

## GA-BW based HMM in Brain Image Segmentation

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### Abstract

*Image segmentation is an important preprocessing step in a sophisticated and complex image processing algorithm. In segmenting real-world images, the cost of misclassification could depend on the true class. For example, in a two-class (negative or positive class) problem, the cost of misclassifying positive to negative class could not be equal to that of misclassifying negative to positive class. However, existing algorithms do not take into account the unequal misclassification cost. Here, we introduce a procedure to minimize the misclassification cost with class-dependent cost. The procedure assumes the hidden Markov model (HMM) which has been popularly used for image segmentation in recent years. In this proposed method Baum-Welch (B-W) Algorithm is used to calculate the HMM model parameters. However, the B-W algorithm uses an initial random guess of the parameters, therefore, after convergence the output tends to be close to this initial value of the algorithm, which is not necessarily the global optimum of the model parameters. To achieve an optimum result Genetic Algorithm (GA) combined with Baum-Welch (GA-BW) is proposed and the idea is to use GA exploration ability to obtain the optimal parameters within the solution space. By using this proposed method, brain tumor region and non tumor region is segmented and classified within the state of art.*

**Keywords:** Hidden markov model, genetic algorithm, hmm training, baum-welch algorithm

### INTRODUCTION

The HMM has been used for image segmentation in recent years. The most important step in HMM is HMM parameters optimization, since getting optimal values of the model parameters

will automatically increase the recognition accuracy. This procedure is referred to as HMM training [1–8]. Usually, the well known Baum-Welch algorithm is used to perform HMM training, an initial guess of the parameters is made randomly, then

more accurate parameters are computed in each iteration until the algorithm converge. Using B-W algorithm, it is possible to get better results after every iteration, however, this procedure can be biased toward the local maxima which is close to the initial values of the algorithm and fail to achieve global optima, which is necessary to produce the best recognition rate [2, 9–12]. Thus, there is need for an algorithm that can escape from the local optimum and then probe the entire solution space to reach the global optimum of the model parameters.

Unlike the B-W algorithm, GA can attain global optima by searching in multiple points within the solution space simultaneously. GA imitates the phenomena of evolution in nature and applies crossover and mutation operations to the encoded solutions to simulate biological genetic operations. Crossover creates new generations by exchanging parent's genes portions, in order to add variations to the solution. Mutation changes only some points in the encoded solution and generates new traits in the offspring, which provide GA the capacity to escape from a local optimum of the solution to a global one [8].

Within the last decade many approaches have been proposed to apply GA for HMM training in speech recognition and in other research areas like web information extraction, molecular biology, biological sequence analysis and video content analysis [1–8]. The experimental results of HMM parameters estimation suggest that using GA or hybrid GA-BW achieve better results than BW or other heuristic algorithms.

In this paper two HMM training methods have been analyzed, the first is a MATLAB toolbox based on B-W algorithm; the other is our implementation of GA using MATLAB GA toolbox. In terms of global searching GA is highly powerful method however, it is very slow to converge. To overcome this limitation a hybrid GA-BW has been used.

## HMM TRAINING SYSTEMS

The model parameters of an HMM can be expressed as a set of three elements  $\lambda = \{A, B, \pi\}$  Where:  $A = \{a_{ij}\}$  is the state transition probability matrix, each element  $a_{ij}$  represent the probability that the HMM model will transit from state  $i$  to state  $j$ . Elements of matrix  $A$  must satisfy the next two conditions:

$$a_{ij} \geq 0 \quad \text{where } 1 \leq i, 3 \leq j \quad (1)$$

$$\sum a_{ij} = 1 \quad \text{where } 1 \leq i \leq 3 \quad (2)$$

$B = \{b_{ij}(k)\}$  is the observation probability matrix, such that  $b_{ij}$  is the probability that the observation that has been generated by state  $i$ .

