Unsupervised Learning for MRI Brain Tumor Segmentation with Spatially Variant Finite Mixture Model in Reversible Jump MCMC Algorithm

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Abstract. MRI brain tumor segmentation is an important topic in medical image processing. Manual segmentation is risky and time-consuming when the MRI is of low quality. The automatic segmentation can be a solution to manage this problem. This paper proposed an improved modeling approach for unsupervised learning trough Spatially Variant Finite Mixture Model (SVFMM). The main contribution is the automation of the SVFMM algorithm to find the optimum number of clusters. This is achieved by employing the birth-death random process in Bayesian Reversible Jump MCMC. Validation of the proposed model is done by calculating the Correct Classification Ration (CCR) in comparison to the original SVFMM and Gaussian Mixture Model (GMM). The proposed model provides similar performance in image segmentation compared to the original SVFMM but is better than GMM. However, SVFMM-RJMCMC is faster and more efficient in finding the optimum number of clusters.

1. Introduction
A brain tumor in Indonesia is a deadly disease with high rate of mortality. According to WHO report there were 4,229 mortalities in 5,323 cases of brain tumors [1]. The detection of a brain tumor could be done through Magnetic Resonance Imaging (MRI). It is a non-invasive medical procedure with various Tesla power. The higher the Tesla power, the better the image quality. Dr. Soetomo General Hospital in Surabaya, provides the MRI services with 1.5 Tesla and 3 Tesla power. The MRI 1.5 Tesla is the high demand service, since it has a minimum in cost and also covered by the Indonesian government's social security (BPJS). However, the low quality of the MRI image could lead the inaccuracies in the detection of a brain tumor. Image segmentation is one of the methodologies that could handle this problem. The manual segmentation is often found risky and time-consuming, while the medical treatment needs the high accuracies, faster identification, and clear sight of the tumor image in MRI.

Several studies based on the clustering methodology are developed to manage the MRI brain segmentation. Traditional methods that have been known are the hierarchical clustering and partitioning algorithm, such as Ward’s method [2], K-Means clustering [3], and Fuzzy C-Means (FCM) clustering [4]. The traditional method is simple but considered less able to explain the data patterns [5]. The unsupervised learning in the form of model-based clustering is a favorable
methodology since the researcher could explore the image pattern and it does not require large amounts of data. Gaussian Mixture Model (GMM) is one of the model-based clustering through finite mixture models (FMM) that often deal in image segmentation. However, the GMM has a limitation due to its assumption of pixel independencies. This is made the GMM less robust to noise. Nguyen [6] solves this limitation and considering the spatial dependencies among the pixels by adding the prior to the clustering label that follows the Gibbs distribution. This is called the hybrid of GMM and the Markov Random Field (MRF) named as the Spatially Variant Finite Mixture Model (SVFMM).

The segmentation using GMM and SVFMM, on the other hand, still leaves the time-consuming in finding the optimum number of clusters. In view of this shortcoming, this paper performs the Reversible Jump Markov chain Monte Carlo (RJMCMC) algorithm to shorten the time of segmentation processed and provide the optimum number of clusters automatically. Moreover, we try to evaluate the RJMCMC-SVFMM algorithm in comparison with the original SVFMM and GMM by calculating the Correct Classification Ratio (CCR). Dr. Soetomo provides all the datasets used in this paper under the medical consent.

2. Spatially Variant Finite Mixture Model

This study uses the MRI brain tumor image as data input. The MRI image would be transformed into the gray-scale image that will provide the gray-scale intensities in each image pixel. Suppose \( y_i \) denote the gray-scale intensities of \( i^{th} \) pixel of an MRI image, and we assume that there are \( N \) pixels in an image that belong to \( K \) clusters. The GMM is a composition of \( K \) Gaussian distributions whose form is given by [7]

\[
f(y|\pi, \mu, \sigma) = \sum_{j=1}^{K} p_j f_j(y|\mu_j, \sigma_j^2),
\]

where \( f_j(y|\mu_j, \sigma_j^2) \) is the Gaussian p.d.f of the \( j^{th} \) mixture component. The \( p_j \) is the proportions of the mixture component model that satisfy the following constraints \( \sum_{j=1}^{K} p_j = 1 \) and \( 0 \leq p_j \leq 1 \), for \( j = 1, 2, \ldots, K \). The Likelihood of the GMM is written as follows

\[
f(y|\pi, \mu, \sigma) = \prod_{i=1}^{N} \sum_{j=1}^{K} p_j f_j(y_i|\mu_j, \sigma_j^2),
\]

where \( \mu_j \) and \( \sigma_j \) are the location parameter and the scale parameter of the \( j^{th} \) component of mixture respectively, which have the domain value of \(-\infty \leq \mu_j \leq \infty\), and \( \sigma_j > 0 \).

