Gaussian mixture model based segmentation methods for brain MRI images

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Abstract   Image segmentation is at a preliminary stage of inclusion in diagnosis tools and the accurate segmentation of brain MRI images is crucial for a correct diagnosis by these tools. Due to in-homogeneity, low contrast, noise and inequality of content with semantic; brain MRI image segmentation is a challenging job. A review of the Gaussian Mixture Model based segmentation algorithms for brain MRI images is presented. The review covers algorithms for segmentation algorithms and their comparative evaluations based on reported results.

Keywords   Statistical · MRI · Brain

1 Introduction

Medical image segmentation algorithms extensively use statistical pattern recognition techniques (Bezdek et al. 1993; Jain et al. 2000; Balafar et al. 2010a). For image segmentation, a known set of classes are considered. For brain images, usually three tissue classes are considered: gray matter, white matter, and cerebrospinal fluid. Each of the pixels in an image is modeled as belonging to one of these classes. For each pixel, a set of features such as pixel intensity is considered. For each pixel, features form a pattern. The probability of belonging each pixel in each class is calculated by classification of these patterns. As part of the process, the variation of each pixel feature for each class need to be determined. Conditional probability distribution describes this variation.

These algorithms assign a probability to each pixel for belonging to a class. The probability for each pixel is obtained using probability density function (PDF) (Song et al. 2007) of target classes. These methods need accurate estimation of PDF. The parameters of the PDF can be determined by two approaches: parametric and nonparametric approaches. Nonparametric approaches do not consider any assumptions to obtain the parameters of the PDF

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from data. As a result, these approaches are more accurate than other ones but expensive (Zijdenbos and Dawant 1994). Parametric approaches use a known form for PDF function. Implementation of these approaches is easy but does not match real distribution of data, so sometimes lacks accuracy (Zijdenbos and Dawant 1994).

In parametric approaches, the forms of the class conditional are known, such as Gaussian distributions. Generally, a Maximum Likelihood (ML) or Maximum A Posteriori (MAP) approach is used to estimate the statistical model parameters. In addition, for the optimization process, one can use the Expectation- Maximization (EM) algorithm. Also, using a regularization term, local interactions between pixels (voxels) are incorporated in the process to make segmentation more robust against noise (Balafar 2011a; Balafar et al. 2011). Usually, MRF (Leemput et al. 1999; Zhang et al. 2001; Liang and Wang 2009) or Hidden Markov Chains (Bricq et al. 2008) are used as regularization term. In Bricq et al. (2008), a unifying Hidden Markov Chain (HMC) model for brain segmentation is proposed. The proposed method considers partial volume effect, and includes in-homogeneity correction (Balafar et al. 2010b), and a probabilistic atlas as prior.

Alternatively, in nonparametric approaches, the form of the distribution is not known. In addition, the number of clusters is not predefined and image data is used to estimate the number. Also, no initialization or assumptions is required. Mean-shift algorithm is instance of such approach. In some of nonparametric approaches such as the k-Nearest Neighbor classifier, class conditional distribution is not required.

Supervised or automatic algorithms are used to determine the distributions. In supervised methods, operator-selected regions from each tissue class are used to determine these distributions. Usually, in unsupervised algorithms, the image data is used to estimate these distributions by iterative procedure. Usually, it is assumed that prior to the segmentation operation, the a priori probability of occurrence of each class within the image and the number of classes is known. Generally, Bayesian rule (Bezdek et al. 1993) is used to determine the a posteriori probability that a pixel belongs to each tissue class. Additionally, segmentation is done using a maximum a posteriori (MAP) rule, where the pixel is assigned to the class in which a posteriori probability is the greatest.

