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Splitting of Gaussian Models via Adapted BML Method Pertaining to Cry-Based Diagnostic System

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ABSTRACT

In this paper, we make use of the boosting method to introduce a new learning algorithm for Gaussian Mixture Models (GMMs) called adapted Boosted Mixture Learning (BML). The method possesses the ability to rectify the existing problems in other conventional techniques for estimating the GMM parameters, due in part to a new mixing-up strategy to increase the number of Gaussian components. The discriminative splitting idea is employed for Gaussian mixture densities followed by learning via the introduced method. Then, the GMM classifier was applied to distinguish between healthy infants and those that present a selected set of medical conditions. Each group includes both full-term and premature infants. Cry-pattern for each pathological condition is created by using the adapted BML method and 13-dimensional Mel-Frequency Cepstral Coefficients (MFCCs) feature vector. The test results demonstrate that the introduced method for training GMMs has a better performance than the traditional method based upon random splitting and EM-based re-estimation as a reference system in multi-pathological classification task.

Keywords: Adapted Boosted Mixture Learning; Gaussian Mixture Model; Splitting of Gaussians; Expected-Maximization Algorithm; Cry Signals

1. Introduction

Gaussian Mixture Model (GMM) has the capability to form smooth approximations to arbitrarily shaped densities and it has proved to be an effective probabilistic model for biometric systems, most notably in speaker recognition systems and speaker identification [1]. The GMMs are estimated from available training data using a special case of the Expectation-Maximization (EM) algorithm based on the maximum-likelihood (ML) [2]. A finite amount of sample data produce detrimental effects that commit statistical errors in training of the GMMs. Nevertheless, this iterative algorithm comes with a guarantee that there will be no decreasing in likelihood function after each iteration and therefore converges to locally optimal parameters [3]. Performance degradation due to parameter estimation errors is a function of the number of free parameters in the classifier [3], so there are still some problems when increasing model complexity. For example, in Automatic Speech Recognition (ASR) systems using HTK with the method based on random splitting and EM-based re-estimation [4]: First, there is no guarantee that the newly added mixture from random splitting always increases the likelihood function prior to re-estimation. Second, convergence to the optimum point in EM-based re-estimation is not guaranteed due to the sensitivity to initial parameters of the randomly split Gaussians. More recently, the traditional boosting method has been used to solve some problems of mixture models [5,6]. Another new method called Boosted Mixture Learning (BML) to learn Gaussian mixture Hidden Markov Model (HMM) is introduced to overcome the aforementioned problems in other available conventional techniques for estimating the GMM parameters [4]. In [7] the discriminative splitting idea has been used for log-linear mixture densities in a speech recognition task. For this purpose, the parameters of Gaussian model have been transformed into their equivalents in log-linear model as presented in [8,9], and then trained in a Maximum Mutual Information (MMI) framework.

GMMs represent a statistical pattern recognition approach that enables optimal processing of data both for training (EM algorithm) the classifier and performing on-line classification. Cry-based diagnostic system for newborn infants can be valuable in medical problems which are currently undetectable until it is too late for treatment. Recently several classifiers such as General Regression Neural Network (GRNN), Multi-Layer Perceptron (MLP), Time Delay Neural Network (TDNN), Probabilistic Neural Network (PNN), Radial Basis Function (RBF) and hybrid systems under several approaches such as bagging and boosting [10] were examined for discriminating between normal and sick infant's cry sig-

nals [11-17]. In our previous work [18], we made use of cry signals to distinguish between healthy and sick infants both full-term and premature. Most of the previous studies [11-17,19] concentrate on health status of infants via a binary classification task, but this paper focuses on identifying several different pathological conditions. In this article a method for splitting of Gaussian mixture densities is presented based on the boosting algorithm to maximize the frame-level ML objective function. The performed experiments on the diagnosis of infants' diseases show that it has fairly superior performance to the conventional method based on random splitting and EM-based re-estimation.

