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Markovian Segmentation of Brain Tumor MRI Images

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ABSTRACT

Image segmentation is a fundamental operation in image processing, which consists to di-vide an image in the homogeneous region for helping a human to analyse image, to diagnose a disease and take the decision. In this work, we present a comparative study between two iterative estimator algorithms such as EM (Expectation-Maximization) and ICE (Iterative Conditional Estimation) according to the complexity, the PSNR index, the SSIM index, the error rate and the convergence. These algorithms are used to segment brain tumor Magnetic Resonance Imaging (MRI) images, under Hidden Markov Chain with Indepedant Noise (HMC-IN). We apply a final Bayesian decision criteria MPM (Marginal Posteriori Mode) to estimate a final configuration of the resulted image X. The experimental results show that ICE and EM give the same results in term of the quality PSNR index, SSIM index and error rate, but ICE converges to a solution faster than EM. Then, ICE is more complex than EM.

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1. INTRODUCTION

Hidden Markov model[2] is very explored in many fields like finance[4], imagery[14],[12], medical field[16],[26] and chemistry[29], it has an important place in processing image[28] precisely in image segmentation. Markovian segmentation is a non supervised statistical method of segmentation. It can be used to estimate an image result= fx1; :::::; xN g from the observed image Y = fy1; :::::; yN g 2 R where N is a number of pixel component the image.

It exists three basic Markovian models[30] of segmentation: fields[12],[24], chains[25],[26] and the trees[23],[27]. Each model has its principle to model the image Y to be segmented. The advantage of field is to take account into the contextual information in the image. To model an image with this model, we divide the image in cliques, each clique contains four pixels neighbors at least, this modelling makes the computing speed and the time of execution very less compared to the other Markovian models[14]. To transform the image in a Markov chain, we can use either Hilbert Peano transformer[18],[19], zigzagging, line by line parcours, column by column parcours. These parcours transform the image taking account into the neighborhood between two pixels in the image. Each pixel in the Markov chain yn depends only on its neighbor yn+1 in the image, it respects the property of Markov. This model is very faster compared with the tree and the field. Markovian tree is a general case of chain, it consists to transform the image in bitree[20] or quadtree[21],[22], it is organized by hierarchical way in T hierarchical levels S such as S1 < S2 < :::: < ST , each pixel child in the tree ys+ depends only on its pixel parent ys . Tree is a competitor to the field becauseit's characterized by its speed to estimate the parameters, it adapts much with the multi resolution image segmentation, the spatial relation of the neighborhood is not respected by the tree, contrary to the field, we can consider the tree like a directed graph and the field like a non directed graph. These models called classical hidden Markovian model. Other Markovian models exist recently in the literatures[30] pairwise Markov models[36] and triplet Markov models.

The pairwise Markov model is a generalization of a classical model. Triplet Markov model[37] is also a generalization of pairwise model, it's composed of three processes (observed process, auxiliary process, hidden process). It treats the non stationary data. Our study focuses on a classical hidden Markov chain model to segment the brain tumor MRI images.

Hidden Markov model models the image Y according to the selected model (field, chain, tree). It used the Bayesian theorem to calculate the a posteriori probability P (XjY) to find a final configuration of the image result of segmentation $X \in \Omega = \{\omega_1, ..., \omega_K\}$ K is a number of membership classes, it is initialized by the user.

$$P(X|Y) = \frac{P(X).P(Y|X)}{P(Y)} \tag{1}$$

where:

1. P(X|Y) : is the probability of the posteriori law X knows Y.
2. P(X) : is the probability of the priori law.
3. P(Y|X) : is the probability of the attached data law.
4. P(Y) : is a constant of normalization P(Y) = 1

To estimate these probabilities, it should to apply the iteratives estimators of parameters EM[13], ICE[6], MCEM(Monte Carlo Expectation-Maximization)[13].... In this work, we have limited our study on two iterative estimators such as EM and ICE, we are using these algorithms to estimate a parameter of Hidden Markov Chain with Independant Noise(HMC-IN) model to segment the brain tumor MRI images[11], we have realized a comparative study between ICE and EM. We are used MPM Algorithm[5] to estimate a final configuration of X. Also, we extract a brain tumor using thresholding technic[11].