In Bayesian approaches, all involved quantities in image are treated as random variables and the laws of probability is used to derive probabilistic algorithms for images. Bayesian decision theory (Duda and Hart 1973) is a quite powerful tool for probability. Bayesian decision theory assigns costs to each correct or wrong decision. In addition, the probabilities of occurring events are used to choose the decision with minimum risk. In Bayesian decision theory, the risk is the cost times the probability of a wrong action being taken. In image processing, Markov Random Fields (MRF) and a multidimensional extension of Markov chains are the most important Bayesian approach. A k–Markov chain is a sequence of random variables, $(X_1, X_2, \ldots, X_n)$. In k–Markov chain, the k preceding $X_{i-k}, \ldots, X_{i-1}$ are used to determine the marginal density of random variable X_i. A Markov Random Field, Markov network is an undirected graph describing a set of random variables having Markov property. A stochastic process has Markov property if conditional property distribution of future states of the process depends only upon the present state. MRFs can be factorized according to the cliques of the graph G. A clique in an undirected graph is a subset of its vertices that every two vertices in the subset are connected by an edge of the graph. Usually, the pixels of image are considered as random variables and mutually neighbouring pixels are considered as a clique. The Hamersley–Clifford theorem (Geman and Geman 1984) is the central result with regard to MRFs. In this theorem, joint density is considered positive and it is written in exponential form:

$$p_x(X) = \frac{1}{Z} \exp\left(-\sum_{c \in CL(G)} U_c(c)\right) \quad (1)$$

Well known from physicists, this is the Gibbs distribution. Where X is random variables, $p_x(X)$ is joint density and $CL(G)$ is the set of all cliques of the graph G. $U_c(c)$ is referred as factor potential or clique potential which is a function upon the variables in the clique c and describes the interactions between the variables in c. Z is partition function which is used for normalizing and describe by the following equation:

$$Z = \sum_X \exp\left(-\sum_{c \in CL(G)} U_c(c)\right) \quad (2)$$

In the Hamersley–Clifford theorem, only local interactions within the cliques are considered instead of computation of the joint density of all variables in the graph. A MRFs based 3D image segmentation algorithm is presented in Held et al. (1997). In this algorithm, manually labelled training samples are used to determine the parameters of an MRF model. Additionally, a simulated annealing algorithm is used to segment the image.

Gaussian mixture model is one of common statistic methods in parametric approaches. In this model, each pixel is assigned to one of a fixed number of known classes (Pan and Lu 2007). Usually, the intensity of input image is considered as input for Gaussian mixture model which is sensitive to noise (Balafar 2011b) and in-homogeneity. In addition, it cannot model non-Gaussian distribution problem caused by partial volume effects, desired tissues in presence of non-desired tissues caused by deviation and complex tissue spatial layout. For brain MRI segmentation, Lee et al. (2009) proposed an extended Gaussian mixtures model to overcome non-Gaussian distribution problem. Schroeter et al. (1998) present two methods for robust parameter estimation of Gaussian mixture to segment desired tissues of brain MRI in presence of no-desired tissues. The first method introduces an outlier rejection scheme, and the second method s forms mixtures of different kind of distributions.

There are two general methods to obtain parameters of Gaussian mixture model: expectation-maximization (EM) (Wang 2007) and Lioyd clustering algorithm (Jeong et al. 2003, 2004). Parameter obtaining methods are computationally expensive. A fast modified EM algorithm is proposed by M'hiri et al. (2007). Combining the Hidden Markov Random Field (HMRF) model and the Expectation-Maximization (EM) algorithm yields an accurate and robust segmentation algorithm, in turn, slows the approach. The authors used the Bootstrap re-sampling to speed up the processing time.

In order to make Gaussian mixture model more robust against complex spatial layout of the tissues, Greenspan et al. (2006) proposed the parameter-tied, constrained Gaussian mixture model (CGMM). The mixture model composed of a large number of Gaussians for each tissue is used to capture the complex spatial layout of the tissues. The parameters of the Gaussians related to a tissue are tied using intensity as global feature. The parameters are learned using the expectation-maximization (EM) algorithm.

