

MRI-Based Brain Tumor Segmentation using Modified Stable Student's t from Burr Mixture Model with Bayesian Approach

Pravitasari, A. P.^{*1,2}, Iriawan, N.¹, Safa, M. A. I.¹, Irhamah¹,
Fithriasari, K.¹, Purnami, S. W.¹, and Ferriastuti, W.³

¹*Department of Statistics, Faculty of Mathematics, Computing,
and Data Science, Institut Teknologi Sepuluh Nopember, Surabaya,
Indonesia*

²*Department of Statistics, Faculty of Mathematics and Natural
Sciences, Universitas Padjajaran, Bandung, Indonesia*

³*Department of Radiology, Faculty of Medicine, Universitas
Airlangga, Surabaya, Indonesia*

E-mail: anindya.apriliyanti@unpad.ac.id

** Corresponding author*

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ABSTRACT

Finite Mixture Models have been developed for brain tumor image segmentation using the Magnetic Resonance Imaging (MRI) as a media. The goal is to obtain the best fit model with the appropriate segmentation results to describe the Region of interest (ROI). Image segmentation techniques with mixture model are used for clustering pixels based on the same color intensity (grayscale). Many studies of mixture models using asymmetric distributions, such as skew normal and skew- t distribution, have been expanded, owing to the fact that the data pattern in the MRI is not always symmetrical. Furthermore, the research uses some approaches

to adaptively capture data pattern and capable of accommodating the skew and even the thicker tails than normal distribution. This technique is called the Neo-Normal. MRI-based segmentation using Modified Stable Student's t from Burr (MSTBurr) distribution was proposed with the aim of creating an adaptive segmentation method which would be adapt to MRI data pattern distribution changes. The segmentation model is optimized by employing the Bayesian method coupled along with the Markov chain Monte Carlo (MCMC) approach because the analytical solutions are considered complicated. The results of the analysis demonstrated indicate that the MSTBurr Mixture Model (MSTBurr-MM) could capture the pattern of MRI brain tumor image better than the Gaussian Mixture Model (GMM) approach.

Keywords: Bayesian, Image Segmentation, Mixture Model, MSTBurr, Neo-Normal.

1. Introduction

Brain tumors are abnormal cell growths in the brain or metastases in other organs (ABTA, 2015). According to Dr. Soetomo Regional General Hospital (RSUD) in Surabaya, Indonesia, the number of brain tumor cases increases yearly with women being the higher carrier. The Magnetic Resonance Imaging (MRI) is used to detect this disease with specifications provided in 1.5 Tesla and above (3 Tesla or 7 Tesla) because the higher it is, the better the image quality. This study therefore aims to provide an approach to improving the quality of MRI-brain tumor, by applying an image segmentation technique using the statistical model.

Image segmentation aims to separate the ROI regions from the Non-ROI area. The results, therefore, are more easily obtained for further analysis (Shapiro and Stockman, 2001). The Model-Based Clustering, is often used to carry out this procedure. This grouping technique optimizes the similarity between objects based on probabilistic data distribution (Grün, 2018), making it possible to be built using mixture model analysis. GMM is one of finite mixture model widely used and implemented in image segmentation. Its use has the disadvantage of being less flexible to the general form of data (Ji et al., 2017), due to the characteristic of the normal distribution which is symmetrical and short-tailed in shape (Ji et al., 2016). This study aims at utilizing another approach by using the other type of distribution in the finite mixture model (FMM), which is considered to be more flexible and capable of capturing the image pattern.

The technique naturally used to capture data pattern and capable of accommodating the skew and thicker tails is called the Nearly-Normal or Neo-Normal distributions (Choir et al., 2019). MSTBurr has been developed with the aim of creating an adaptive distribution to naturally change patterns (Iriawan, 2012). In this paper, this distribution is used to conduct the mixture model. However, analytical solution for estimating its parameter is tasking since the likelihood function cannot be simplified. Therefore, in order to optimize the parameter, the Bayesian approach coupled with Markov chain Monte Carlo (MCMC) is utilized (Iriawan, 2000). The proposed method is expected to be able to produce a segmented image of the brain tumor site better, and give an alternate suggestion to Dr. Soetomo.