This paper is organized as follows: In Section 2 we give a brief review of GMM. Section 3 explains the different parts of introduced learning algorithm. In Section 4, preprocessing steps and experiments are reported, and in section 5 a follow-up analysis of the results and a conclusion are presented at the end to finalize this paper.

2. Gaussian Mixture Model

A complete GMM for a *D* dimensional continuous value data vector called *X* can be represented by the weighted sum of M Gaussian component densities $\lambda = \{c_k, \mu_k, \Sigma_k\}$ $k = 1,\ldots,M$ as follows:

$$F_M\left(X|\lambda\right) = \sum_{k=1}^{M} c_k \mathcal{N}_k\left(X;\mu_k,\Sigma_k\right), \sum_{k=1}^{M} c_k = 1 \qquad (1)$$

where each mixture component $\mathcal{N}_k$ is a *D*-dimensional multivariate Gaussian distribution and c_k, μ_k, Σ_k are the mixture weights, mean vector and covariance matrix respectively. Since GMMs are used usually in unsupervised learning and clustering problems with unknown number of mixtures and their parameters, the choice of model configuration is almost determined by the amount of data available for estimating the GMM parameters in a particular application. GMM, as a parametric probability density function with the following adapted learning method could be a successful candidate for cry-based physical or psychological status identification system.

3. Adapted Boosted Mixture Model

Generally, boosting method combines weak learners or base classifiers in a weighted majority voting scheme to improve the overall classification accuracy for almost any type of learning algorithm [20,21]. The main idea of boosting is that instead of always treating all data points as equal, component classifiers should specialize on certain examples. Moreover, some recent work has shown that the boosting method can effectively increase the margin of all training samples, which can be explained by a theoretical view related to functional gradient techniques [4,22]. We should note that the boosting algorithm does not always improve the accuracy of a learning algorithm nor does it always increase the margin.

In the presented method a new component $\mathcal{N}_k$ and its weight w_k can be trained based discriminatively based on a predefined objective function, denoted as $\mathcal{C}$, in an optimal way. Then, they will be added to the previous mixture model F_{k-1} which has $k-1$ mixture components to grow into a new mixture model F_k.

$$F_k\left(X\right) = \left(1-c_k\right)F_{k-1} + c_k\mathcal{N}_k\left(X\right) \qquad (2)$$

Objective function is defined as the log likelihood function of the mixture model F_k, based on all training data $\{X_1, X_2, X_T\}$.

$$\mathcal{C}\left(F_k\right) = \sum_{t=1}^{T} \log F_k\left(X_t\right) \qquad (3)$$

where w_k is a weight to combine the new mixture component with the current model. When a new mixture component $\mathcal{N}_k$ is added, it will increase the ML objective function with respect to F until the criterion which will be explained later is met.

$$C\left(\left(1-\varepsilon\right)F_{k-1} + \varepsilon N_k\right) > C\left(F_{k-1}\right) \qquad (4)$$

where ε is a small deviation constant. Thus, the new mixture component $\mathcal{N}_k$ should be estimated in order to increase the ML objective function the most. By employing Teylor's series and predefined inner product of mixture models p and Q over training samples,

$$\langle \mathrm{P},\mathrm{Q}\rangle = \frac{1}{\mathrm{T}}\sum_{\mathrm{t}=1}^{\mathrm{T}} \mathrm{P}\left(\mathrm{X_t}\right)\mathrm{Q}\left(\mathrm{X_t}\right) \qquad (5)$$

the optimal new component can be obtained by:

$$\mathcal{N}_{\mathrm{k}}^{*} = \underset{\mathcal{N}_{\mathrm{k}}}{\mathrm{argmax}} \langle \nabla\mathcal{C}\left(\mathrm{F_{k-1}}\right), \left(\mathcal{N}_{\mathrm{k}} - \mathrm{F_{k-1}}\right)\rangle$$

$$= \underset{\mathcal{N}_{\mathrm{k}}}{\mathrm{argmax}} \sum_{\mathrm{t}=1}^{\mathrm{T}} \frac{\mathcal{N}_{\mathrm{k}}\left(\mathrm{X_t}\right)}{\mathrm{F_{k-1}}\left(\mathrm{X_t}\right)} \qquad (6)$$