Markov random field (MRF) is commonly used to capture spatial relations exist in the neighbor of each pixel. Sometimes, image segmentation methods contribute neighborhood information in segmentation process using MRF model (Li 1995). In medical images, most neighborhood pixels have the same target class. Segmentation method can model this spatial relation using MRF. By using neighborhood information, segmentation methods become more robust against noise. Usually, EM is used to estimate the parameters of MRF which is time consuming due to iterative nature of EM. Woolrich and Behrens proposed a

computationally efficient method for determining the MRF parameters which determines the amount of spatial regularization (Woolrich and Behrens 2006).

Usually MRF is incorporated in clustering models (Balafar et al. 2010c,d) to improve their robustness. Awate et al. (2007) proposed a MRF based fuzzy-segmentation method for brain MRI which is more robust against noise. Rajapakse et al. (1997) modeled brain MRI segmentation by a finite Gaussian mixture and used MRF to model smoothness and make Gaussian mixture model more robust against noise. For the same purpose, Li et al. (2003) proposed a MRF Gibbs model for brain MRI segmentation to integrate the local spatial information into EM and used the model for brain MRI segmentation. Ruan et al. (2000) proposed a MRF based solution for Partial effect in brain MRI segmentation by considering a separate class for mixtures of tissues.

The following works have been done in supervised segmentation: maximum likelihood (Clarke et al. 1993), Bayesian classifiers (Bezdek et al. 1993), discriminant analysis (Amato et al. 2003), and k-Nearest Neighbor classifiers (Bezdek et al. 1993; Clarke et al. 1993; Anbeek et al. 2005). Unsupervised, parametric (a mixture of Gaussians) clustering algorithm is applied for volume identification (Leemput et al. 1999; Held et al. 1997; Wells et al. 1996). The expectation maximization (EM) is used for parameter estimation. The algorithm is a two-step iterative procedure which simultaneously allows segmentation and in-homogeneity correction. In order to reduce misclassification errors arising from noise and partial volume averaging, Markov random field (MRF) Chellappa and Jain (1993) is used to incorporate contextual information in classification by allowing neighbor pixels to influence classification and considering the possible neighbors for pixels in each tissue using a priori information (Leemput et al. 1999; Held et al. 1997). Leemput et al. (2003) proposed an extension for EM to further address the partial volume problem. Zhang et al. (2001) further proposed a hidden MRF model for similar purpose. In order to automatically determine the MRF parameters, Woolrich and Behrens (2006) reported a computationally efficient algorithm for determining the amount of spatial regularization. Marroquin et al. (2002) proposed a variant of the EM algorithm for image segmentation. For each tissue, the proposed algorithm estimates a separate bias field. Ng and McLachlan (2004), M'hiri et al. (2007) reported a speed enhancement for EM. Additionally, Marroquin et al. (2003) proposed an alternative for EM to overcome high computation time due to iterative nature of EM. González Ballester et al. (2002) and Tohka et al. (2004) reported a statistical models namely a novel trimmed minimum covariance determinant (TMCD) for the estimation of the parameters of partial volume models to address partial volume averaging.

In Silva (2007), a nonparametric Bayesian model, known as Dirichlet process mixture model (DPMM) is proposed to overcome the limitations of current parametric finite mixture models. The DPMM permits unknown number of components in the mixture and allows robust segmentation of brain with unknown or incomplete specifications.

In Silva (2009), Markov chain Monte Carlo (MCMC) sampling techniques is used for exploring normal mixture models with an unknown number of components in the context of magnetic resonance imaging (MRI) segmentation. In contrast to EM-based procedures, in the paper, the number of components and the mixture component parameters are estimated jointly. In this paper, two different Markov chain Monte Carlo (MCMC) methods are compared, the reversible jump MCMC model (rjMCMC) and the Dirichlet process mixture model (DPM).

In Scherrer et al. (2009), a local cooperative unified segmentation (LOCUS) approach based on distributed local MRF models for brain segmentation is presented. The volume is partitioned into sub volumes and a set of *local* and *cooperative* Markov random field (MRF) models are distributed. In order to ensure consistency, neighbor local MRFs are estimated

cooperatively. The intensity in-homogeneity correction is not required due to precisely fitting of Local estimation with the local intensity distribution.