The structure of this paper is organised as follows :
Section 1 presents Hidden Markov Chain with Independant Noise model.
Section 2 shows EM algorithm, ICE algorithm, complexity of these estimators and MPM algorithm.
Section 3 illustrates the experimental results.

Finally, we have a conclusion and some open questions.

2. HIDDEN MARKOV CHAIN WITH INDEPENDANT NOISE

Now, we present the Hidden Markov Chain with Independent Noise (HMC-IN). This model is a classical Markovian model, it contains two processes : hidden Markovian process X and observed process Y. It's called Hidden Markov Chain with Independent Noise (HMC-IN), because it ignores the noise information contained in the which the image Y [17].

Let the process Z = (X, Y), where $X = (X_n)_{n=1}^{N} \in \Omega$ and $Y = (Y_n)_{n=1}^{N} \in R$.
The process Z = (X, Y) is a HMC-IN, if and only if :

1. The process X is a Markov Chain, it's homogeneus and stationary, its law is as follows :

$$P(X) = P(X_1 = x_1).\prod_{n=1}^{N-1} P(X_{n+1} = x_{n+1} | X_n = x_n) \tag{2}$$

2. The observations Y are conditionally independent of X
3. Each observation y_n, $\forall n \in N$ depends only on its hidden class x_n.

$$P(Y_n = y_n|X) = P(Y_n = y_n|X_n = x_n) \tag{3}$$

Each process of a hidden Markov chain has its parameters, a hidden Markovian process X has its initial law P I and its matrix of transition A. An observed process Y has also its parameters, these parameters depend on the law of probability following by this process.

To estimate these parameters. We apply three phases:

1. Initialization phase.
2. Iterative estimation phase.

3. Final decision phase.

a. In the initialization phase, we initialize the parameters $\theta^0 = (PI^0, A^0, \mu^0, (\sigma^2)^0)$ of each law. It's an important phase. For a priori law parameters $\theta^0_x = (P^0, A^0)$, we have:
   1. The initial law $PI^0(i) = p(x_1 = i)\ \forall i \in \Omega$ of size K.
   2. The transition matrix $A^0(i, j) = p(x_{n+1} = \omega_j | x_n = \omega_i)$ between the classes i and j $\forall_i, j \in \Omega$ of size K∗K.

For the attached data law parameters $\theta^0 y|x$, if we assume that the observations follow the Gaussian law $p(y_n|x_n = \omega_t)$, we initialize $\theta^0_{y|x} = (\mu^0 (\sigma^0)^2)$, for each class $\forall_i \in \Omega$ we have:
   1. The mean μ^0_t of size K.
   2. The variance (σ^0_i) 2 of size K.

b. In the iterative estimation phase, we calculate the parameters $\theta^q = (\theta^x_q, \theta^{x|y}_q)$ of each law for each number of iterations $q \in Q$ using the estimator algorithms such as EM[31],ICE[32], SEM(Stochastic Expectation-Maximization)[13],[33]
c. In the final phase of decision, we estimate a final configuration of the hidden process X (image result). Using MPM or MAP [38] Bayesian criteria.

HMC-IN model estimates K2 + 3K parameters in each iteration q.

3. EM AND ICE ALGORITHMS

In this section, we present the EM, ICE estimators, its complexity and MPM algorithm. They are based on Baum Welch algorithm [1].

EM uses the deterministic strategy to calculate the parameters, it is based on maximizing a likelihood $P(x, y|\theta)$ It has many difficulties to converge [3].

