance and supplemented the objective function with a spatial penalty term, which models the spatial continuity compensation. Liao et al. [35] developed a spatially constrained fast kernel clustering algorithm to improve the computational efficiency. Li et al. [36] introduced the local binary fitting (LBF) energy into the energy functional of region-based active contour models to handle the intensity inhomogeneity by drawing upon local intensity means. Wang et al. [37] introduced more complicated statistical characteristics of local intensities based on the LBF model by describing the local information with Gaussian distributions, and thus proposed the local Gaussian distribution fitting (LGDF) model. However, since a model will be estimated for each voxel, the local model-based approaches are generally time-consuming.

Last but not least, each 3D brain MRI image contains millions of voxels, whose values distribute with very complex structures due to the existence of noise, INU, partial volume effect (PVE) and other artifacts. Therefore, the statistical assumption that the voxel values from each tissue type are sampled independently from an identical Gaussian distribution is usually less valid for MRI images. To address this issue, other mathematical tools, such as the fuzzy set theory [38], have been utilized [39,40]. Moreover, statistical models have been combined with the fuzzy set theory to form the so-called probabilistic fuzzy models for describing the uncertainty embedded in brain MRI data. Tran et al. [41] proposed the fuzzy GMM model to improve parameter estimation. Zeng et al. [42] developed the type-2 fuzzy GMM model for density modeling and classification. Although the fuzzy theory provides another perspective on modeling the uncertainty, it can hardly overcome the essential drawbacks of statistical approaches.

Recently, the variational Bayes inference has been introduced to learn statistical models [43–45]. Variational approaches assume that statistical parameters are also stochastic variables, and hence have the flexibility to handle the complex distribution of voxel values. In these approaches, the posterior distribution of both statistical parameters and latent voxel labels can be inferred by using the variational EM (VEM) algorithm [44]. Although the variational Bayes inference can effectively avoid overfitting, inferring the posterior distribution is computationally more complex than estimating GMM parameters. Therefore, when applying it brain MRI image segmentation, it is almost impossible to build a variational model for every voxel.

1.2. Outline of our work

In this paper, we introduce variational Bayesian inference to brain MRI image segmentation, and thus propose an automated segmentation algorithm based on learning local variational Gaussian mixture (LVGM) models. To cope with the complexity and dynamic nature of MRI images, we assume the parameters of Gaussian models that represent the distribution of voxel values are also stochastic variables and replace the traditional model estimation with variational Bayesian inference. To address the challenges raised by INU, we use small MRI volumes sampled from the original image to train a relatively large number of LVGM models and avoid voxel-wised estimation of local models. We also construct a co-registered probabilistic brain atlas for each MRI image to incorporate the prior knowledge about brain anatomy into the segmentation process. Therefore, the proposed LVGM learning algorithm combines the merits of atlas-based and statistical approaches. We have evaluated our algorithm against five commonly used brain MRI image segmentation methods on both synthetic and clinical studies.

2. Variational Bayesian inference

For a dataset $X=\left\{x_s \in R^D : s=1,2,\cdots,N\right\}$, each data x_s is assumed to be drawn independently from one of K Gaussian distributions $\mathcal{N}(\mu_k,\Sigma_k)$ with a prior probability ω_k. All statistical parameters, denoted by $\Theta=\{\omega_k,\mu_k,\Sigma_k{:}1\le k\le K\}$, are further assumed to be stochastic variables that follow the Dirichlet distribution and independent Gaussian–Wishart distribution, respectively. Let the latent class labels of observed data be denoted by $Z=\{z_s\in R : s=1,2,\cdots,N\}$. The complete-data likelihood $p(X,Z,\Theta)$ can be calculated as

$$p(X,Z,\Theta)=p(XZ,\mu,\Lambda)p(Z\omega)p(\omega)p(\mu,\Lambda) \tag{1}$$

where $\Lambda_k=\Sigma_k^{-1}$ is the precision matrix.

Instead of estimating the posterior probability of latent voxel labels Z, the variational Bayesian inference aims to infer a posterior distribution $p(Z,\Theta X)$ by introducing a variational distribution $q(Z,\Theta)$ to approximate it. For any choice of $q(Z,\Theta)$, the following decomposition of the model evidence $\ln p(X)$ holds [44]

$$\ln p(X)=KL(q\|p)+L(q) \tag{2}$$

where

$$KL(q\|p)=-\iint q(Z,\Theta)\frac{p(Z,\Theta X)}{q(Z,\Theta)}dZd\Theta \tag{3}$$