2. MSTBurr Mixture Model

In this study, FMM is used to determine segmentation, this model is represented as a combination of several sub-populations from the same or different distributions. Suppose y is defined as the pixel grayscale intensities of the image, the mixture distribution of the univariates multimodal can be approximated using equation (1) (Iriawan, 2012).

$$f(y|\boldsymbol{\theta}, \mathbf{w}) = \sum_{j=1}^K w_j f_j(y|\theta_j) \quad (1)$$

where $f_j(y|\theta_j)$ is the j^{th} density function of j^{th} subpopulation/ component, K is the number of components in the mixture distribution, $\boldsymbol{\theta}$ is a vector of parameters with the elements of $(\theta_1, \theta_2, \dots, \theta_K)$, \mathbf{w} is a vector of proportion parameter which the elements of (w_1, w_2, \dots, w_K) , and w_j is proportion parameter of mixture components that satisfy $0 \leq w_j \leq 1, j = 1, 2, \dots, K$ and $\sum_{j=1}^K w_j = 1$. The likelihood of n pixel grayscale intensities is given by

$$L(\mathbf{y}|\boldsymbol{\theta}, \mathbf{w}) = \prod_{i=1}^n f(y_i|\boldsymbol{\theta}, \mathbf{w}) = \prod_{i=1}^n \sum_{j=1}^K w_j f_j(y_i|\theta_j) \quad (2)$$

where y_i must come from the domain $0 < y_i < 255$. It is the domain of grayscale intensities, which 0 represents the darkest grayscale (black), and 255 represents the lightest one (white).

The general mixture model in equation (1) would become the specific distribution when $f_j(y|\theta_j)$ is described to the specific density. In GMM, $f_j(y|\theta_j)$ is the form of Gaussian or normal densities. This study will employ of the MSTBurr distribution which is a type of Neo-Normal technique.

The basic idea of using Neo-normal distribution is in accordance with the various patterns (symmetrical and or asymmetrical) on each MRI data cluster. It can accommodate both symmetrical and asymmetrical patterns adaptively through its skew parameter. Iriawan (2000) developed a Neo normal distribution technique named the Modified Stable Student's t from Burr distribution (MSTBurr). It was developed with the aim of making an adaptive distribution to the changes of the pattern data naturally.

The MSTBurr is the Burr II distribution that stabilized to Student's t by employing the factor k in the following standardized form

$$k = \frac{\Gamma\left(\frac{n+1}{2}\right) \left(1 + \frac{1}{\alpha}\right)^{(\alpha+1)}}{\sqrt{n\pi} \Gamma\left(\frac{n}{2}\right)}, \quad (3)$$

where n is the degree of freedom that can be approach with the number of data. The probability density function for MSTBurr is shown in equation (4).

$$f(y|n, \alpha, \mu, \phi) = \frac{\frac{k}{\phi} \exp\left(-k\left(\frac{y-\mu}{\phi}\right)\right)}{\left(1 + \frac{\exp\left(-k\left(\frac{y-\mu}{\phi}\right)\right)}{\alpha}\right)^{(\alpha+1)}} \quad (4)$$

with $0 < y < 255$, $0 < \mu < 255$, $k > 0$, $\alpha > 0$, where μ is the location parameter, ϕ is the dispersion parameter, and α is the skewness parameter. Based on equation (1) we can write MSTBurr with K mixture components in equation (5).

$$f(y|\mathbf{n}, \boldsymbol{\alpha}, \boldsymbol{\mu}, \Phi, \mathbf{w}) = \sum_{j=1}^K w_j \frac{\left(\frac{k}{\phi_j} \exp\left(-k\left(\frac{y-\mu_j}{\phi_j}\right)\right)\right)}{\left(1 + \frac{\exp\left(-k\left(\frac{y-\mu_j}{\phi_j}\right)\right)}{\alpha_j}\right)^{(\alpha_j+1)}} \quad (5)$$