The SVFMM is a hybrid of GMM and MRF which use the Gibbs distribution as the prior for labeling the pixel [8]. In SVFMM, the \( p_{ij}, j = 1, \ldots, K \), rearranged as \( p_{ij}, i = 1, \ldots, N \). It is the probability of \( i^{th} \) pixel that belongs to the \( j^{th} \) cluster. The MRF follows the Hammersley-Clifford theorem which states that the random variable have to corresponding to a Gibbs distribution having p.d.f as follows

\[
f(p) = \frac{1}{Z} \exp(-\beta \sum_{i=1}^{N} V_{C_i}(p)),
\]

where \( Z \) is a normalized constant, the vector \( p = (p_{i1}, p_{i2}, \ldots, p_{ij}, \ldots, p_{iK}) \) is set of the pixel label that denotes the probability of \( i^{th} \) pixel belongs to the \( j^{th} \) cluster, \( V_{C_i}(p) = \sum_{m \in C_i} g(\theta_{l,m}) \) is the clique potential function from pixel label \( p_{ij} \) to its neighborhood pixel where

\[
\theta_{l,m} = \sum_{j=1}^{K} (p_{ij} - p_{mj})^2,
\]

\( g(\theta) \) is a function \( \theta \), i.e. \( g(\theta) = (1 + \theta^{-1})^{-1} \). \( C = C_1 \cup C_2 \cup \ldots \cup C_n \) is a set of pixel cliques and \( \beta \) is the smoothness degree parameter. Applying the MRF to adapt the spatial correlation between labels values, then the construction of the log-likelihood function for SVFMM would be as follows

\[
\log f(\mathbf{p}, \mathbf{\theta}|\mathbf{y}) \propto \sum_{i=1}^{N} \log \left( \sum_{j=1}^{K} p_{i} f_j(y_i|\theta_j) \right) + \log f(\mathbf{p}) = \sum_{i=1}^{N} \log \left( \sum_{j=1}^{K} p_{i} f_j(y_i|\theta_j) \right) - \beta \sum_{i=1}^{N} \sum_{m \in C_i} (p_{ij} - p_{mj})^2.
\]

Nguyen [8] recommend the estimation through the Expectation-Maximization (EM) algorithm, since the model is not in the closed form.
3. Reversible Jump Markov chain Monte Carlo (JCMCMC) for SVFMM

The RJMCMC algorithm is used for determining the optimum number of clusters automatically. The steps of the RJMCMC algorithm contain the estimated parameters of the SVFMM which is done by the EM algorithm called as EM-SVFMM algorithm. This algorithm is written in Algorithm 1, while the algorithm of RJMCMC-SVFMM is formulated in Algorithm 2.

**Algorithm 1.** EM Algorithm for SVFMM, namely EM_SVFMM.

1. Initialization parameters \( \{\mu_j^{(0)}, \sigma_j^{(0)}, p_i^{(0)}\} \), mean \( \mu_j^{(0)} \); variance \( \sigma_j^{(0)} \); and proportion \( p_i^{(0)} \), and set \( t = 0 \).
2. E-Step: Calculate \( z_{ij} \)
   \[
   z_{ij}^{(t+1)} = \frac{p_i^{(t)} f(y_i | \mu_j^{(t)}, \sigma_j^{(t)})}{\sum_{l=1}^{K} p_l^{(t)} f(y_i | \mu_l^{(t)}, \sigma_l^{(t)})}.
   \]  
3. M-Step: Re-estimating parameters \( \{\mu_j, \sigma_j, p_i\} \)
   a) Update the mean \( \mu_j \)
   \[
   \mu_j^{(t+1)} = \frac{\sum_{i=1}^{N} z_{ij}^{(t+1)} y_i}{\sum_{i=1}^{N} z_{ij}^{(t+1)}}.
   \]  
   b) Update the variance \( \sigma_j \)
   \[
   \sigma_j^{(t+1)} = \frac{\sum_{i=1}^{N} z_{ij}^{(t+1)} (y_i - \mu_j^{(t+1)})^2}{\sum_{i=1}^{N} z_{ij}^{(t+1)}}.
   \]  
   c) Update the proportion \( p_i \)
   \[
   p_i^{(t+1)} = \frac{\sum_{m \in C_{m_i}^{(t)}} (\sum_{m \in C_{m_i}^{(t)}} y_i - \mu_j^{(t+1)})^2}{\sum_{m \in C_{m_i}^{(t)}} z_{ij}^{(t+1)}}
   \]