In Tohka et al. (2010), a local MRF-based segmentation method is presented. The authors believe local MRFs describe image data better than a global MRF. The image domain is divided into a set of sub-domains using Sub volume probabilistic atlases (SVPA). The image domain can be divided in multiple ways. Tissue probability maps (TPMs) is used to find proper division. TPMs specify the probability of belonging a certain voxel to a tissue. Homogeneous MRF models are defined on local image sub-domains. Then, local MRF models are used to construct a global MRF-based image model.

2 Background

2.1 Imaging modalities

The human body consists primarily of water and bones. Moreover, tracing elements exist in different parts of human body, such as iodine in the thyroid, tellurium in the liver and iron in blood. Medical imaging techniques use different properties of these elements. The important modalities are X-ray, computed tomography (CT), positron emission tomography (PET), single-photon emission computed tomography (SPECT), ultrasound and magnetic resonance imaging (MRI).

The X-ray, invented by Wilhelm in 1895, is based on the measurement of the transmission of X-ray through the body. The disadvantage of X-ray is the high level of radiation which can cause the disease such as cancer and eye cataract. In X-ray computer assistance tomography (CT), image is reconstructed from a large number of X-rays. In PET, radio nuclides are injected into patient's body which attach to a specific organ. SPECT is a nuclear medicine tomographic imaging techniques which able to produce true 3D image. It uses gamma rays. Ultrasound measures the reflection of ultrasonic waves transmitted through the body and is the best modality for investigation of soft tissues.

The MR imaging (MRI), invented in 1970, is a popular method in medical imaging. MRI scanning relatively is safe and unlike other medical imaging modalities, can be used as often as necessary. Moreover, it can be adapted to image the brain.

Clinical MRI is based on the hydrogen nucleus due to their abundance in the human body and their magnetic resonance sensitivity. For image formation, a large static magnetic field is used to perturb magnetic moments of proton exists in the hydrogen nucleus from their equilibrium and observing how perturbed moments relaxes back to their equilibrium. Naturally, the protons are oriented randomly. But in existence of a static magnetic field, they line up with the field and the net magnetization of protons tends toward the direction of the field. In the existence of enough energy, it is possible to make the net magnetization zero. In the relaxation process an induced electronic signal is recorded. The strength and duration of the signal depend on three quantities:

1. ρ (proton density)
2. spin–lattice relaxation time: the time which describes how fast the net magnetization relaxes back to its equilibrium (T1).
3. spin–spin relaxation time: the time in which Magnetization components decrease to zero (T2).

In scanning of a person's body, by using different parameters setting, it is possible to obtain three different images of the same body: T1-weighted, T2-weighted and ρ-weighted.

2.2 Databases for segmentation validation

Every new segmentation method needs to be validated by comparing their result with a truth model. This comparison is done by a quantitative index to measure the efficacy of new algorithm. Usually, segmentation made by experts is used as truth model. Also new segmentation methods can be evaluated using segmentation of physical phantoms images (Pham et al. 2000) or synthetic images.

2.2.1 Brainweb

Brainweb (http://www.bic.mni.mcgill.ca/brainweb/), a synthetic image database has been developed by the McConnell Brain Imaging Centre of the Montreal Neurological Institute (MNI). A manually segmented head image passes through an MR simulator to produce the synthetic images. MR simulator allows producing synthetic images with different levels of noise and intensity in-homogeneity. At first version, Brainweb provided two anatomical models, one of a normal brain and the other of a brain with multiple sclerosis lesions. The ground truth (manual) segmentation has nine normal tissue classes. Additionally, it has partial-volume content levels for each image pixel. Recently, other twenty normal models have been added. Currently added models have 11 normal tissue classes (Aubert-Broche et al. 2006a,b).

2.2.2 The internet brain segmentation repository (IBSR)

The Center for Morphometric Analysis (CMA) at the Massachusetts General Hospital (MGH) provides the Internet Brain Segmentation Repository (IBSR) (http://www.cma.mgh.harvard.edu/ibsr/), an on-line database of head MR images of more than 40 subjects along with truth models for their segmentation. Truth models for some of MR images have 43 individual structures and for others have three tissue classes, gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF).