2.1 Bayesian MCMC

The Bayesian approach is used to estimate the MSTBurr mixture model's parameters owing to the non-close form of the posterior distribution, which acts as the multiplication between the likelihood function and the prior distribution. Based on equation (5), the function is formed by observing the latent variable, z_{ij} , as follows:

$$L(\mathbf{y}, \mathbf{z}|\mathbf{n}, \boldsymbol{\alpha}, \boldsymbol{\mu}, \Phi, \mathbf{w}) = \prod_{i=1}^n \prod_{j=1}^K \left(\frac{w_j \left(\frac{k}{\phi_j} \exp\left(-k\left(\frac{y_i-\mu_j}{\phi_j}\right)\right)\right)}{\left(1 + \frac{\exp\left(-k\left(\frac{y_i-\mu_j}{\phi_j}\right)\right)}{\alpha_j}\right)^{(\alpha_j+1)}} \right)^{z_{ij}} \quad (6)$$

The prior distribution for MSTBurr has been discussed by Iriawan (2000), while its proportion of the mixture distribution components is discussed by Gelman et al. (2014). The following are prior distributions for each parameter:

$$\begin{aligned} \mu_j &\sim \text{Gaussian}(\omega, \sigma^2), \\ \varphi_j &\sim \text{InversGamma}(a, b), \\ \alpha_j &\sim \text{GeneralisedSymmetricalBeta}(\tau, \tau, l, u), \\ w_j &\sim \text{Dirichlet}(\beta_1, \beta_2, \dots, \beta_k). \end{aligned}$$

Since the likelihood function and prior distribution are known, the joint posterior density could be provided. Therefore, full conditional posterior distribution is needed to generate parameter values that will be estimated using

the MCMC. The following are the Full conditional posterior distributions for each parameter. For simplicity, the formula are perform in logarithm.

- a) The full conditional posterior of $\alpha_j, j = 1, 2, \dots, K$ is shown in equation (7), where *const* is all parts of the equation that do not contain the α_j parameter.

$$\begin{aligned} \log f(\alpha_j | \mathbf{y}, \mathbf{z}, n_j, \mu_j, \phi_j, w_j) = & \text{const} - \sum_{i=1}^n k \left(\frac{y_i - \mu_j}{\phi_j} \right) + \\ & (\tau_j - 1) (\ln(\alpha_j - l_j) + \ln(u_j - \alpha_j)) - \\ & (\alpha_j + 1) \sum_{i=1}^n \ln \left(1 + \frac{\exp\left(-k \left(\frac{y_i - \mu_j}{\phi_j} \right)\right)}{\alpha_j} \right). \end{aligned} \quad (7)$$

- b) The Full conditional posterior for $\mu_j, j = 1, 2, \dots, K$ is shown in equation (8),

$$\begin{aligned} \log f(\mu_j | \mathbf{y}, \mathbf{z}, n_j, \mu_j, \phi_j, w_j) = & \text{const} - \sum_{i=1}^n k \left(\frac{y_i - \mu_j}{\phi_j} \right) - \frac{1}{2} \left(\frac{\mu_j - \omega_j}{\sigma_j} \right)^2 - \\ & (\alpha_j + 1) \sum_{i=1}^n \ln \left(1 + \frac{\exp\left(-k \left(\frac{y_i - \mu_j}{\phi_j} \right)\right)}{\alpha_j} \right), \end{aligned} \quad (8)$$

where all parts of the equation that do not contain the μ_j parameter are compiled to *const*.

- c) The Full conditional posterior for $\phi_j, j = 1, 2, \dots, K$ is shown in equation (9),

$$\begin{aligned} \log f(\alpha_j | \mathbf{y}, \mathbf{z}, n_j, \mu_j, \phi_j, w_j) = & \text{const} - \sum_{i=1}^n k \left(\frac{y_i - \mu_j}{\phi_j} \right) - \\ & (a_j + 1) \ln(\phi_j) - \frac{b_j}{\phi_j} - \\ & (\alpha_j + 1) \sum_{i=1}^n \ln \left(1 + \frac{\exp\left(-k \left(\frac{y_i - \mu_j}{\phi_j} \right)\right)}{\alpha_j} \right), \end{aligned} \quad (9)$$

where all parts of the equation that do not contain the ϕ_j parameter are defined by *const*.