The new mixture component is generated along the direction of functional gradient where the objective function grows the most. There is no closed-form of the optimization problem for GMMs, but it can be solved by optimizing a lower bound on the boosting learning formula with the EM algorithm [4]. After estimating $\mathcal{N}_k^{*}$, the mixture weight c_k^{*} can be obtained by using the following line search:

$$c_k^{*} = \underset{c_k \in [0,1]}{argmax}\ \mathcal{C}\left(\left(1-c_k\right)F_{k-1} + c_k\mathcal{N}_k^{*}\right) \qquad (7)$$

3.1. Process of Adding a New Component

In this method, a single Gaussian model initialized by ML training is estimated to fit the data at first, and then

in each step it is split into two Gaussians followed by learning via introduced method. In the splitting or adding process the part of training vectors in which $\mathcal{N}_k(X)$ has a higher value than the reminder of the mixture model, denoted by $F_k - \{\mathcal{N}_k\}$ is selected. Then this subset of data indicated by X_{sub} should be modeled by a small GMM consisting in two Gaussian components called $\mathcal{N}_k^*$ and $\mathcal{N}_{k+1}$. The initial component came from the EM-based re-estimation, and then the second component and its weight were estimated based upon adapted BML method. We considered the estimated component—the second one—as an initial component and run the algorithm again. This process continues repeatedly, until it reached the optimal maximum log-likelihood estimate of parameters over X_{sub}. This procedure for finding the best two new components $\mathcal{N}_{k+1}$ and $\mathcal{N}_k^*$ continued for $k = 1,\ldots,K$. Amongst all the created K mixture models, denoted by F_{K+1}, the one that gave the highest value of the objective function was selected and added to the mixture by adjusting its weight. This iterative density splitting process in ML frame work is repeated as long as the added component causes an increase in the predefined objective function.

3.2. Partial and Global Updating

During previous step, instead of finding the new mixture weight from the line search, there is an alternative method called partial updating in which each new component and its weight are estimated at the same time, which is preferable since it may result in more robust and reliable estimation.

$$\{\mathcal{N}_k^*, c_k^*\} = \underset{c_k, \mathcal{N}_k}{argmax} \; \mathcal{C}\left((1-c_k)F_{k-1} + c_k\mathcal{N}_k\right) \tag{8}$$

The iterative re-estimation formula for model parameters $\Phi_k^{(n+1)} = \{\mu_k^{n+1}, \Sigma_k^{n+1}\}$ at the $(n+1)^{th}$ iteration can be evaluated as follows: [4]:

$$w^n(X_t) = \frac{\mathcal{N}_k\left(X_t \middle| \Phi_k^{(n)}\right)}{c_k{}^n \mathcal{N}_k\left(X_t \middle| \Phi_k^{(n)}\right) + (1-c_k{}^n)F_{k-1}\left(X_t \middle| \Psi_{k-1}\right)}$$

$$\gamma_t\left(\Phi_k^{(n)}\right) = \frac{w^n(X_t)}{\sum_{t=1}^{T} w^n(X_t)}$$

$$c_k{}^{n+1} = \frac{1}{T}\sum_{t=1}^{T} c_k{}^n w^n(X_t)$$

$$\mu_k{}^{n+1} = \sum_{t=1}^{T} \gamma_t\left(\Phi_k^{(n)}\right).X_t$$

$$\Sigma_k{}^{n+1} = \sum_{t=1}^{T} \gamma_t\left(\Phi_k^{(n)}\right).\left(X_t - \mu_k{}^{n+1}\right)\left(X_t - \mu_k{}^{n+1}\right)^{Tr} \tag{9}$$