2.2.3 The section for biomedical image analysis (SBIA)

For generating simulated inter-subject head deformations, a software has been developed by the Section for Biomedical Image Analysis (SBIA) in the department of Radiology at the University of Pennsylvania (http://www.\protect\kern+.1667em\relaxrad.upenn.edu/sbia/). Xue et al. (2006) used these simulated inter-subject head deformations for validation studies of atlas-based segmentation methods.

3 Literature review

The reported results for neighborhood based extensions for statistical segmentation algorithms are presented. Three main brain tissues are considered which corresponds to grey matter (GM), white matter (WM) and cerebral spinal fluid (CSF). In order to investigate their effectiveness, the results of the algorithms are compared quantitatively.

3.1 Phantom based brain images

In Zhang et al. (2001), a Hidden Markov Random Field Model and the Expectation-Maximization Algorithm are used for image segmentation. The HMRF-EM and MEM are applied

on two generated images consisting of two constant regions. Two images are degraded with the same simulated bias field but with different Gaussian noise levels (3 and 15%). Both algorithms give perfect segmentation results, in presence of 3% noise level. However, for 15% noise level, the HMRF-EM algorithm visually gives segmentation results much better than the MEM algorithm.

In Greenspan et al. (2006), the parameter-tied, constrained Gaussian mixture model (CGMM) is proposed. Average similarity index for different algorithms with variant noise levels (3, 5, 7, 9%) are: CGMM (0.93 0.93 0.92 0.895) and KVL (0.925, 0.915, 0.895 and 0.865). In the presence of very low noise levels, the CGMM method performs Comparable with KVL algorithm. CGMM outperforms the KVL algorithm when noise levels are high. The similarity of the CGMM decreases more slowly than KVL algorithm when noise level increases.

In Silva (2009), Markov chain Monte Carlo (MCMC) sampling techniques is used for exploring normal mixture models with an unknown number of components. In this paper, two different Markov chain Monte Carlo (MCMC) methods are compared, the reversible jump MCMC model (rjMCMC) and the Dirichlet process mixture model (DPM). DPM, rjMCMC, KVL and MPM-MAP are applied on simulated image volumes from Brainweb. Average similarity index for different methods with variant noise levels (3, 5, 7, 9%) are: DPM (0.942, 0.93, 0.9 and 0.89), rjMCMC (0.92, 0.897, 0.882 and 0.875), KVL (0.922, 0.923, 0.901 and 0.874) and MPM-MAP (0.955, 0.942, 0.905 and 0.875). DPM produces similarity index higher than rjMCMC in all noise levels. In addition, DPM outperforms competing methods in 9% noise level.

In Bricq et al. (2008), a unifying Hidden Markov Chain (HMC) model for brain segmentation which includes partial volume effect, in-homogeneity correction, and a probabilistic atlas as prior is proposed. HMC, EMS (Leemput et al. 2003), SPM5 (Ashburner and Friston 2005) are applied on Brainweb image volumes with noise levels varying from 0 to 9 and 20% in-homogeneity. The proposed method outperforms competing methods in studied noise levels. The similarity index for all three methods decreases, when the noise level increases. Also, the effect of incorporating multimodality in HMC and EMS is investigated. The multimodality increases the similarity indexes. HMC using both T1 and T2 images produces similarity index higher than similarity index on T1 images and higher than similarity index for multimodal EMS.