ICE is an iterative algorithm based on a principle of SIP[3] and Monte Carlo method [7],[10],[34]. It uses a hybrid strategy (deterministic+stochastic) to estimate the parameters.

3.1. EM Algorithm

EM proceeds in two steps Expectation(E) and Maximization(M) :

For each iteration q 2 Q:

1. Step(E):
   – We calculate $\alpha^q_n(i)$, $\beta^q_n(i)$,$\gamma^q_n(i,j)$ and $\xi^q_n(i)$

2. Step(M):
   – We calculate the parameters of each law of HMC-IN:
   – Concerning a priori law parameter's, we calculate :

$$PI^q(i) = \xi^q_1(i), \forall i \in \Omega \tag{4}$$

$$A^q(i,j) = \frac{\sum_{n=1}^{N-1} \gamma^q_n(i,j)}{\sum_{n=1}^{N-1} \xi^q_n(i)}, \forall i,j \in \Omega \tag{5}$$

   – Concerning a data attached law parameter's, we calculate :

$$\mu^q_i = \frac{\sum_{n=1}^{N} y_n.\xi^q_n(i)}{\sum_{n=1}^{N} \xi^q_n(i)}, \forall i \in \Omega \tag{6}$$

$$(\sigma^q_i)^2 = \frac{\sum_{n=1}^{N} (y_n - \mu^q_i)^2.\xi^q_n(i)}{\sum_{n=1}^{N} \xi^q_n(i)}, \forall i \in \Omega \tag{7}$$

   – After calculating the attached data parameters, we calculate a Gaussian density f [2], $\forall i \in \Omega \forall n \in N$ in each iteration $q \in Q$.

$$f^q_i(y_n) = \frac{1}{\sqrt{2\pi(\sigma^q_i)^2}} \exp[-\frac{(y_n - \mu^q_i)^2}{(\sigma^q_i)^2}] \tag{8}$$

3.2. Ice Algorithm

This estimator proceeds also in two steps:

For each iteration $q \in Q$

1. We calculate $\alpha_n^q(i)$, $\beta_n^q(i)$,$\gamma_n^q(i,j)$ and $\xi_n^q(i)$
   We simulate a sample of Xq for one random simulation using the parameters of the iteration q [9].

2. We calculate a priori law and attached data law parameter's

$$PI^q(i) = \xi_1^q(i), \forall i \in \Omega \tag{9}$$

$$A^q(i,j) = \frac{\sum_{n=1}^{N-1} \gamma_n^q(i,j)}{\sum_{n=1}^{N-1} \xi_n^q(i)}, \forall i,j \in \Omega \tag{10}$$

$$\mu_i^q = \frac{\sum_{n=1}^{N} y_n.1[x_n = i]}{\sum_{n=1}^{N} 1[x_n = i]} \forall i \in \Omega \tag{11}$$

$$(\sigma_i^q)^2 = \frac{\sum_{n=1}^{N} (y_n - \mu_i^q)^2.1[x_n = i]}{\sum_{n=1}^{N} 1[x_n = i]} \forall i \in \Omega \tag{12}$$

We also calculate a density f^q using the equation (3.1.)

EM and ICE use a deterministic strategy to calculate the a priori law parameter's. To estimate the attached data parameter's EM uses also a deterministic strategy and ICE uses a stochastic strategy.

3.3. Baum Welch Algorithm

Calculation parameters by EM or ICE is based on Baum Welch Algorithm. This algorithm[1] proceeds as we calculate:

1. The Forward probabilities α
2. The Backward probabilities β
3. The marginal a posteriori probability ξ
4. The joint a posteriori probability ϒ

In Forward Backward Algorithm, we calculate the Forward and the Backward probabilities: Forward Algorithm α_n (i) = p (y_1, ..., y_n , x_n) proceeds in two steps :

1. Initialization:(n=1)

$$\alpha_1(i) = \frac{PI(i).f_i(y_1)}{\sum_{j\in\Omega} PI(i).f_j(y_1)}, \forall i \in \Omega \tag{13}$$