- d) The Full conditional posterior for $w_j, j = 1, 2, \dots, K$ is shown in equation (10),

$$f(w_j | \mathbf{y}, \mathbf{z}, n_j, \alpha_j, \phi_j) \propto \prod_{j=1}^K w_j^{\sum_{i=1}^n z_{ij}} = \prod_{j=1}^K w_j^{\left(\sum_{i=1}^n z_{ij} + 1\right) - 1}. \quad (10)$$

This is a *Dirichlet* $\left(1 + \sum_{i=1}^n z_{i1}, \dots, 1 + \sum_{i=1}^n z_{iK}\right)$ distribution.

e) The posterior of $\mathbf{z}_i, i = 1, 2, \dots, n$

Latent variable z_{ij} for $i = 1, 2, \dots, n$ and $j = 1, 2, \dots, K$, only has two possibilities values, that is 0 or 1. Based on the Bayes theorem, therefore, the probability of every i^{th} data on each j^{th} cluster is calculate using

$$f(z_{ij}|y_i, n_j, \alpha_j, \mu_j, \phi_j, w_j) = \frac{f(y_i|n_j, \alpha_j, \mu_j, \phi_j) w_j}{f(y_i)}, \quad (11)$$

for $j = 1, 2, \dots, K - 1$, And for K^{th} cluster is calculate using

$$f(z_{ij}|y_i, n_j, \alpha_j, \mu_j, \phi_j, w_j) = 1 - \sum_{j=1}^{K-1} \frac{f(y_i|n_j, \alpha_j, \mu_j, \phi_j) w_j}{f(y_i)}.$$

The biggest probability of $f(z_{ij}|y_i, n_j, \alpha_j, \mu_j, \phi_j, w_j)$, the value of related z_{ij} is set to one, and zero for other j^{th} clusters. Therefore, the value of \mathbf{z}_i , where $\mathbf{z}_i = (z_{i1}, z_{i2}, \dots, z_{iK})$ follows the *Multinomial* $(1, \gamma_{i1}, \dots, \gamma_{iK})$ distribution with

$$\gamma_{ij} = \frac{f(y_i|n, \alpha_j, \mu_j, \phi_j) w_j}{f(y_i)}. \quad (12)$$

Full conditional posterior for each parameter will construct a sequence of steps in a Gibbs sampling algorithm estimating the K component mixture model. This algorithm would be iteratively run until it reaches convergence and help in optimizing the estimated parameter numerically (Susanto et al., 2018). The details of the step are presented in Algorithm 1.

Algorithm 1 : Gibbs sampling for estimating the MSTBurr mixture model

- 1) Pick the convenient initial value of the parameters $\alpha_1^0, \dots, \alpha_K^0, \mu_1^0, \dots, \mu_K^0, \phi_1^0, \dots, \phi_K^0, w_1^0, \dots, w_K^0, z_{1j}^0, \dots, z_{nj}^0$, and set $t = 0$
- 2) Update each variable in turn at the t^{th} iteration, $t = t + 1$
 - a) Update $\alpha_j, j = 1, 2, \dots, K$, by generating sample α_j^t from equation (7),
 - b) Update $\mu_j, j = 1, 2, \dots, K$, by generating sample μ_j^t from equation (8),
 - c) Update $\phi_j, j = 1, 2, \dots, K$, by generating sample ϕ_j^t from equation (9),

- d) Update $w_j, j = 1, 2, \dots, K$, by generating sample w_j^t from *Dirichlet* $\left(1 + \sum_{i=1}^n z_{i1}, \dots, 1 + \sum_{i=1}^n z_{iK}\right)$ distribution,
 - e) Update \mathbf{z}_i , by generating sample \mathbf{z}_i^t from *Multinomial* $(1, \gamma_{i1}, \dots, \gamma_{iK})$ distribution.
- 3) Repeat step 2) while $t = 1, 2, \dots, T$ (T is number of samples generated).