where $w^n(X_t)$ denotes the weight assigned to sample X_t at the n^{th} iteration, similar to sample weights used in the traditional boosting algorithms and $\Psi_k = \{\Phi_k, \Psi_{k-1}\}$. Moreover, in order to speed up converging process and finding the minimum number of Gaussian component in the final mixture, the current mixture model F_k should be updated globally over training data samples before adding the next component. For example in the GMM with k components, denoted by F_k, the k^{th} component can be re-estimated for $k = 1,\ldots,K$ when the reminder of the mixture mode is assumed to be fixed. It means that after obtaining a mixture model F_K, we could update each component $\mathcal{N}_k$ and its weight over all training feature vectors by using the same updating equations. The parameters updating phase, subsequent to splitting the selected density in half, brings about an increase in the objective function through the localized training of each component separately.

3.3. Initialization of Sample Weights

A problem may arise when the initial values of the weights are chosen by boosting theory as follow:

$$w^0(X_t) = 1/F_{k-1}\left(X_t \middle| \Psi_{k-1}\right) \tag{10}$$

The dynamic range of F_{k-1} is large in a way that it could be dominated by only a few number of outliers or samples with low probabilities. We use the so-called "Weight decay" method [23] to overcompensate for the low probability by smoothing sample weights based on power scaling.

$$w^0(X_t) = (1/F_{k-1}\left(X_t \middle| \Psi_{k-1}\right))^p, 0 < p < 1 \tag{11}$$

where p is a decay parameter or an exponential scaling factor. In the second method the idea of sampling boosting in [24] is applied to form a subset of training feature vectors according to the mean and variance values of the decayed weights. Afterwards, vectors contained in the previously created subset are utilized with equal weights to estimate the new component parameters. Assume $\overline{M}$ and σ^2 denote the mean and variance of weights calculated in equation (9) as defined below.

$$\overline{M} = mean\left\{log\ w^0(X_t)\right\}$$

$$\sigma^2 = variance\left\{log\ w^0(X_t)\right\} \tag{12}$$

Then, the aforementioned subset with large weights is selected as described below:

$$X_{sub} = \left\{X_t \middle| log\, w^0(X_t) > \overline{M} + \beta\sigma\right\} \tag{13}$$

where β is a linear scaling factor to control the size of subset X_{sub}. In the experiments, we set $p = 0.05$ and $\beta = -0.5$ to overcome over fitting and these same parameter values which utilized for BML algorithm in [4].

3.4. Criterion for Model Selection

The process of adding new mixture component to the previous mixture model is continued incrementally and recursively until the optimal number of mixtures is met. The set of Gaussian components selected should represent the space covered by the feature vectors. For this purpose, the selected strategy to stop the adding process is a criterion-based called Bayesian Inference Criterion (BIC). It can be represented as the following [25]:

$$BIC\left(k\right) = -\mathcal{C}\left(F_k\right) + M_k \log\left(T\right) \tag{14}$$

where $\mathcal{C}\left(F_k\right)$ is the log-likelihood function of the mixture model over all training data, M_k is the number of parameters used in model F_k, and T denotes total number of training data. **Figure 1** shows a brief review of all mentioned processes to train a GMM for each available pathological condition in order. A simple procedure to evaluate the presented learning method is to monitor the progress of the method during learning phase with a created training dataset, whose samples have been drawn from a known mixture of multivariate Gaussian distributions. Given training data with 600 two-dimensional samples, we wish to estimate the parameters of the GMM, $\lambda = \{c_k, \mu_k, \Sigma_k\}$, which in some sense best matches the distribution of the training feature vectors.

Figure 2 shows the final trained GMM and the whole discriminative splitting process after each substitution step. We compare the log-likelihood score between our method and the mentioned traditional method at the end of the discriminative training of this model. The negative log-likelihood score of the estimated GMM bears a close resemblance to that of the trained model with the traditional method consisting of the correct number of Gaussian components on the same data, whose values are 2.7682×10^3 and 2.7684×10^3 respectively.

