ÉCOLE DE TECHNOLOGIE SUPÉRIEURE
UNIVERSITÉ DU QUÉBEC

MANUSCRIPT-BASED THESIS PRESENTED TO
ÉCOLE DE TECHNOLOGIE SUPÉRIEURE

IN PARTIAL FULFILLEMENT OF THE REQUIREMENTS FOR
THE DEGREE OF DOCTOR OF PHILOSOPHY
Ph. D.

BY
Hesam FARSAIE ALAIE

DIAGNOSIS OF DISEASES IN NEWBORN INFANTS BY ANALYSIS OF CRY SIGNALS

MONTREAL, JUNE 8th 2015

BOARD OF EXAMINERS (THESIS PH.D.)

THIS THESIS HAS BEEN EVALUATED

BY THE FOLLOWING BOARD OF EXAMINERS

Prof. Chakib Tadj, Thesis Supervisor
Department of Electrical Engineering at École de technologie supérieure

Prof. Christian Gargour, Chair, Board of Examiners
Department of Electrical Engineering at École de technologie supérieure

Prof. Jérémie Voix, Member of the jury
Department of Mechanical Engineering at École de technologie supérieure

Prof. Patrick Kenny, External Evaluator
Computer Research institute of Montréal

THIS THESIS WAS PRENSENTED AND DEFENDED

IN THE PRESENCE OF A BOARD OF EXAMINERS AND THE PUBLIC

MAY 8th 2015

AT ÉCOLE DE TECHNOLOGIE SUPÉRIEURE

ACKNOWLEDGMENTS

Thanks are in order for all the people who have helped me in realizing this doctorate thesis.

My heartfelt gratitude is in order for my director at École de Technologie Supérieure, Dr. Chakib Tadj for his supervision and support. His invaluable support helped me to get into the doctorate program and overcome all the difficulties through the period of my PhD study. He let me find my own path whilst at the same time showing me which alternate paths I might be missing and giving me advice in courses, in thesis writing, in securing grants, in dealing language problems between English and French, in personal problem in my life.

I also would like to thank the jury members who evaluated my thesis and for their constructive suggestions and helpful advice.

Apart from academic people mentioned above, I would also like to thank all my colleagues in MMS laboratories for all the technical help and support during the period of my PhD study in Montréal.

I would like to dedicate this thesis to my parents, Ahmad and Fatemeh, my brother Hossein and thanks them for all the support, they provided for me during this stage of my life. This was simply not possible without their encouragement and unconditional love. Thanks mom and dad for all your love.

Finally, I acknowledge the financial support from Bill & Melinda Gates Foundation.

DIAGNOSIS OF DISEASE IN NEWBORN INFANTS BY ANALYSIS OF CRY SIGNALS

Hesam FARSAIE ALAIE

SUMMARY

Crying is the first sound the baby makes when he enters the world outside of his mother's stomach, which is a very positive sign of a new healthy life. Well, we elders can talk but the newborn infant isn't old enough to do that yet. Cry is all a baby can do to express any discomfort it feels. When initially reading it, the first thing that comes to mind is why the cry is such an important aspect of health care for newborn infants? Although studying on infant's cry was pioneered in the late 1960s, but it never crossed anybody's mind that sick infants might be identified from their cries. Statistical reports by World Health Organization state that the congenital anomalies or birth defects affect approximately 1 in 33 infants born every year and almost all of the world's infant deaths happen in developing countries. Therefore, it is imperative to provide an inexpensive health care system, with no need of complex and advanced technology for poor mothers with newborn babies in low-income countries to survive more babies beyond the first months of life. In spite of the fact that there are a lot of maternal issues that can raise the risks of complications and anomalies in newborn infants, we are curious to examine the ability of solely the concealed information inside infant's cry to clarify the infant's physiological anatomy and psychological condition. The creative idea behind of such a non-invasive diagnostic system is based on the evidence extracted from past research studies for potential ability of infant's cry to distinguish between healthy and sick infants. This innovative idea can tackle key global health and development problems.

The purpose of this study is to develop a newborn cry-based diagnostic system to classify healthy and sick infants with different pathological conditions. First, an informed choice of pathological states and collecting of the infant cry data base is necessary and still in progress to complete the infant cry data base. In many of today's application domains, it is often unavoidable to have data with high dimensionality and small sample size. Both small sample size problem and dimensionality reduction methods have been studied extensively but the combination of imbalanced data and small sample size presents a new challenge to the community. In this situation, learning algorithm often fail to generalize inductive rules over the sample space when presented with this form of imbalance. In fact, the combination of small sample size and high dimensionality hinders learning because of difficulty involved in forming conjugations over the high degree of features with limited samples. In the next part, data preprocessing, including selection and extraction of pathologically-informed features suitably with the best possible precision and then quantifying them for each pathological condition without any human intervention is considered in the system. In order to obtain the full benefit of the information embedded in the cry signal, Mel Frequency Cepstrum Coefficient (MFCC) analysis will be done on both expiratory and inspiratory cry vocalizations separately in this study. To avoid the need of human effort in labeling the boundaries of the corresponding corpus, automatic labeling of cry signals is required for an

ideal cry-based diagnostic system. However, to alleviate the segmentation task in this study, it has been manually performed so far.