2.2 Cluster Validation

The optimum number of cluster in this study is measured by the Silhouette Coefficient (SC) and provided by its maximum value. The following Algorithm steps are required to achieve this: (Thinsungnoena et al., 2015)

Algorithm 2 : Calculation of Silhouette Coefficient

- 1) Calculate p_i^j as the average squared Euclidean distance to i^{th} data with other data in a single cluster.
- 2) Calculate q_i^j as the minimum of average squared Euclidean distance of i^{th} data to other data from the different cluster.
- 3) Calculate the SC value of every i^{th} data at j^{th} cluster using formula of

$$SC_i^j = \frac{q_i^j - p_i^j}{\max(p_i^j, q_i^j)}. \tag{13}$$

- 4) Calculate SC for each j^{th} cluster using formula of

$$SC_j = \frac{1}{n_j} \sum_{i=1}^{n_j} SC_i^j. \tag{14}$$

- 5) Calculate the overall SC using formula of

$$SC = \frac{1}{K} \sum_{j=1}^K SC_j. \tag{15}$$

3. Application of MRI Brain Tumor Image Segmentation

This study uses real data sets from Dr. Soetomo Surabaya, which is already medically certified. Furthermore, it tries to segment the two types of sequences

in MRI brain tumor image. The first type is a slice of a brain image with the swelling area of a the tumor known as ax T2 Flair, which means the axial slice of the brain T2 Fluid Attenuated Inversion Recovery, without any contrast. The second is the slice of a brain image with contrast, named ax T1 memp+C. The ROI of ax T2 Flair, therefore, is larger than the ax T1 memp+C. Figures 1 (a) and (b) displays the before and after preprocessing images of ax T2 Flair and ax T1 memp+C. Preprocessing is conducted for image enhancement and the fat is removed along the skull bone capable of distracting the next segmentation process.

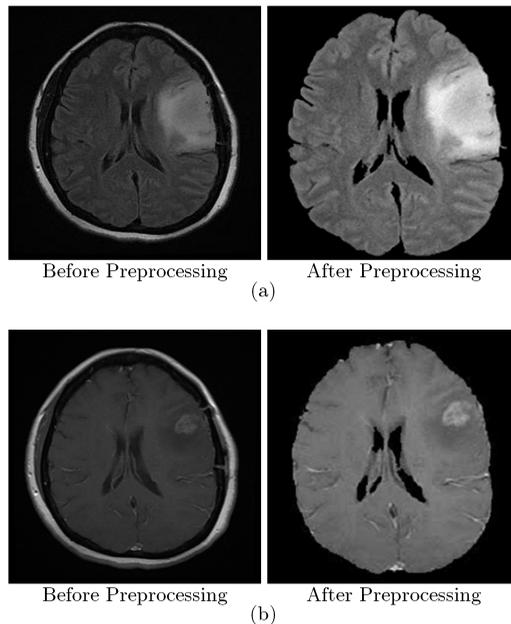


Figure 1: Image of MRI sequence (a) ax T2 Flair and (b) ax T1 memp+C, before and after preprocessing

The histogram of the preprocessing images is shown in Figure 2. It indicates that the MRI image is a mixture which shows a multimodal histogram. In Figure 2 (a), three modes of the histogram can easily be captured, while only two modes in Figure 2 (b). After preprocessing, Figures 1 (a) and (b), it can be seen that the number of ROI pixels on ax T1 memp + C is less than ax T2 Flair with the ROI in Figure 2 (b) looks smaller but somewhat less visible. This point of view are still in subjective matter, however applying the mixture model framework for analyzing this image is considered suitable for the segmentation. The preprocessing images will be segmented with MSTBurr-MM and the result

compared with the GMM. The programming code for the GMM segmentation is adopted from the research of Sianipar (2017).