4. Experiments

4.1. Preprocessing and Features Extraction

It would be worthwhile to find a clear correlation between infants' medical statuses and extracted cry characteristics. This concept could prove useful in the early infant diagnosis system. Several different cry characteristics and features were described in [19,26] and have been shown to work well in practice for distinguishing between a healthy infant's cry and that of infants with asphyxia, brain damage, hyperbilirubinemia, Down's syndrome, and mothers who abused drug during their pregnancies. Therefore, selecting the most informative features to distinguish between healthy baby class and pathological infant classes with different pathology conditions has a significant role in pathological classification tasks. **Table 1** shows the list of available different pathological conditions and the number of samples in each class; totaling 63 cry signals for each healthy and sick infants classes including both full-term and premature per class.

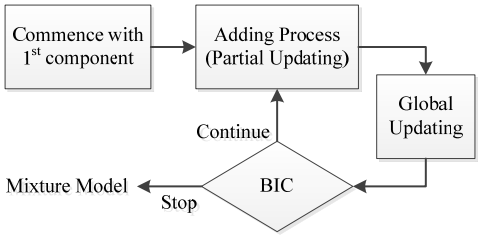


Figure 1. Block diagram of adapted BML technique.

In a similar way to typical speech recognition systems, the pre-processing and the feature extraction phases are modeled in such a way that irrelevant information to phonetic content of the cries should be eliminated as far as possible *i.e.* nurses talking and environmental noises. On the other hand, the Mel-Frequency Cepstral Coefficients (MFCCs) are selected to be extracted from the cries which contain the vocal tract information [27]. This type of excitation source characteristics is one of the popular schemes in speaker recognition and identification systems [27-30]. It is common practice to pre-emphasis the signal prior to computing the speech parameters by applying the filter $P\left(z\right) = 1 - 0.97z^{-1}$ [31,32]. In all related practical applications, the short terms or frames should be utilized, which implies that the signal characteristics are uniform in the region. Prior to any frequency analysis, the Hamming windowing is necessary to reduce any discontinuities at the edges of the selected region. A common choice for the value of the window length is 10 - 30 ms [32-34].

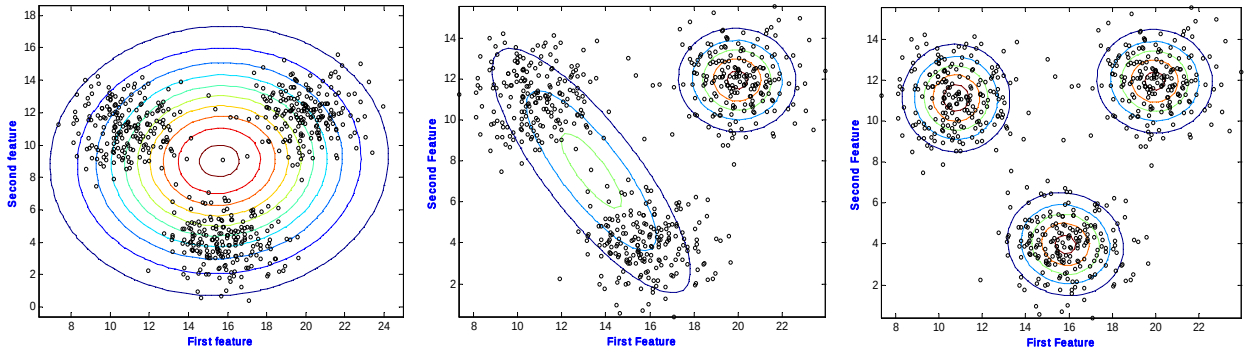
A total number of 12 MFCCs $\{C_n, n = 1,\ldots,12\}$ are computed directly from the data [31,35]. For better performance, the 0^{th} cepstral coefficient C_0 is appended to the vector which is simply a version of energy (*i.e.*, weighting with a zero-frequency cosine). Therefore, each frame is represented by a 13-dimensional MFCCs feature vector [33].