Finite mixtures are a flexible and powerful probabilistic tool for modeling univariate and multivariate data among all available approaches to do modeling and classification tasks. In this regard, we come up with Gaussian Mixture Models (GMMs) that is a special case of Hidden Markov Models (HMMs) with one state, as a new representation of cry signals according to extracted feature streams. The next part of this thesis is dedicated to enhancement of learning of GMMs that are usually trained using the iterative Expectation Maximization (EM) algorithm. However, considering the risk of overfitting due to small training sample size in some pathological conditions, and the fact that the number of mixtures is fixed in the traditional EM-based re-estimation algorithm, a new learning method based on boosting algorithm is introduced to learn growing mixture models in an incremental and recursive manner.

The idea of Universal Background Model (UBM) used in speaker recognition and verification systems is employed to represent general feature characteristics of infant cry signals. Then, a variant of boosted mixture learning (BML) method is employed in order to derive subclass models for each enrolled disease from the GMM-UBM by adaptation of GMM parameters. The crux of the design was to fuse two subsystems that are based on expiratory and inspiratory sounds in baby cry recordings into a single effective system. Such systems are expected to be more reliable due to the presence of multiple, (fairly) independent pieces of evidence. We present log-likelihood ratio score fusion to stop worrying on the feature compatibility and rigid fusion.

Apart from all of the above-mentioned modeling and learning methods, our work is different from previous works in that while other systems usually deal with binary classification tasks between healthy and sick infant with only one specific disorder. Our cry-based diagnostic system has a hierarchical scheme that focuses into multi-pathology classification problem via combination of individual classifiers. Moreover, it is worthwhile mentioning that the chosen diseases have not been previously studied.

Keywords: Gaussian mixture model; Universal background model; Mel-frequency Cepstral Coefficient; Likelihood ratio scores; Newborn infant cries; Expiratory sound; Inspiratory sound.

LE DIAGNOSTIC DES PATHOLOGIES CHEZ LES NOUVEAU-NÉS PAR L'ANALYSE DES SIGNAUX DE CRIS

Hesam FARSAIE ALAIE

RÉSUMÉ

Le cri est le premier son qu'un bébé peut générer à la naissance, et qui est également un signe positif d'une nouvelle vie saine. Ainsi, le cri est tout ce qu'un nourrisson peut faire pour exprimer un quelconque malaise qu'il ressent. Nous pouvons alors nous demander : pourquoi un cri est-il un aspect important des soins de santé dispensés aux nouveau-nés ? Bien que les études sur les cris des nouveau-nés aient été initiées depuis la fin des années 1960, peu de travaux ont été réalisés en vue de l'identification automatique de pathologies à partir du cri.

Les rapports statistiques de l'Organisation mondiale de la santé indiquent que les anomalies congénitales ou malformations à la naissance affectent environ 1 nouveau-né sur 33 chaque année, et tous les décès d'enfants dans le monde ont majoritairement lieu dans les pays en développement. Il est donc impératif de fournir, aux pauvres mères dans les pays à bas revenu, un système économique de soins de santé qui aide leurs nouveau-nés à survivre au-delà des premiers mois de la vie, sans avoir à recourir à des technologies complexes et avancées. Malgré le fait qu'il y ait beaucoup de problèmes de santé maternelle qui peuvent augmenter les risques des complications et des anomalies chez les nouveau-nés, nous sommes avides de savoir à quel point l'information dissimulée dans le cri pourrait permettre l'identification de l'anatomie physiologique ainsi que de la condition psychologique chez un nouveau-né. L'idée créative d'un tel système non invasif de diagnostic est basée sur les données probantes ressorties des recherches antérieures qui à leur tour révèlent la possibilité de distinguer entre enfants malades et enfants sains à partir du cri. Cette idée innovatrice peut aborder les principaux enjeux en matière de santé et de développement.

Le but de cette étude est de développer un système de diagnostic basé sur les cris afin de classifier les bébés sains et malades avec différents états pathologiques. D'abord, il est important de faire un choix précis des états pathologiques pour la phase de collection des cris des nouveau-nés. Cette opération est encore en cours pour compléter la base de données de cris. De plus, dans de nombreux domaines d'applications, il est souvent incontournable de disposer de données à très haute dimensionnalité et de taille d'échantillons réduite. Les problèmes de la taille des échantillons et de la réduction de la dimensionnalité ont fait l'objet des nombreuses recherches, mais l'association des données déséquilibrées et la taille réduite des échantillons réduite présente un nouveau défi pour la communauté. Dans cette situation, les algorithmes d'apprentissage échouent souvent à généraliser des règles inductives sur l'espace de l'échantillon et surtout lorsqu'ils sont employés avec cette forme de déséquilibre.

En effet, l'utilisation d'un échantillon, de taille réduite et de haute dimensionnalité, peut avoir un impact négatif sur l'apprentissage en raison de la difficulté dans la formation des relations par rapport au niveau déjà élevé des caractéristiques avec un nombre limité d'échantillons. Dans la partie qui suit, une étape de prétraitement des données, y compris la sélection et l'extraction des caractéristiques pathologiques appropriées avec la meilleure précision possible ainsi que leur quantification pour chaque pathologie, sans aucune intervention humaine, sera considérée pour l'élaboration de notre système. Afin d'exploiter l'information contenue dans le signal du cri, l'analyse des coefficients cepstraux sur l'échelle de Mels (MFCC) sera effectuée dans cette étude de façon séparée sur chacun des types de vocalisations expiratoire et inspiratoire du cri. En tenant compte de la nécessité d'éviter les efforts humains dans l'étiquetage des frontières dans le corpus utilisé, une étape de segmentation automatique des signaux de cris est requise pour un système de diagnostic idéal. Cependant, en vue d'alléger la tâche de segmentation dans cette étude, il était nécessaire jusqu'à présent de l'effectuer manuellement.