2. Induction: (n > 1)

$$\alpha_{n+1}(i) = \frac{f_i(y_{n+1}).\sum_{j\in\Omega} \alpha_n(j).A(i,j)}{\sum_{k\in\Omega} f_k(y_{n+1}).\sum_{j\in\Omega} \alpha_n(j).A(i,j)}, \forall i \in \Omega \tag{14}$$

Backward Algorithm β_n (i) = p(y_{n+1} , ..., yN |x_n) also proceeds in two steps in the opposite direction starting with n = N:

1. Initialization:(n=N)

$$\beta_N(i) = 1, \forall i \in \Omega \tag{15}$$

2. Induction: (n < N)

$$\beta_n(i) = \frac{\sum_{j\in\Omega} A(i,j).f_j(y_{n+1}).\beta_{n+1}(j)}{\sum_{k\in\Omega} f_k(y_{n+1}).\sum_{j\in\Omega} \alpha_n(j).A(i,j)}, \forall i \in \Omega \tag{16}$$

We also calculate two probabilities for two law, the marginal a posteriori law $\xi_n(i)$ and the joint a posteriori law $\gamma_n(i, j)$ where:

$$\xi_n(i) = p(x_n = i|y_n) = \alpha_n(i).\beta_n(i), \forall i \in \Omega \tag{17}$$

and

$$\gamma_n(i,j) = p(x_n = i, x_{n+1} = j|y_n) = \frac{\alpha_n(i).A(i,j).f_j(y_{n+1}).\beta_{n+1}(j)}{\sum_{k\in\Omega} f_k(y_{n+1}).\sum_{l\in\Omega} \alpha_n(l).A(l,k)} \tag{18}$$

3.4. Complexity of ICE and EM algorithms

The aim of this section is to compare the complexity of ICE and EM algorithms, for this reason, we calculate the complexity of each task executable by these estimators, we calculate the complexity of Forward algorithm n(i), the complexity of Backward algorithm n(i), the complexity to calculate a marginal a posteriori algorithm n(i) and to calculate the joint a posteriori algorithm n(i; j). Then, the complexity to calculate parameters P I(i); A(i; j); i; i2 and the simulation of X by the ICE algorithm in each iteration q 2 Q. We have N observations (size of the Y) and K states (number of classes). We are resumed the complexity of each task executed by EM and ICE in this table:

Table 1. Complexity of EM and ICE algorithms

Task	EM	ICE
Forward	O(K2N)	O(K2N)
Backward	O(K2N)	O(K2N)
Joint a posteriori probability	O(K2N)	O(K2N)
Marginal a posteriori probability	O(KN)	O(KN)
Initial law P I	O(K)	O(K)
Matrix of transition A	O(K2N)	O(K2N)
Mean	O(KN)	O(KN)
Variance 2	O(KN)	O(KN)
Simulation X	not executable by this algorithm	O(KN)

From this table, we notice that the complexity of ICE is superior than the complexity of EM. Because, ICE simulates the hidden process X [35] one time in each iteration q 2 Q. This task makes ICE more complex than EM.

3.5. MPM Algorithm

To find a final configuration of X. This estimator maximizes for each pixel y_n, $\forall n \in N$. The marginal a posteriori probability [5]:

$$x_{nmpm} = argmax_{x_n}(P(X_n = x_n|Y_n = y_n)) \tag{19}$$

We use this mathematical formula to estimate a membership class $\bar{x}$ nmpm, for each pixel y_n, $\forall_n \in N$.

$$\bar{x}_{nmpm} = argmax_{i\in\Omega}(\alpha_n(i).\beta_n(i)) = argmax_{i\in\Omega}((\xi_n(i))) \tag{20}$$

By this approach, we estimate a final configuration of the process X.
MPM has a complexity of O (K N).

4. EXPERIMENTAL RESULTS

4.1. Experiments

We segment a brain MRI images to three regions.