4.2. Multi-Pathology Classification

In training phase of algorithm, in order to estimate the parameters of GMMs for pathology classes, almost 63% of total cry signals were employed and the reminder for system evaluation. The GMM classifier is employed to identify infants' pathological conditions. The Maximum Likelihood (ML) decision criterion is applied to assist in choosing between hypotheses.

$$Pathology\,Class\,\# = \underset{j}{\operatorname{argmax}}\,\mathcal{L}_j\left(X\right) \tag{15}$$

where $\mathcal{L}_j\left(X\right)$ shows the likelihood of a feature vector X given a Gaussian model λ_i for i^{th} pathology class.



(a) (b) (c)

Figure 2. Estimated contour (a) of first Gaussian component, (b) after splitting GMM into 2 components, (c) of final GMM.

Table 1. Cry database.

Infants	State	Pathologies	Number
Full term	Healthy	N/A	38
	Sick	Bovine protein allergy	13
		Tetralogy of Fallot	5
		Thrombosis in the vena cava	13
Premature	Healthy	N/A	25
	Sick	Tetralogy of Fallot	9
		Cardio complex	14
		X chromosomal abnormalities	9

This multi-pathology classification was done by using predefined feature vectors extracted from different frame durations (10, 20, 25, 30 msec) with the same overlap percentage (30%) between two consecutive windows to assess what improvements it may have.

Nevertheless, our results show that, on the average, it had a better accuracy rate compared with the traditional method based on random splitting and EM-based re-estimation for GMMs as our reference system. It is worth mentioning that the GMMs created by the traditional method for each class were trained by setting the number of components equal to that of mixture model learned by adapted BML method. The coefficient of variation (CV) is used to represent the reliability of performance tests. It gives the standard deviation as a percentage of the mean values which is computed from frequency distribution over all pathology classes as follows [36]:

$$CV = \frac{StandardDeviation}{Mean} \times 100\% \qquad (16)$$

Due to space limitation, **Table 2** shows only the results for two frame length (10 ms and 20 ms) as the most reliable results. Note that the states correspond to the order given in **Table 1**. It can be seen that both methods delivered great performances for most pathology classes, but based on the frequency distribution of the cry samples. The presented method for 20 ms frame size had

Table 2.Obtained accuracy rate (%) for multi-pathology task.

	20 msec		10 msec	
State	EM-Based	ABML	EM-Based	ABML
1	100	100	100	100
2	100	100	80	80
3	100	100	100	100
4	75	100	75	75
5	100	88.9	100	100
6	100	100	100	100
7	80	60	80	80
8	100	100	100	100
Mean	94.16	94.58	92.08	92.08
CV	10.9	12	11.8	11.8

better final accuracy rate. Moreover, the larger the CV, the more the performance varies.

5. Conclusion

An adapted mixture learning method for GMMs based on boosting algorithm is introduced in this paper. Advanced techniques of signal processing, and machine learning were employed in different parts of the learning process such as adding a new component per step, weighting function for samples, model selection, and global re-estimation of parameters. The focus of this paper has been on the application of discriminative training via introduced GMM-ABML as it pertains to the pathology detection through infants' cry signals. For each pathology class in our cry database, the adapted BML method trained a mixture model with a separate Gaussian pool as a cry-pattern. The results show that, on the average, it delivers a higher classification accuracy rate (94.58%) than the traditional method based on random splitting and EM-based re-estimation. It might be early to reach strong conclusions since there are not enough cases of the pathological classes, but the results have the potential

to serve as a mixture learning method for further research. We are currently trying to use alternative discriminative criteria like MMI rather than ML and collecting more sample cries for further tests.

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