Les mélanges finis sont des outils de modélisation probabilistes, flexibles et puissants parmi toutes les approches disponibles. Elles permettent la modélisation et la de classification de données univariables et multivariables. Nous avons ainsi choisi d'utiliser les modèles de mélanges gaussiennes (GMM), qui représentent un cas particulier des Modèles de Markov cachés (HMMs) avec un seul état, pour la représentation des signaux cris selon les vecteurs de caractéristiques extraites. La partie suivante de cette thèse est dédiée à l'amélioration de l'apprentissage des GMMs. Cette étape est généralement réalisée à l'aide d'un algorithme itératif EM, pour Expectation-Maximisation. Cependant, compte tenu, d'une part, du risque du sur-apprentissage (overfitting) en raison de la petite taille de des échantillons de certaines conditions pathologiques, et d'autre part, du fait que le nombre de mélanges est fixé dans l'algorithme de ré-estimation traditionnelle EM, une nouvelle méthode d'apprentissage fondée sur un algorithme de 'boosting' est introduite afin d'entrainer les modèles de mélanges croissantes d'une façon incrémentale et récursive.

L'idée du modèle universel (UBM), largement employé dans les systèmes de reconnaissance du locuteur et de vérification, est utilisée pour représenter les caractéristiques principales des signaux de cris des nourrissons. Une variante de l'algorithme d'apprentissage appelée BML, pour Boosted Mixture Learning est employée, afin d'obtenir des modèles de chaque pathologie étudiée à partir d'un GMM-UBM par une adaptation des paramètres du GMM. L'essentiel dans la manipulation d'un système efficace de diagnostic est la fusion des deux sous-systèmes basés sur les vocalisations expiratoires et inspiratoires détectées dans les enregistrements des cris des bébés. De tels systèmes sont censés être plus fiables du fait de la présence de plusieurs éléments de preuve indépendants. En tenant compte de la compatibilité

des caractéristiques et de la rigidité de la fusion, nous illustrons le rapport de fusion du Log-vraisemblance.

Indépendamment de toutes les méthodes d'apprentissage et de modélisation susmentionnées, notre travail se différencie des travaux antérieurs par le fait que dans les autres systèmes, une tâche binaire de classification est utilisée et qui sert à distinguer entre bébés sains et bébés malades ayant seulement une pathologie spécifique. Alors que notre système de diagnostic est fondé sur un schéma hiérarchique qui se focalise sur le problème de classification multipathologies via la fusion de divers classificateurs individuels. Par ailleurs, il convient de souligner que les pathologies sélectionnées n'ont pas été étudiées auparavant.

Mots clés: Modèles de mélanges gaussiennes ; Modèle universel (UBM) ; Coefficients Cepstraux; Rapport de vraisemblance ; cris des nouveau-nés ; Expiration ; Inspiration.

TABLE OF CONTENTS

Page

INTRODUCTION 1

CHAPITRE 1 REVIEW OF THE STATE OF THE ART 9
1.1 Fundamental concepts 9
1.1.1 Definitions and elucidation 9
1.1.2 Types of cries in infants 14
1.2 Background 16
1.2.1 Mortality rate and birth defects 16
1.2.2 Primary research 20
1.2.3 Early-infant medical researches 24
1.2.4 Review of studies on machine learning and classification problems 28
1.3 Cry pattern classification 35
1.3.1 Brief description on various classifiers 37
1.3.1.1 ANN and SVM 37
1.3.1.2 Decision tree 39
1.3.1.3 Naïve Bayes 40
1.3.1.4 K-nearest neighbor 41
1.3.2 Why Gaussian Mixture Models? 41
1.3.2.1 Introduction to GMMs 43
1.3.2.2 Learning of GMMs 44
1.3.2.3 Boosting algorithm 46
1.4 Brief objectives, methodologies and contributions 47
1.5 Summary 50

CHAPITRE 2 CRY-BASED CLASSIFICATION OF HEALTHY AND SICK INFANTS USING ADAPTED BOOSTED MIXTURE LEARNING METHOD FOR GAUSSIAN MIXTURE MODELS 53
2.1 Abstract 54
2.2 Introduction 54
2.3 GMMs for Cry-Pattern Classification 56
2.4 Newborn Cry-Based Diagnosis System (NCDS) 58
2.4.1 Cry Database 58
2.4.2 Pre-processing and feature extraction 58
2.4.3 Adapted BML method for GMMs 62
2.4.4 Initialization of sample weights 64
2.4.5 Process of adding a new component 65
2.4.6 Partial and global updating 66
2.4.7 Criterion for model selection 67
2.4.8 Decision rule 68
2.5 Experiments 69

2.6 Conclusion 76
2.7 Acknowledgment 77

CHAPITRE 3 SPLITTING OF GAUSSIAN MODELS VIA ADAPTED BML METHOD PERTAINING TO CRY-BASED DIAGNOSTIC SYSTEM 79
3.1 Abstract 80
3.2 Introduction 80
3.3 Gaussian mixture model 82
3.4 Adapted boosted mixture model 83
3.4.1 Process of adding a new component 84
3.4.2 Partial and global updating 85
3.4.3 Initialization of sample weights 86
3.4.4 Criterion for model selection 87
3.5 Experiments 89
3.5.1 Preprocessing and feature extraction 89
3.5.2 Multi-pathology classification 90
3.6 Conclusion 92
3.7 Acknowledgment 93