   where \( n_i \) stands for the set of neighbors falling in a window around the pixel \( y_i \), \( p_{mj} \) is the label of pixel \( y_m \) in \( j^{th} \) cluster. We select the root with positive value since it produces \( p_{ij} > 0 \).
4. Check for convergence, both for the log-likelihood function in equation (4) and the parameter values. If the convergent criterion has not been fulfilled, then return to step 2 and set \( t = t + 1 \).

**Algorithm 2.** RJMCMC for SVFMM, namely RJMCMC-SVFMM

1. Update the parameter \( \mu_j \)
2. Update the parameter \( \sigma_j^2 \)
3. Update the parameter \( p_{ij} \)
4. Update the latent variable \( z_{ij} \)
5. Updating Split/ Merge process of the component
6. Updating Birth/ Death process from the unoccupied component

Step 1–4 are utilizing Algorithm 1, Step 5–6 change the number of \( j^{th} \) mixture components individually. Split/ Merge step is a random chance between split \( (j_1 \rightarrow j_1 + 1) \) or merges \( (j_2 + 1 \rightarrow j_2) \) where \( j_1 = 1, 2, ..., K \).

The merge process for certain \( i \) are contains the steps as follows:

a. If there are two groups \( j_1 \) and \( j_2 \) that will joint, then combine the opposite pairs \((j_1, j_2) \rightarrow j^*\)

b. Set the value for \( \{p_{ij^*}, \mu_{j^*}, \sigma_{j^*}\} \) with the subsequent equations
   \[
   p_{ij^*} = p_{ij_1} + p_{ij_2},
   p_{ij^*} \mu_{j^*} = p_{ij_1} \mu_{j_1} + p_{ij_2} \mu_{j_2},
   \]

   \[
   p_{ij^*} \sigma_{j^*}^2 = p_{ij_1} \sigma_{j_1}^2 + p_{ij_2} \sigma_{j_2}^2 + 2 p_{ij_1} p_{ij_2} \sigma_{j_1} \sigma_{j_2} \cos \theta_{ij_1, ij_2},
   \]

   \[
   \text{where } \theta_{ij_1, ij_2} \text{ is the angle between } \mu_{j_1} \text{ and } \mu_{j_2}.
   \]
\[ p_{ij}(\mu_j + \sigma_j) = p_{ij1}(\mu_j + \sigma_j) + p_{ij2}(\mu_j + \sigma_j). \]  

(11)

The split process steps for certain \( i \) are

a. If we have two groups \( j_1 \) and \( j_2 \) that will be separated, then the selected components are

randomly separated into \( j^* \rightarrow j_1 + j_2 \)

b. Create \( u = (u_1, u_2, u_3) \), a random vector that satisfy \( 0 < u_c < 1 \), \( c = 1, 2, 3 \) to form new

parameters with the the subsequent equations:

\[ p_{ij1} = p_{ij}u_1, \]

\[ p_{ij2} = p_{ij}(1 + u_1), \]

\[ \mu_{j1} = \mu_j - u_2\sigma_j \left( \frac{p_{ij2}}{p_{ij1}} \right)^{\frac{1}{2}}, \]

\[ \mu_{j2} = \mu_j - u_2\sigma_j \left( \frac{p_{ij1}}{p_{ij2}} \right)^{\frac{1}{2}}, \]

\[ \sigma_{j1}^2 = u_3(1 - u_2^2) \sigma_j^2 \left( \frac{p_{ij2}}{p_{ij1}} \right), \]

\[ \sigma_{j2}^2 = (1 - u_3)(1 - u_2^2) \sigma_j^2 \left( \frac{p_{ij1}}{p_{ij2}} \right). \]

(14) \hspace{1cm} (15) \hspace{1cm} (16) \hspace{1cm} (17)

c. Repeat Step b. until \( \mu_{j1} < \mu_{j2} \).