In Scherrer et al. (2009), a local cooperative unified segmentation (LOCUS) approach based on distributed local MRF models for brain segmentation is presented. LOCUS is applied on eight BrainWeb phantoms, with variant noise levels (3, 5, 7, and 9%) and different in-homogeneity (20 and 40%) for each noise level. LOCUS is compared with published results for SPM5 (Ashburner and Friston 2005) and FAST (Zhang et al. 2001). For WM, FAST outperforms competing methods and LOCUS has the second performance. For GM, LOCUS outperforms competing methods in the presence of high noise levels and has the second performance in 3% noise level. The mean Dice similarity indexes for different methods are: SPM5 = 86.4%, FAST = 88.4% and LOCUS-T = 88.5%. The mean computation times for 3D image volume segmentation are: LOCUS = 4 min, FAST = 8 min and SPM5 ≥ 10 min.

All above mentioned methods try to capture complex spatial layout. HMRF-EM and HMC use Hidden Markov models to capture complex interaction between pixels. These methods speed up process due to hidden variables they use. CGMM and LOCUS use distributed local models to capture complex spatial layout. CGMM uses large number of Gaussians while LOCUS uses distributed local MRFs for this purpose. MCMC uses sampling to capture necessary number of components.

There are not any reported results for EM extension (NWEM). Therefore, this method is implemented and applied on simulated image volumes from Brainweb. Average similarity index for this method with variant noise levels (3, 5, 7, 9%) are: (0.962, 0.9486, 0.9291, 0.9083). NWEM produces the average similarity indices ρ higher than previous report results in this section. In contrast to other mentioned methods, NWEM uses average of the neighbourhood values instead of Markov models to smooth the result.

3.2 Real images

The results of applying EM extensions on the MRI images are reported in the IBSR by the Centre for Morphometric Analysis at Massachusetts General Hospital. 20 normal data volumes with T1-weighted sequence are used. The average similarity index values of EM extensions for 20 normal are presented. The Jaccard similarity index for different methods are: adaptive MAP = 0.5655, biased MAP = 0.56, fuzzy c-means = 0.52, Maximum Aposteriori Probability (MAP) = 0.552, Maximum-Likelihood = 0.543, tree-structure k-means = 0.524 and Manual (4 brains averaged over 2 experts) = 0.854.

In Zhang et al. (2001), a Hidden Markov Random Field Model and the Expectation-Maximization Algorithm are used for image segmentation. The HMRF-EM and MEM are applied on several real 2-D MR images with simulated bias field. The HMRF-EM algorithm visually produces better results.

Also, HMRF-EM is applied on two data sets with very different bias field patterns and image qualities. First dataset contains real 3-D images taken by different scanners and second one consists of several coronal scans from IBSR. In both cases, HMRF-EM visually performs well.

In Tohka et al. (2004), a novel trimmed minimum covariance determinant (TMCD) method for partial volume effect (PVE) estimation is applied on 20 normal image volumes from IBSR. The average jaccard values are 0.6637 (WM) and 0.6807 (GM). The proposed method outperforms reported results from IBSR website.

In Greenspan et al. (2006), a parameter-tied, constrained Gaussian mixture model (CGMM) is proposed. The CGMM algorithm is applied on 18 volumes from 20 normal image volumes in IBSR website. The CGMM results are compared with reported results from the IBSR website, as well as with the *Marroquin algorithm* (Marroquin et al. 2002). Marroquin's algorithm is an atlas-based Bayesian segmentation algorithm. Jacc similarity index and standard deviations for different methods are: CGMM = 0.67, SD = 0.05, marro = 0.67, SD = 0.1. The CGMM algorithm outperforms reported results from the IBSR. The results indicate comparable performance for CGMM algorithm and the Marroquin algorithm but with lower standard deviation for CGMM algorithm.

Also, the CGMM algorithm is applied on 18 new added image volumes and the results are compared with the KVL algorithm. Dic similarity index and standard deviations for different methods are: CGMM = 0.818, SD = 0.052, KVL = 0.821, SD = 0.035. The CGMM algorithm performs comparably to the KVL algorithm.

In Bricq et al. (2008), a unifying Hidden Markov Chain (HMC) model for brain segmentation which includes partial volume effect, in-homogeneity correction, and a probabilistic atlas as prior is proposed. HMC, EMS (Leemput et al. 2003), SPM5 (Ashburner and Friston 2005) are applied on 18 new added normal image volumes. Dic similarity index for different methods are: HMC = 0.8323, EMS = 0.824 and SPM5 = 0.82. The similarity index for proposed method is higher than competing methods, meaning that proposed method produces more accurate segmentation results.