CHAPITRE 4 CRY-BASED INFANT PATHOLOGY CLASSIFICATION USING GMMS 95
4.1 Abstract 96
4.2 Introduction 97
4.2.1 Early studies and birth defects 97
4.2.2 Related studies 100
4.3 Recording procedure and cry data base 101
4.4 Feature extraction 103
4.4.1 Preprocessing stages 104
4.4.2 Static and dynamic MFCCs 105
4.5 Statistical modeling and descriptions 108
4.5.1 Likelihood ratio detector 109
4.5.2 Gaussian mixture models 111
4.5.3 System description 112
4.5.4 Applying the GMM-UBM 114
4.5.5 BML adaptation of sub-models or health-dependent-infant cry model 116
4.6 Evaluations and experiments 119
4.6.1 Defining GMM-UBM and adaptation methods 119
4.6.2 Log-likelihood score computation 120
4.6.3 Health-condition detection system 123
4.6.3.1 Healthy infant detector 123
4.6.3.2 Sick infant detector with a specific disease 129
4.6.4 Fusion, calibration and decision 131
4.6.5 Results and discussion 133
4.7 Conclusion and further discussion 145
4.8 Acknowledgment 148

CONCLUSION 149

RECOMENDATIONS 155

LIST OF TABLES

Page

Table 1.1 Comparison of the first three cry signals after pain stimulus 15

Table 1.2 Deaths and percentage of total deaths for the 11 leading causes of infant death: United States, 2010 17

Table 1.3 Maternal age versus risk of DS 17

Table 1.4 Similarities between hunger, first birth, and pleasure cry 21

Table 1.5 Comparison table between cry characteristics of several diseases 22

Table 1.6 Comparison table between cry characteristics of healthy and sick infants 23

Table 1.7 Confusion matrix 24

Table 1.8 Cry features of infants with severe pathologies 25

Table 1.9 Cry features of infants with undetectable disease with not clear prognosis 27

Table 1.10 Confusion matrix of Neural Network with SCG algorithm 30

Table 1.11 The winning combination with 10 features 31

Table 1.12 Confusion matrix of RBF network 31

Table 1.13 Determination of FN1 32

Table 1.14 Determination of decision parameter 33

Table 1.15 Confusion matrix of the ensemble method 33

Table 1.16 Comparison accuracies of FFNN with PCA and statistic reduction 34

Table 1.17 Comparison table between best results of classifiers and their ensembles 34

Table 1.18 Obtained accuracy rate in each decomposition level for PNN classification 36

Table 2.1 Cry database 59

Table 2.2 Obtained accuracy rate for multi-pathology classification (%) 71

Table 2.3 Confusion Matrix for defined Binary classification task 75

Table 2.4 Obtained two statistical measures for Binary-classification problem.....76

Table 3.1 Cry database 90

Table 3.2 Obtained accuracy rate (%) for multi-pathology classification task.....92

Table 4.1 Different units available in the CDB 102

Table 4.2 List of health-conditions 103

Table 4.3 Number and duration of the recorded cry signals that were available in the training CDB at the time.....117

Table 4.4 Number of infants and recorded cry signals available in the testing CDB at the time.....122

Table 4.5 Number of cry samples that contain EXP/INSV-labeled segments and 3-sec cry units in our test CDB 122

Table 4.6 Comparison of the different healthy infant detector systems based on the Equal error rate and Area under the curve for all of the test samples 128

Table 4.7 Comparison of the different healthy infant detector systems based on the EER and AUC for the test samples that have more than 3 INSV units (32 and 23 cry samples of healthy and sick infants respectively).....128

Table 4.8 Results of the sick infant detector systems for Respiratory and Neurological disorders 130

Table 4.9 Training parameters used in SVM, PNN and MLP 132

Table 4.10 Number of folds and rounds 133

Table 4.11 Average accuracy, sensitivity and specificity over the used classifiers in the healthy infant detection task 137

Table 4.12 Accuracy rates for the used classifiers in the healthy infant detection task 138

Table 4.13 Sensitivity rates for the used classifiers in the healthy infant detection task 139

Table 4.14 Specificity rates for the used classifiers in the healthy infant detection task 139

Table 4.15 Average accuracy, sensitivity and specificity over the used classifiers in the sick infant (affected by neurological problems) detection task 143

Table 4.16 Average accuracy, sensitivity and specificity over the used classifiers in the sick infant (affected by respiratory disorders) detection task 144

LIST OF FIGURES

Page

Figure 1.0 The desired system....14

Figure 1.1 Rhythmic pattern of a typical infant cry 14

Figure 1.2 Pattern of Pain Cry....15

Figure 1.3 Infant mortality by gestational age in the U.S. in 2010 18

Figure 1.4 Relation of weight and gestational age for (a) male and (b) female singletons 19

Figure 1.5 Median values, the 25^{th} and 75^{th} percentiles of the....28

Figure 1.6 Block diagram of auto diagnostic system by using pattern recognition 28

Figure 1.7 Linear prediction analysis on 1 second of cry signal....29

Figure 1.8 Structure of a basic RBF network....30

Figure 1.9 Obtained densities for uni-modal Gaussian model, GMM, and VQ....42

Figure 1.10 The general system diagram 48

Figure 1.11 The growing process of finite mixture model....49

Figure 1.12 Modeling and decision....50

Figure 2.1 Time domain representation of a cry signal....59

Figure 2.2 Pre-processing steps....62

Figure 2.3 Block diagram of learning GMM using....68

Figure 2.4 Mapping of estimated GMMs to pathological conditions 69

Figure 2.5 Mean classification accuracy rates....72

Figure 2.6 Coefficient of variation....73

Figure 2.7 Number of components....74

Figure 3.1 Block diagram of adapted BML technique....88

Figure 3.2 Estimated contour (a) of the first Gaussian component, (b) after splitting GMM into 2 components, (c) of final GMM....89