We compare EM and ICE algorithms in term of quality such as PSNR index, SSIM index, Error rate and Convergence.

Then, we extract a region of interest using thresholding technics[11],[15].

- We use K-means algorithm [8] to initialize the configuration of X^0.
- Concerning the initial law PI^0 we have:

$$PI^0 = \begin{pmatrix} 0.33 \\ 0.33 \\ 0.33 \end{pmatrix}$$

- Concerning the matrix of transition A^0, we have:

$$A^0 = \begin{pmatrix} 0.5 & 0.25 & 0.25 \\ 0.25 & 0.5 & 0.25 \\ 0.25 & 0.25 & 0.5 \end{pmatrix}$$

- The mean μ^0 and the variance $(\sigma^0)^2$ are initialized by K-means from the configuration of X^0.
- We have a number of iterations Q = 30.

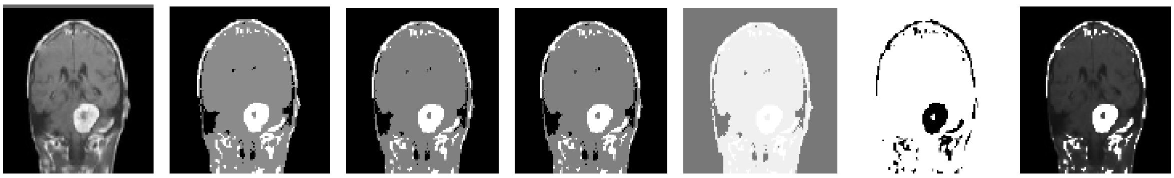
We have used this type of initialization parameters in all experiments presented in this work. We have realized ten experiments for ten MRI images. We assume that the MRI images using in this computation are filtered. After segmentation phase. We have taken the image result of segmentation X obtained by ICE in each experiment and we have extracted from this image the region of interest (tumor). Using the thresholding technic, this technic consists to eliminate all regions of the image, and just left the region of interest which it's necessary to extract from the celebrale image X. To facilitate the diagnosis the type of tumor (benign or malignant), we take the original image Y and we mark the position of the tumor by the white color. We have surrounded the tumor by a red contour. In particular, we present the obtained results in each experiment, they are available in the following figures.

(a) Original image Y (b) Configuration X^0 (c) EM (d) ICE (e) Indexed Regions (f) Interest Region (g) Final Result

Figure 1. Experiment 1

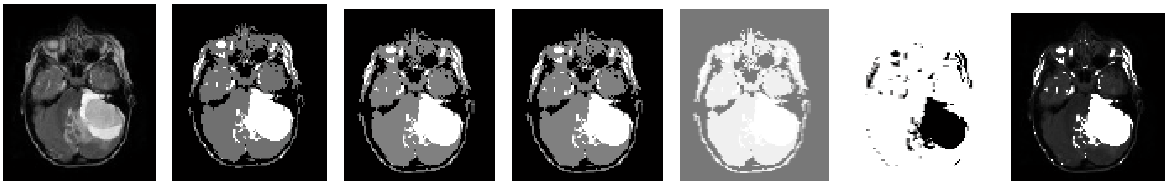
(a) Original image Y (b) Configuration X^0 (c) EM (d) ICE (e) Indexed Regions (f) Interest Region (g) Final Result

Figure 2. Experiment 2



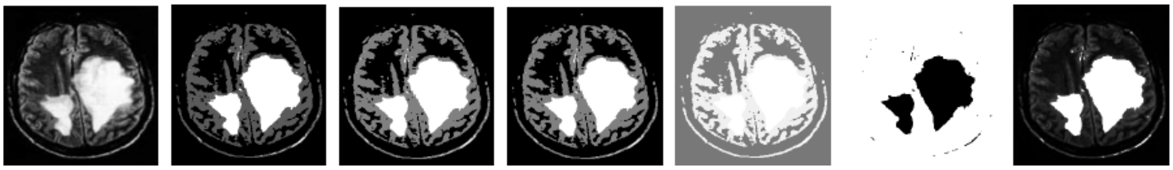
(a) Original image Y | (b) Configuration X^0 | (c) EM | (d) ICE | (e) Indexed Regions | (f) Interest Region | (g) Final Result