Elements of matrix  $B$  must satisfy the next two conditions:

$$b_{ij} \geq 0 \quad \text{where } 1 \leq i, j \leq 3 \quad (3)$$

$$\sum b_{ij} = 1 \quad \text{where } 1 \leq i \leq 3 \quad (4)$$

$\pi = \{\pi_i\}$  is the initial state distribution vector, and every  $\pi_i$  expresses the probability that the HMM chain will start at state  $i$ . Elements of vector  $\pi$  must satisfy the next two conditions:

$$\pi_i \geq 0 \quad \text{where } 1 \leq i, j \leq 3 \quad (5)$$

$$\sum \pi_i = 1 \quad (6)$$

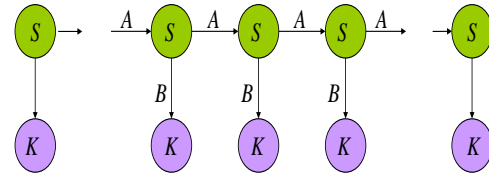
HMM Training is the process of HMM parameter calculation. Compute the probability of given observation sequence. From observation sequence compute the most likely hidden state sequence, find the model that produces the most likely sequence. And from model and observation update the model parameter that best fit the observation.

### HMM TRAINING USING BW-ALGORITHM

The B-W algorithm provided by Mix Gaussian toolbox, has been used to train the HMM [9]. After an initial guess of the HMM parameters is made, the B-W

algorithm is run for 20 iterations to get more accurate parameters. As result we get a continuous HMM and it will be biased towards local maxima. S

### HMM Formalism



- $\{S, K, \Pi, A, B\}$
- $\Pi = \{\pi_i\}$  are the initial state probabilities
- $A = \{a_{ij}\}$  are the state transition probabilities
- $B = \{b_{ik}\}$  are the observation state probabilities

**Fig. 1: HMM Formalism.**

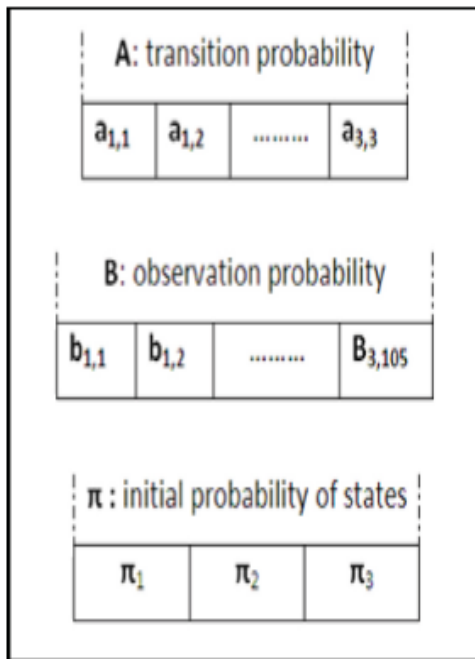
### HMM TRAINING USING HYBRID GA-BWALGORITHM

In Mixt Gaussian toolbox implementation a 3 hidden state continuous density mixture Gaussian HMM with 105 observation symbols have been used. Thus the HMM model parameters is  $\lambda = \{A, B, \pi\}$  where  $A$  is a 3 by 3 transition probability matrix,  $B$  a 3 by 105 matrix,  $\pi$  is the initial probability of states vector of size 3.

### Encoding Method

It is vital to find genetic representation of the model parameters by applying GA to solve optimization problem. In genetics, chromosomes are comprised by a set of

basic elements called genes, in our case the elementary information is the elements of every probability matrixes  $A$ ,  $B$  and  $\pi$ . We choose to concatenate the rows of each matrix in the model parameters, thus the chromosomes will be represented as an array of real numbers as shown in Figure 2.