Figure 4.1 Leading causes of infant deaths in 193 countries in 2010 98

Figure 4.2 Cumulative power spectrum of (a-c) EXP units, (b-d) INSV units for each health condition....106

Figure 4.3 Pre-processing and MFCC feature extraction steps....107

Figure 4.4 Balanced data pooling approaches for two defined GMM-UBM....115

Figure 4.5 Mean of the LLR scores over INSV cry units inside the (a) healthy and (b) sick infants for the healthy infant verification system....121

Figure 4.6 DET curves for two alternative hypothesized models λPI − UBM (a-c) and λHyp (b-d) and for INSV (a-b) and EXP (c-d) cry units with a 10 ms frame length in the healthy infant verification system....124

Figure 4.7 DET curves for two alternative hypothesized models λPI − UBM (a-c) and λHyp (b-d) and for INSV (a-b) and EXP (c-d) cry units with the 30 msec frame length in the healthy infant verification system 125

Figure 4.8 Type I and type II errors of the tested different healthy infant detector systems for each of the adaptation methods 136

Figure 4.9 Type I and type II errors for the SVM with different kernel functions in the healthy infant detection task 137

Figure 4.10 Comparison of the accuracy rates of all of the classifiers in the healthy infant detection task 138

Figure 4.11 Type I and type II errors of the classifiers used in the healthy infant detection task using 400 repeated 3-fold CVs for the test samples that contain more than 3 EXP and INSV-labeled cry units 140

Figure 4.12 Type I and type II errors for the different classifiers in the sick infant (affected by neurological problems) detection task....142

Figure 4.13 Comparison of the accuracy rates of all of the classifiers in the sick infant (affected by neurological problems) detection task....142

Figure 4.14 Type I and type II errors for the different classifiers in the sick infant (affected by respiratory disorders) detection task....144

Figure 4.15 Comparison of the accuracy rates of all of the classifiers in the sick infant (affected by respiratory disorders) detection task....145

Figure 4.16 Introduced system overview 152

LIST OF ABREVIATIONS, INITIALS AND ACRONYMS

AGA	Appropriate for gestational age
AIC	Akaike information criterion
ANN	Artificial neural network
ANOVA	Analysis of variance
ASR	Automatic speech recognition
AUC	Area under cover
BIC	Bayesian information criterion
BML	Boosted mixture learning
CDB	Cry data base
CDC	Center for disease control
CE	Cross entropy
CNS	Central nervous system
CV	Coefficient of variation
DCT	Discrete cosine transform
DET	Detection error tradeoff
DS	Down syndrome
DWT	Discrete wavelet transform
EER	Equal error rate
EM	Expectation maximization
EXP	Expiration
FAR	False acceptance rate
FFNN	Feed-forward neural network
FFT	Fast Fourier transform
FIR MLP	Finite impulse response multilayer response
FN	False negative
FP	False positive
FRR	False rejection rate
GMM	Gaussian mixture model
GMM-ML	Gaussian mixture model-maximum likelihood

GFCC	Gamma-tone frequency Cepstral coefficients
GRNN	General regression neural network
GSFM	Genetic Selection of a Fuzzy Model
HMM	Hidden Markov model
HPF	High Pass Filter
HTK	Hidden Markov model toolkit
INSV	Inspiration voiced
KNN	K-nearest neighbor
LBW	Low birth weight
LGA	Large for gestational age
LLR	Log-likelihood ratio
LP	Linear prediction
LPC	Linear prediction coefficients
LVQ	Linear vector quantization
MAP	Maximum a posteriori
MFCC	Mel frequency Cepstral coefficients
MFDWC	Mel frequency discreet wavelet coefficients
ML	Maximum likelihood
MLP	Multilayer perceptron
MMI	Maximum mutual information
ms	Millisecond
NCDS	Newborn cry-based diagnosis system
NICU	Neonatal intensive care unit
NIST	National institute of standard and technology
OP	Operation point
PCA	Principle component analysis
PNN	Probabilistic neural network
PSD	Power spectral density
RBF	Radial basis function
RDS	Respiratory distress syndrome

ROC	Receiver operating characteristic
SCG	Scaled conjugate gradient
SFFS	Sequential forward floating search
SGA	Small for gestational age
SIDS	Sudden infant death syndrome
SMO	Sequential minimal optimization
SRE	Speaker recognition evaluation
SVM	Support vector machine
TDNN	Time delay neural network
TN	True negative
TP	True positive
UBM	Universal background model
VAD	Voice activation detection
VQ	Vector quantization
WHO	World health organization
WPT	Wavelet packet transform
WTCC	Wavelet transform-based Cepstral coefficient

INTRODUCTION

Context of Research Work

Crying is the first and clear sign of life which is seen clearly shortly after the baby's live birth. Reasons of infant's cry are the same reason of speech in adult i.e. to let others know about their needs or problems. In other words, every baby is born with the ability to express their needs through sound. Therefore this multimodal signal carries a lot of information about the baby. For example, Mrs. Priscilla Dunstan[1] has decoded five universal infant cry patterns as an easiest way to settle an inconsolable baby who can make a parent feel quite helpless and powerless. These patterns are sort of a baby language based on phonetic sounds, which are created as part of the automatic reflexes that all newborn babies make.