Figure 3. Experiment 3



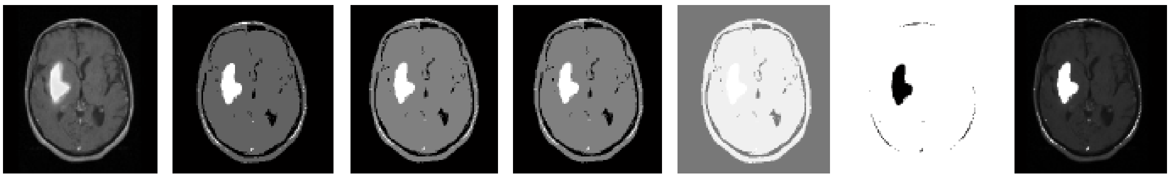
(a) Original image Y | (b) Configuration X^0 | (c) EM | (d) ICE | (e) Indexed Regions | (f) Interest Region | (g) Final Result

Figure 4. Experiment 4



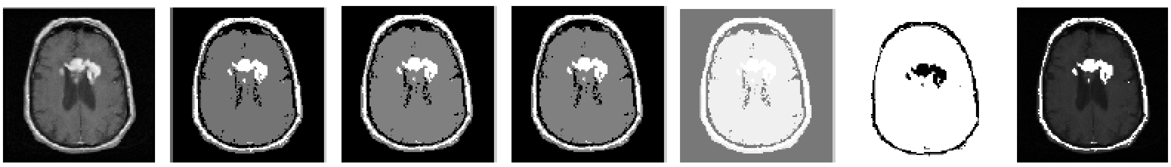
(a) Original image Y | (b) Configuration X^0 | (c) EM | (d) ICE | (e) Indexed Regions | (f) Interest Region | (g) Final Result

Figure 5. Experiment 5



(a) Original image Y | (b) Configuration X^0 | (c) EM | (d) ICE | (e) Indexed Regions | (f) Interest Region | (g) Final Result

Figure 6. Experiment 6

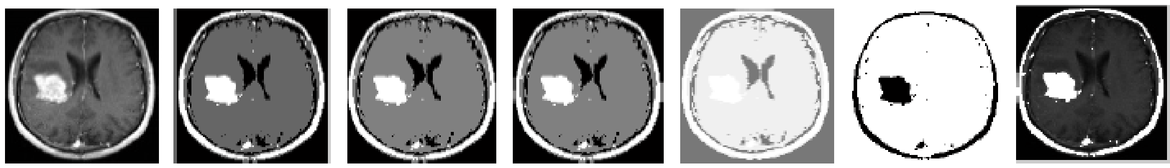


(a) Original image Y | (b) Configuration X^0 | (c) EM | (d) ICE | (e) Indexed Regions | (f) Interest Region | (g) Final Result

Figure 7. Experiment 7

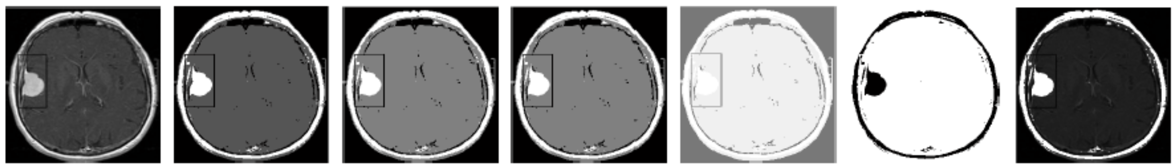
(a) Original image Y (b) Configuration X^0 (c) EM (d) ICE (e) Indexed Regions (f) Interest Region (g) Final Result