The step of birth/ death is a random chance between birth \( (j_1 \rightarrow j_1 + 1) \) and death \( (j_1 + 1 \rightarrow j_1) \). The steps in the birth process are:

a. Build a parameter \((p_{ij}, \mu_j, \sigma_j)\) as formulated in the merge process for new components

b. Rescaling for the weighting parameters \( p_{ij} \) into \( \sum_{j=1}^{2} p_{ij} = 1 \),

while the death process are:

a. Dismiss all unoccupied components from the process

b. Rescaling the remaining value of \( p_{ij} \).

4. Validation and Measure of Evaluation

The proposed algorithm is compared with the previous state of the art method (GMM and original EM-SVFMM). In RJMCMC-SVFMM, the optimum number of clusters is conducted automatically with merge/split and birth/death process, while the GMM and EM-SVFMM should be validated manually by calculating the Silhouette Coefficient (SC). The \( SC_j^i \) is formulated in equation (18) [9],

\[ SC_j^i = \frac{\xi_j^i - \xi_{\text{max}}^i}{\xi_j^i - \xi_{\text{min}}^i}, \]

(18)

where \( \xi_j^i \) denotes how similar a data to its cluster and \( \xi_j^i \) indicates how similar a data to the other clusters. \( SC_j \) of a cluster in equation (19) is the average value of \( SC_j^i \). The overall SC of the image is the average of all \( SC_j \) from all clusters which formulated in equation (20).

\[ SC_j = \frac{1}{n_j} \sum_{i=1}^{n_j} SC_j^i \]

(19)

\[ SC = \frac{1}{K} \sum_{j=1}^{K} SC_j \]

(20)

The closer the SC to 1, the more precisely the data should be distributed and classified in the \( K \) cluster.

Evaluation of the segmentation performance is done quantitatively by calculating the Correct Classification Ratio (CCR) [10]. It is the ratio of similarity between a number of pixels in ROI and the ground truth. The higher of CCR value indicates the better performance of the segmentation results. The formula of CCR is given by equation (21).

\[ CCR = \frac{\sum_{j=1}^{2} |GT \cap Seg_j|}{|GT|}, \]

(21)

where \( GT = \bigcup_{j=1}^{2} GT_j \) is ground truth and \( Seg_j \) defines the segmented pixel based on the model. The Non-ROI is indexed with \( j = 1 \), while the ROI is indexed with \( j = 2 \).
5. Segmentation of MRI Brain Tumor

The data used in this study are passed by the medical consent from Dr. Soetomo. The data are recorded as slices from sequences named T\textsubscript{1} memp+C and T\textsubscript{2} Flair, both are in axial point of view. The T\textsubscript{1} memp+C sequence is an arrangement slices that have been added with a contrast media, either by oral or injection. This contrast media made the tumor is more visible than in the T\textsubscript{2} Flair sequence, which the more visible feature is the swelling or edema. The four datasets are visualized in Figure 1 (a). Image 1 and Image 3 are slices from the T\textsubscript{1} memp+C, while the remaining are from the T\textsubscript{2} Flair sequence. Figure 1 (b) are the datasets after pre-processing. The preprocessing is done by evacuating the fat around the skull which could debilitate the segmentation procedure. Image 2 and Image 3 are used in the research of Iriawan, et al [7] that also runs the EM-SVFMM in the analysis. Figure 2 is the set of gray-scale image histogram after preprocessing.

![Figure 1](image1.png)

**Figure 1.** The original MRI image (a) and the image after preprocessing (b)
Figure 2. Histogram after preprocessing for (a) Image 1, (b) Image 2, (c) Image 3, and (d) Image 4

The segmentation process is done under the GMM, EM-SVFMM, and RJMCMC-SVFMM Algorithm for each dataset. The GMM and EM-SVFMM are validating manually by calculating the Silhouette Coefficient (SC), while the RJMCMC-SVFMM is validating automatically since the algorithm includes the birth-death process that leads to the optimum number of cluster. The summary of SC for GMM and EM-SVFMM and the optimum number of the cluster under the RJMCMC-SVFMM algorithm are summarize in Table 1. The marked cell indicates the maximum value of SC, which denotes the optimum number of clusters.