Analysis of infant cry signals was pioneered in the late 1960s in Scandinavia. After some sound spectrographic cry analysis of infants with various diseases, in some cases it has been noticed that there are fixed cry attributes, which are rarely seen in cries of healthy infants. Instead, these attributes occur very often in cries of infants with diseases. Therefore it was found that concealed information contained in infant cry signal can reflect a diverse range of diseases and conditions that could affect an infant's health. In early studies of infant cry, the acoustic structure of infant crying was analyzed and some of the important variables controlling the production of their cries were described. Afterwards, focus of attention was shifted into the sounds produced by the hungry, lonely, pain, hurt, or generally discomforted infants. Although there have been some books and products created through the years to unlock the secret language of babies, their potential for use in the early diagnosis and treatments in newborns remains largely in an open and undeveloped state.

---

[1] http://www.dunstanbaby.com/

Statement of research problem

In recent years, there has been an increasing interest in cry analysis of sick newborn infants. Due to high rate of mortality rate (about 2.7 million infants) in 193 countries in 2010 (Congenital anomalies, 2014), researchers have begun to take an interest in newborn infants with congenital anomalies or babies who are preterm or at risk with infected Central Nervous System (CNS). Moreover, the sudden death of an infant may occurs in some cases which is not predictable by medical history and remains unexplained after detailed death scene investigation, but some of them are actually result of accidents, abuse, and previously undiagnosed conditions, such as metabolic disorders.

Recently, there has been a lot of interest in diagnosis tools that are affordable, easy-to-use and can rapidly diagnose disease at the point of care and thereby reduce death, disability in resource-poor communities. One of many bold ideas attracting investment from the Gates Foundation's Grand Challenges Explorations initiative to address global health and development challenges is to provide special care and treatment that can prevent disability and death early in life in resource-poor communities. Since approximately 1 percent of the world's infant deaths occur in developed countries based on the fact sheet[2], the situation is worse for many developing countries. Consequently, identifying illness in newborns from their cries via a robust, inexpensive, and simple to use in point-of-care settings have the ability to greatly improve the quality and efficacy of healthcare available to newborns in developing countries, where the burden of disease is highest.

It never crossed anybody's mind a few years ago that sick infants might be identified from their cries. However, based on current evidence for potential ability of infant's cry to distinguish healthy infant from those with medical problems, there is a good chance to be

[2] The World factbook (Fact sheet N° 348-Updated May 2104)
Available in: http://www.who.int/mediacentre/factsheets/fs348/en/

successful in finding such a Newborn Cry-based Diagnosis System (NCDS). This innovative idea can tackle key global health and development problems.

In this work, we focus on the means of the discriminative learning of GMM to suit the given cry samples consisting of healthy and sick newborn infants with different pathological conditions. A novel idea is used to adapt the parameters of the corresponding GMM-UBM to derive either healthy or pathology subclass models separately. It is the principal contribution that we offer in this research domain where lots of interests were expended for the classification of cries of infants in pathological conditions.

Objective and methodology

Our objective is to develop classification system to determine prognosis for newborn infants with congenital diseases. The system creates a GMM-based pattern for either the expiratory or inspiratory sounds of cry signals. It provides score level fusion of aforementioned models in order to offer improvement in diagnostic and prognostic accuracy. Indeed, our objective is to provide a cry-based classification system that is capable of modeling the acoustic differences between wide range of developmental and pathological conditions affecting both vulnerable preterm and full-term neonatal population. Once developed, the system is simple to use: a recorder of the voice connected to a computer takes samples of the cry of the infant. The result will be available after finishing data processing and cry classification process instantly. Figure 0.1 shows various test results which will be provided by the system.

In order to attain this objective, the following approaches were conceived:

1. The paradigm that is to be developed should be generic in concept in order that the proposed solution can be applied to any kind of infant disease with no or very little adjustments.

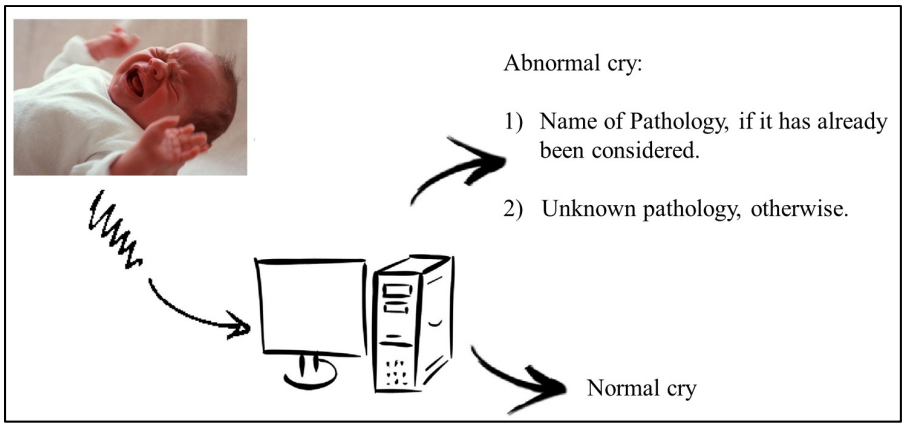


Figure 0.1 The desired system

2. For the system to be robust, inexpensive and simple to use due to inspiration behind the startup idea of developing such a system, it must be able to work with cry signals recorded in hospital environment without any advanced methods such as enhancement and recognition technologies for the reverberation challenge.