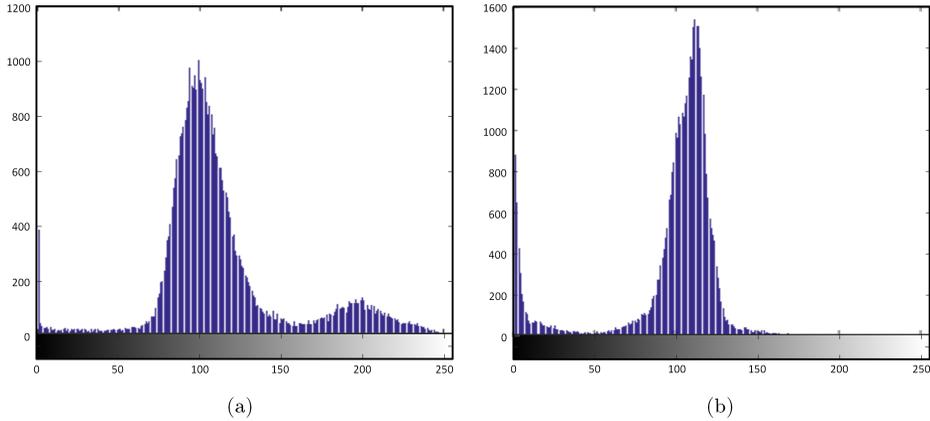


Figure 2: Histogram after preprocessing, for sequence (a) ax T2 Flair and (b) ax T1 memp+C

The images will be segmented into $K = 2, 3, \dots, 7$ number of clusters. The optimum number of cluster would be selected by calculating their SC . Table 1 shows the results of segmentation using both methods for MRI Sequence ax T2 Flair and ax T1 memp+C. While the Figure 3 and Figure 4 show the difference of SC both MSTBurr-MM and GMM for MRI Sequence ax T2 Flair and ax T1 memp+C. The $K = 2$ will be eliminated from the candidate optimum number of cluster since the segmented image just only able to recognize the brain and its background.

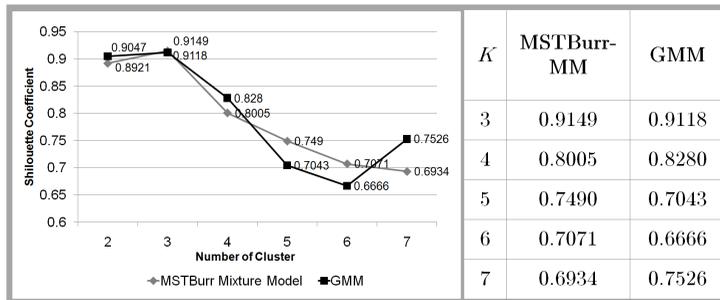


Figure 3: The SC values of MSTBurr-MM and GMM for sequence ax T2 Flair

In Figure 3, it can be determined that the optimum number of clusters in both MSTBurr-MM is greater than GMM with almost the same SC value. This indicates that MSTBurr-MM gives a better result than GMM in segmenting

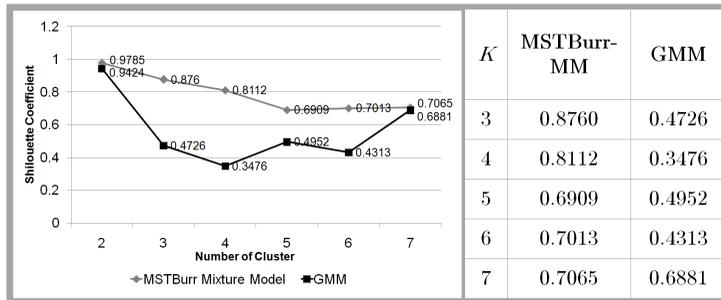


Figure 4: The SC values of MSTBurr-MM and GMM for sequence ax T1 memp+C

MRI sequence ax T2 Flair, though less parsimonious than GMM. The different result is shown in Figure 4, which is visualizing the difference of SC values for MSTBurr-MM and GMM in MRI sequence ax T1 memp+C. This Figure 4 demonstrates the optimum number of three clusters for MSTBurr-MM that is almost double from the GMM on seven clusters. This result indicates that MSTBurr-MM is more parsimony, since with a smaller number of clusters, the model has already able to represent the pattern of MRI image. Table 2 shows the optimum number of clusters, the SC value, the member of parameter of MSTBurr and GMM for a different sequence of MRI.