From Table 1, we can see that the GMM reaches the optimum number of clusters at $K = 8$ clusters for Image 1 and Image 2, $K = 7$ for Image 4 and $K = 9$ for Image 3. The EM-SVFMM grabs optimum at $K = 7$ for Image 1, Image 2, and Image 3, while Image 4 reaches optimum at $K = 8$. The RJMCMC-SVFMM seizes optimum at $K = 4$ clusters for Image 1, $K = 5$ clusters for Image 3, and $K = 6$ clusters for Image 2 and Image 4. As we see the results from Table 1, the RJMCMC-SVFMM has the minimum number of clusters compared to GMM and SVFMM. Although the number of clusters is smaller, RJMCMC-SVFMM effectively considers the tumor area as ROI. Figure 3 shows the ROI of segmentation results based on the optimum number of clusters for each image and each algorithm.
Table 1. The summary of the optimum number of clusters

| Algorithm         | Dataset | Number of Clusters (K) | 3   | 4       | 5   | 6       | 7   | 8       | 9       |
|-------------------|---------|------------------------|-----|---------|-----|---------|-----|---------|---------|
| GMM               | Image 1 | 0.7792                 | 0.8026 | 0.8294 | 0.8440 | 0.8613 | 0.8822* | 0.8579 |
|                   | Image 2 | 0.7615                 | 0.7772 | 0.8003 | 0.8198 | 0.8443 | 0.8642* | 0.8444 |
|                   | Image 3 | 0.7418                 | 0.7539 | 0.7880 | 0.8076 | 0.8429 | 0.8532 | 0.8788* |
|                   | Image 4 | 0.7222                 | 0.7521 | 0.7745 | 0.8006 | 0.8423* | 0.8212 | 0.7800 |
| EM-SVFMM          | Image 1 | 0.7143                 | 0.7257 | 0.7457 | 0.7736 | 0.8211* | 0.8003 | 0.7628 |
|                   | Image 2 | 0.6152                 | 0.6304 | 0.7371 | 0.7946 | 0.8083* | 0.7972 | 0.7479 |
|                   | Image 3 | 0.7370                 | 0.7783 | 0.8074 | 0.8268 | 0.8782* | 0.8174 | 0.7934 |
|                   | Image 4 | 0.7154                 | 0.7240 | 0.7468 | 0.7860 | 0.8111 | 0.8545* | 0.8025 |
| RJMCMC-SVFMM      | Image 1 |                        |       |         | 4 clusters |       |       |       |
|                   | Image 2 |                        |       |         | 6 clusters |       |       |       |
|                   | Image 3 |                        |       |         | 5 clusters |       |       |       |
|                   | Image 4 |                        |       |         | 6 clusters |       |       |       |

* indicates the maximum SC value

Figure 3. The ROI visualization from optimum segmentation result for different Algorithm.
Figure 4. CCR of GMM, EM-SVFMM, and RJMCMC-SVFMM

All algorithms are executed under a computer with processor Intel Core i7, 8GB RAM, 128GB SSD, and without GPU and VRAM. The evaluation through the CCR is visualized in Figure 4. This figure shows that the segmentation results of RJMCMC-SVFMM have a great performance as well as the EM-SVFMM. This is indicated by the CCR value of EM-SVFMM that coincides with RJMCMC-SVFMM. However, RJMCMC-SVFMM is still better than GMM. Overall the performance of RJMCMC-SVFMM is calculated from the CCR average of about 90.2%. Not to mention that RJMCMC-SVFMM is more efficient since this algorithm could finding the optimum number of clusters automatically with the average running time per image is about 6.8 minutes (for 13 clusters, from $K = 3$ to $K = 15$). The GMM requires running time about 56 seconds per image just for a single cluster, and EM-SVFMM requires about 84 seconds per image per cluster. Moreover, in the GMM and EM-SVFMM still have to calculate the SC in comparing each cluster manually, therefore it consumes time longer.

6. Conclusions and Future Research
This study had succeeded to build the RJMCMC-SVFMM algorithm and compare the performance with GMM and original EM-SVFMM. The results have shown that RJMCMC-SVFMM has similar performance with EM-SVFMM, but is better than GMM. The performance of RJMCMC-SVFMM is showing by the CCR average value of about 90.2%. With the smaller number of clusters compared to GMM and EM-SVFMM, the RJMCMC-SVFMM effectively perceived in detecting the tumor area as an ROI. The RJMCMC-SVFMM likewise more efficient and faster to provide the optimum number of clusters with the running time per image is about 6.8 minutes for 13 clusters.

This study is still used the Gaussian distribution approach to fit the MRI image data pattern, which in fact are not always symmetrical. In this manner for future research, it is essential to explore the actual data pattern in MRI images.

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