The following methodologies were used in the course of our research work and documentation:

1. The cry signals are pre-processed to be prepared for short-term processing, and then, the feature extraction procedure is applied, including MFCCs (Davis et Mermelstein, 1980), delta and delta-delta coefficients (Gauvain et Chin-Hui, 1994). This feature extraction was done through the HTK (Hidden Markov Model Toolkit) software tool (Young et al., 2006b), which is an established tool of speech recognition systems based on hidden Markov models.

2. The concept of universal background model (UBM) (Reynolds, 2009) and background speaker models (Reynolds, 1995b) were used in order to represent the global infant's cry characteristics and calculate the likelihood ratio score. The design of each subclass or health-condition-specific models via adapting the parameters of the UBM made with regards to the corresponding training cry signals separately.

3. The traditional EM-based re-estimation (Dempster, Laird et Rubin, 1977) and maximum a-posteriori (MAP) approach (Gauvain et Chin-Hui, 1994; Reynolds, Quatieri et Dunn, 2000) were employed to train GMMs and adapt the GMM-UBM respectively as a reference system.

4. The concept of Log-likelihood ratio (LLR) (Reynolds, Quatieri et Dunn, 2000) was used for a test sequence of feature vector. Both fast scoring method and score normalization for a sequence of feature vector (Reynolds, Quatieri et Dunn, 2000) were employed to reduce the computational complexity.

5. Mathematical equations were formulated to allow the reader a better understanding of various concepts and idea within this thesis.

Organization of the thesis

The organization of this thesis is as follows:

The first chapter is a review of the past research studies whose goal is to illustrate their contributions with regards to our work as well as to differentiate ours with them, therefore illustrating our contributions to the domain. The three chapters that follow are published works.
The second chapter is an article that was published in the Journal of Modeling and Simulation in Engineering:

- Farsaie Alaie, Hesam, et Chakib Tadj. 2012. « Cry-Based Classification of Healthy and Sick Infants Using Adapted Boosted Mixture Learning Method for Gaussian Mixture Models ». Modeling and Simulation in Engineering, vol. 2012, p. 10.

In this article, we presented the major drawback of the conventional EM-based re-estimation algorithm in designing and training the parameters of GMMs. We presented our preliminary

solution as an adapted boosted mixture learning method to train mixture models in an incremental and recursive manner. We presented GMM as an effective probabilistic model for our cry-based classification system. We also demonstrated that the performance of the healthy infant classifier gradually improve when the frame duration for short-time processing decrease from 30 to 20 msec.

The third chapter is an article that was published in the Journal of Engineering in 2013:

- Farsaie Alaie, Hesam, et Chakib Tadj. 2013. « Splitting of Gaussian Models via Adapted BML Method Pertaining to Cry-Based Diagnostic System ». Engineering, vol. 5, p. 277-283.

In this article, we introduced a discriminative splitting idea for GMMs followed by learning via Adapted boosted mixture learning method. We also demonstrate that this method can stop splitting process to find the minimum number of Gaussian components by maximizing the objective function in each iteration and BIC. We employed this method to classify healthy and sick infants including both full-term and premature based on ML decision criterion.

The fourth chapter is an article that was submitted in the Journal of Speech Communication in January 2015:

- Farsaie Alaie, Hesam, Lina Abou-Abbas, Chakib Tadj. Jan 2015. « Cry-Based Infant Pathology Classification Using GMMs ». Journal of Speech Communication.

In this article, we presented a hierarchical scheme that is a treelike combination of individual detection system to identify healthy and sick infants at risk with neurological and respiratory disorders. Each hypothesized health-condition class is derived from the corresponding UBM by adapted BML procedure. We also demonstrated that due to small number of hypothesized classes using the idea of background speaker models is practical in calculating the likelihood ratio score and has better accuracy compared to UBM. Although it was shown that the

expiration cry sounds have better performance in the classification tasks, the system also adapts a score level fusion of the expiratory and inspiratory sounds-based subsystems to make a more reliable decision.

Finally, the last chapter is dedicated to conclusion of this thesis document as well as some further research recommendations.

CHAPITRE 1

REVIEW OF THE STATE OF THE ART

In this chapter, we present the previous research studies that were related to ours. Many authors have contributed to the development of such this classification system for different types of diseases. A comparison between pattern recognition techniques helped us to better understand what kind of features and classifier could be the best choice for our purpose. Consequently, this chapter tries to emphasize the key role of both feature selection and classification approach in such a system. Whenever there is a need to diffuse confusion, we will define the terminologies used in this research to diminish ambiguity that may arise in the discussion.

1.1 Fundamental concepts

This section has a primary concept of cry analysis and gives you a good view of cry signals and their features. This information is not essential to follow the remainder of this thesis but it may help you better understand where they came from and its importance.

1.1.1 Definitions and elucidation

In adult human speech communication, we use and interpret some of features unconsciously and without really thinking. These so-called prosodic features go beyond phonemes and deal with auditory qualities of sound. They convey attitudes, and emotional states which make human speech sound human. The infant cry signals are all prosody. Thus, the infants express their feeling, and their needs through acoustic correlates of the prosodic features such as pitch, loudness, melody, and intonation. Lester et al in (Benson et Haith, 2009) defined three identifiable cry modes of vocal fold vibration: basic-cry or phonation, high-pitch cry or hyperphonation, noisy or turbulent cry or dysphonation. Most infants have a fundamental frequency or pitch f_0 around 250-450 Hz. In phonation and hyperphonation modes only the

first two formants are usually measured and F1 occurs at approximately 1100 Hz and F2 at approximately 3300 Hz.