Estimates parameters of MSTBurr-MM for the optimum number of cluster is shown in Table 3. The ROI of both sequences is given by the third cluster. For the sequence ax T2 Flair, the ROI has grayscale color mean of 197.263, while the ax T1 memp+C is 153.512. The dispersion parameter ϕ , indicate the spread range of the ROI grayscale color. This parameter shows that sequence ax T2 Flair has larger ROI grayscale range than ax T1 memp+C. The skewness parameter α shows that both sequences have the left skew pattern.

Table 1: Result of segmentation between MSTBurr-MM and GMM

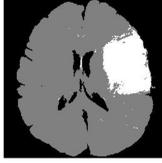
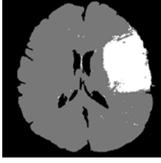
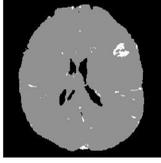
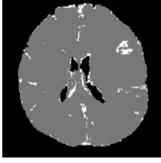
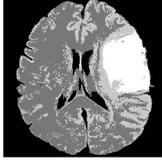
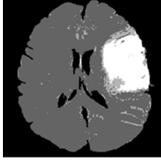
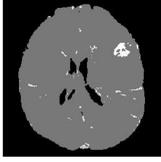
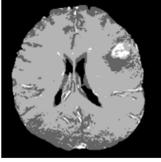
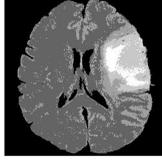
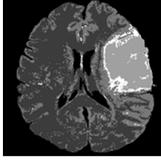
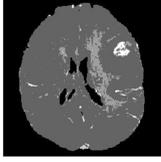
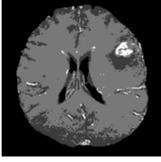
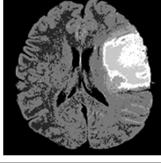
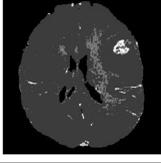
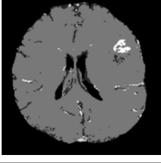
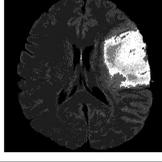
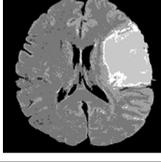
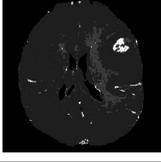
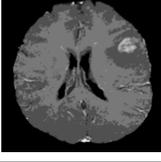
K	Ax T2 Flair		ax T1 memp+C	
	MSTBurr-MM	GMM	MSTBurr- MM	GMM
2				
3				
4				
5				
6				
7				

Table 2: The Summary of Segmentation Results

Method	ax T2 Flair			ax T1 memp+C		
	Optimum K	p	SC	Optimum K	p	SC
GMM	3	9	0.9118	7	21	0.6811
MSTBurr-MM	3	15	0.9149	3	15	0.8760

Table 3: The Parameters of MSTBurr-MM

Sequence	K index	w	μ	ϕ	α	n
ax T2 Flair	1	0.379	0.375	4.579	31.462	24841
	2	0.533	103.194	43.820	13.992	34962
	3	0.087	197.263	59.059	2.858	5733
ax T1 memp+C	1	0.44	2.865	11.854	24.514	28838
	2	0.552	111.498	36.602	0.8972	36148
	3	0.008	153.512	31.769	7.326	550

4. Conclusions

This paper have succeeded to demonstrate the work of MSTBurr-MM for segmenting two type of sequences in MRI brain tumor image. Bayesian approach with the prior as in subsection 2.1, coupled with the MCMC and its Gibbs Sample Algorithm has shown the appropriate posterior for capturing the segmented of MRI pattern images. When large ROIs such as MRI Sequence ax T2 Flair is segmented, both MSTBurr-MM and GMM gave equal performance. The different results show image segmentation with a smaller area of ROI. The MSTBurr-MM is more parsimony and provides better results than the GMM, thereby indicating a smaller optimum cluster number. The segmentation results using the MSTBurr-MM, on the other hand, still leave noise identified as ROI. This is a good case to be continued as a future research, which is by employing the spatial method for image segmentation.

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