In Silva (2007), a nonparametric Bayesian model, known as Dirichlet process mixture model (DPMM) is applied on 13 images (1_24, 2_4, 5_8, 6_10, 7_8, 11_3, 12_3, 13_3, 15_3, 16_3, 100_23, 110_3 112_2) from the 20 normal T1-weighted brain image volumes from IBSR. Dice similarity index for different methods are: DPMM = 0.7071, MPM-MAP = 0.6546. The similarity index for the proposed method is higher than the competing method.

In Scherrer et al. (2009), a local cooperative unified segmentation (LOCUS) approach based on distributed local MRF models for brain segmentation is presented. LOCUS is applied on the 20 normal T1-weighted brain image volumes from IBSR. LOCUS is compared with published results for SPM5 and FAST. Dic similarity index for different methods are: LOCUS = 0.765, SPM5 = 0.81, FAST = 0.765. SPM5 outperforms LOCUS and FAST. This dataset consist of low resolution, low contrast and highly artifacted image volumes. LOCUS and FAST algorithms use MRF models and it seems that MRF models over-regularize the segmentation due to low quality conditions.

Also, LOCUS is applied on the 18 new added normal T1-weighted brain image volumes from IBSR. LOCUS is compared with published results for SPM5 and FAST. Dic similarity index for different methods are: LOCUS-T = 0.815, SPM5 = 0.795, FAST = 0.82. LOCUS-T outperforms SPM5 and gives comparable result with FAST.

There are not any reported results for NWEM (an EM extension). Therefore, this method is implemented and applied on 20 normal data volumes. The average similarity index for this method is 0.7618. NWEM produces the average similarity indices ρ higher than reported results in IBSR.

In Tohka et al. (2010), a local MRF-based method (SVPASEG) which is based on Sub volume probabilistic atlases (SVPA) and tissue probability maps (TPMs) is proposed. SVPASEG and the homogeneous global MRFs model (MRFSEG) are applied on 20 normal image volumes from IBSR. Jacc similarity index for different methods are: MRFSEG-TPM with N3 in-homogeneity correction = 0.684, SVPASEG-TPM with N3 in-homogeneity correction = 0.6915, SVPASEG-TPM = 0.6865, A-MAP = 0.5655, BrainSuite = 0.6295, PVE-TMCD = 0.6695, MPM-MAPCGMM = 0.6725 and CGMM = 0.66. MRFSEG assumes the same model across the brain for each tissue class intensities. Therefore, MRFSEG is not tested without in-homogeneity correction. SVPASEG-TPM with N3 in-homogeneity correction outperforms other competing methods.

Also, the methods are applied on the eighteen newly added image volumes from the IBSR. Dic similarity index for different methods are: SVPASEG-PVE = 0.8634, SVPASEG-TPM = 0.8532, MRFSEG-PVE = 0.833, MRFSEG-TPM = 0.8434, MRFSEG-TPM=, Awate = 0.847, CGMM = 0.8280 and EMS = 0.822. SVPASEG-PVE outperforms other competing methods.

TMCD, CGMM, DPMM, SVPASEG are evaluated on 20 image volumes from IBSR. CGMM used 18 of 20 image volumes and DPMM used 13 of 20 image volumes. Also, 18 new added images from IBSR are used to evaluate CGMM, HMC, LOCUS and SVPASEG. From the mentioned methods, TMCD and HMC consider partial volume effect. HMC and SVPASEG consider inhomogeneity correction and an atlas as pirior.

4 Conclusion

In this paper a critical review for Gaussian Mixture Model based brain segmentation is presented. This paper gives a review of the most recent works in this area and contains database, similarity index, and state-of-art methods which in different works has been used. Also, this

paper presents the results achieved by different works which can be used by researchers to compare their new developed methods.

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