Figure 8. Experiment 8



(a) Original image Y (b) Configuration X^0 (c) EM (d) ICE (e) Indexed Regions (f) Interest Region (g) Final Result

Figure 9. Experiment 9



(a) Original image Y (b) Configuration X^0 (c) EM (d) ICE (e) Indexed Regions (f) Interest Region (g) Final Result

Figure 10. Experiment 10

From these figures, we notice that : HMC-IN divides the image in three regions, among these regions we find the regions containing the brain tumor. Visually, ICE and EM methods capture same details of the real image in these experiments.

4.2. The Results

We have resumed the obtained results in the following tables. We have compared these estimators in ten experiments in term of the PSNR index, the SSIM index, the error rate and the convergence.

Table 2. PSNR index and SSIM index

Experiments	PSNR ICE	SSIM ICE	PSNR EM	SSIM EM
Experiment 1	21,9594	0.5390	21,9500	0.5397
Experiment 2	24,0672	0.5710	24,0672	0.5697
Experiment 3	19,9323	0.4821	19,9322	0.4847
Experiment 4	22,1529	0.4990	22,1529	0.4977
Experiment 5	18.4713	0.4773	18.4713	0.4784
Experiment 6	21,8050	0.5157	21,8058	0.5150
Experiment 7	20,3738	0.3908	20,3738	0.3922
Experiment 8	19,0083	0.3488	19,0083	0.3506
Experiment 9	18,0636	0.3845	18,0631	0.3843
Experiment 10	21.7587	0.3574	21.7587	0.3572

Table 3. Error rate

Experiments	Error rate ICE	Error rate EM
Experiment 1	9,2127	9,2127
Experiment 2	8,1357	8,1357
Experiment 3	7,9766	7,9766
Experiment 4	11,4270	11,4270
Experiment 5	9.6075	9.6075
Experiment 6	10,0450	10,0450
Experiment 7	9,4128	9,4128
Experiment 8	7,0975	7,0975
Experiment 9	13,0872	13,0872
Experiment 10	12.9558	12.9558

Table 4. The Convergence of ICE and EM algorithms

Experiments	ICE	EM
Experiment 1	7 iterations	8 iterations
Experiment 2	6 iterations	7 iterations
Experiment 3	9 iterations	12 iterations
Experiment 4	10 iterations	13 iterations
Experiment 5	6 iterations	8 iterations
Experiment 6	7 iterations	6 iterations
Experiment 7	9 iterations	11 iterations
Experiment 8	7 iterations	9 iterations
Experiment 9	9 iterations	8 iterations
Experiment 10	10 iterations	9 iterations

From these tables, we notice that the values of PSNR index, SSIM index and error rate obtained in each experiment by EM and ICE are similes. EM and ICE give the same result in these ten experiments. Despite of they use the strategies differences to estimate the parameters. The quality of segmentation is comparable for both algorithms, we have no difference in terms of quality. From the values of convergence, EM and ICE are very quick to converge. But, ICE is quick to converge as EM, because the convergence of EM has some difficulties, it depends on its initial parameters.

5. CONCLUSION

In this paper, we have realized a comparative study between two iterative estimators such as EM and ICE to estimate HMC-IN parameter's according the final Bayesian decision criteria MPM, to segment ten medical brain tumor MRI images. We have used the thresholding technic to extract the interest region (tumor position) by the image result of segmentation. Generally, ICE and EM give the same results in term of the quality PSNR index, SSIM index and error rate, but the experimental results show that ICE converges to a solution faster than EM. And, EM is less complex than ICE. This work come up with many open questions. In particular, it's possible to :

1. Use these estimators to segment color textured images.
2. Program these estimators to estimate a parameter of a pairwise or triplet Markov chain models.
3. Segment the MRI images using the triplet Markov chain, considering that X is non stationary.

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