**Fig. 2:** Chromosome Encoding.

### Hybrid GA-BW

We present a hybrid GA-BW algorithm due to slow convergence and high computational power needed by classical GA, especially when the generated chromosomes cannot satisfy the conditions (1), (2), . . . , (6). For this reason, not included in the offspring and they are replaced by new chromosomes. To overcome the slow convergence problem,

the initial generation  $P(0)$  is not generated randomly as in normal GA, but by applying an iteration of B-W algorithm as shown in Figure 3. For every ten generations, three iterations of B-W algorithm are applied to all chromosomes to allow the algorithm to converge faster.

### Fitness Function

The fitness function is an evaluation mechanism of the chromosome; a higher fitness value reflects the chances of the chromosome to be chosen in the next generation. The log likelihood has been used and it represents the probability that the training observation utterances have been generated by the current model parameters and it is a function of the following form [2, 12]:

$$P_n = (\sum \log (P(O_K/\lambda_n)))/M \quad (7)$$

- 1) Apply **B-W** algorithm to generate the initial population **P(0)**, where  $P(0) = \{C_1, C_2, \dots, C_N\}$ , and  $C_i$  is one chromosome
- 2) Calculate the fitness function **F(C<sub>i</sub>)** of every chromosome  $C_i$  within the actual population **P(t)**.
- 3) Select a few chromosomes for the intermediate population **P'(t)**.
- 4) Apply crossover to some chromosomes in **P'(t)**.
- 5) Apply mutation to few chromosomes in **P'(t)**.
- 6) Apply **three** iterations of **B-W** algorithm to the population **P(t)** for each **ten** generations.
- 7)  $t = t+1$ ;  
if **not convergence**, then go to: 2).

**Figure 3.** Hybrid GA-BW algorithm

## Mutation

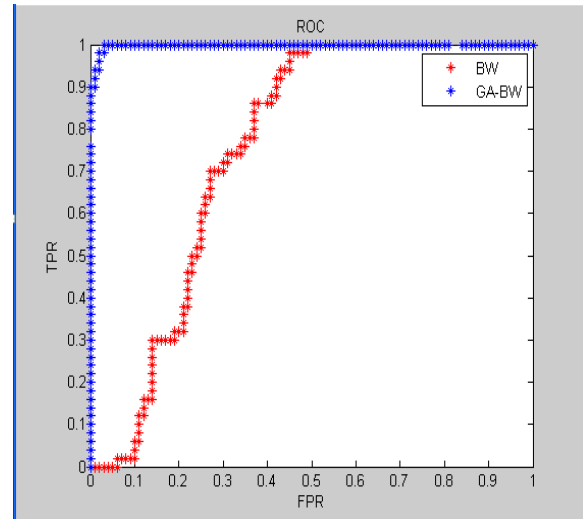
Mutation selects randomly few chromosomes and alters some genes to produce new chromosomes. The “mutation adaptfeasible” function of GA toolbox has been used to satisfy the conditions (1), (2) ... (6).

## Selection and Crossover

Selection mimics the survival of fittest mechanism seen in nature. Chromosomes with higher fitness values have a greater probability to survive in the succeeding generations. Then some elements from the population pool will be selected to apply crossover. Portions of genes will be exchanged between each couple of chromosomes. The default GA Toolbox selection and crossover functions have been used the implementation.

## EXPERIMENTAL STUDY

The experimental study consists of using ROC curve analysis. In Receiver operating Characteristic (ROC) curve a true positive rate is plotted as a function of false positive. A test with prefect discrimination has a ROC curve that passes through upper left corner thus it will have higher the overall accuracy. From Figure 4 GA-BW is at the topmost left corner so it has higher accuracy than BW algorithm. So, it has better classification of tumor region.



**Fig. 4: ROC Convergence.**

## CONCLUSION

In this work two HMM training systems have been analyzed. The first is based on the classical Baum-Welch iterative procedure; the second is based on genetic algorithm.

Under the same conditions the hybrid GABW algorithm performs better than Baum-Welch method. We believe that this improvement is due to global searching ability of GA. So classification of tumor and non tumor region has become better.

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