Here are some terminologies and definitions of popular cry characteristics used in literature on cry analysis (Benson et Haith, 2009; Lederman, 2002; Verduzco-Mendoza et al., 2009; Wasz-Hockert, Michelsson et Lind, 1985).

Prosody: It is the intonation and melody patterns of an utterance.

Cry modes: It is a function of vibrational mode of vocal folds. Specific cry modes include: Phonation, Hyperphonation, Dysphonation and Inspiratory Phonation.

Phonation: Category of cry sounds resulting from harmonic vibration (usually between 350 and 750 vibrations per second) of the vocal chords during an expiratory utterance.

Hyperphonation: Category of cry sounds caused by a change in vocal register resulting in a harmonic vibration (usually between 1000 and 2000 vibrations per second) of the vocal chords during an expiratory utterance.

Dysphonation: Category of cry sounds caused by a change in vocal register resulting in an inharmonic or noisy.

Inspiratory phonation: Category of cry sounds resulting from vibration of the vocal folds during an inspiratory utterance during an expiratory utterance.

Cry mode change: The number of times the cry modes change within any given utterance.

Fundamental frequency: Base frequency, during harmonic vibration (that includes the Cry Modes of Phonation and Hyperphonation) of vocal cord vibration Fundamental Frequency is usually heard as the pitch of the cry.

Formant frequencies ($\mathbf{F_1\ F_2 \ldots F_N}$): They are center frequencies of the theoretically infinite number of resonances of the vocal tract system. The center frequency of the first resonance is defined as the first formant (F_1), and the second is defined as the second formant (F_2), etc. Only the first two or three formants are usually measured.

Maximum pitch: It is the highest measurable point of the fundamental frequency (f_0).

Minimum pitch: It is a frequency after a rapid increase in the f_0 contour.

Pitch of Shift (shift): It is a frequency after a rapid increase in the f_0 contour.

Break: It is defined like the time interval between the end of a phonation and the next inspiration.

Cry latency: It is the time between the pain stimulus and the onset of the first expiratory utterance.

Voicedness: Voicedness is defined as being the ratio of the amount of periodic sound versus the amount of noise.

Stridor: When the voicedness suddenly drops within an area of high energy, one occurrence of stridor is marked. Tangibly, the following thresholds were selected: when the voicedness drops to less than 30% of its maximum while the energy level remains above -35dB, one occurrence of stridor is marked.

Melody type: Fundamental frequency variations that is either falling, rising-falling, rising, falling rising, or fiat.

Noise concentration: High-energy peak at 2000 to 2300 Hz, found both in voiced and voiceless signals. This attribute is clearly audible.

Bi-Phonation: It is an apparent double series of harmonics of two fundamental frequencies. Unlike double harmonic break, these two series seem to be independent of each other.

Gliding: A very rapid up or down movement of f_0.

Continuity: A measure of whether the cry was entirely voiced, partly voiced, or voiceless.

Glottal stops: Short, expiratory bursts of sound created by a sudden opening and sustained closing of the vocal folds.

Vibrato: It is at least four rapid up-and-down movements of f_0 within one expiratory utterance.

Voice-UnVoiced: The cries are voiced or unvoiced (voiceless). In the voiced cry the sound wave is periodic and both fundamental and its harmonics are visible on the spectrogram. In the inaudible unvoiced cries the spectrogram shows a burr turbulence or aperiodic noise with a fundamental which is not visible, nor measurable.

The following is a brief definition of some diseases and disorders that are common among newborn infants and used in related works and ours (Miller et O'Toole, 2003).

Down's Syndrome (trisomy 21): Down syndrome (DS) is the most common cause of mental retardation and malformation in a newborn. It occurs because of the presence of an extra chromosome.

Cri-du-chat: A hereditary congenital syndrome characterized by hypertelorism, microcephaly, severe mental deficiency, and a plaintive catlike cry, due to deletion of the short arm of chromosome 5.

Trisomy 13: A syndrome characterized by mental retardation and defects to the central nervous system and heart, caused by having three copies of chromosome 13.
Trisomy 18: A congenital condition caused by the presence of an extra chromosome 18, characterized by severe mental retardation and multiple deformities.

SIDS: It is a sudden and unexpected death of an apparently healthy infant, not explained by careful postmortem studies. It typically occurs between birth and age 9 months, with the highest incidence at 3 to 5 months.

Sepsis: It is a potentially deadly medical condition that is characterized by a whole-body inflammatory state (called asystemic inflammatory response syndrome or SIRS) and the presence of a known or suspected infection. In neonates, sepsis is difficult to diagnose clinically. It is found in infants during the first month of life.

Bovine protein allergy: Cow's milk allergy is the most common food allergy in young children. Bovine protein allergy constitutes an important place in childhood food allergies. Soy protein-based and hydrolyzed protein formulas have some disadvantages.

Pre term infants: Babies who are born before 37 weeks, and particularly those born before 34 weeks, are at greater risk of suffering problems at birth.

Thrombosis in the vena cava: Renal venous thrombosis occurring in the neonate causes haematuria, oliguria, acute renal failure, and hypertension.

Hypoxia: It is a deficiency in the amount of oxygen reaching body tissues.

Tetralogy of Fallot: It is a type of congenital land cyanotic heart defect. It causes low oxygen levels in blood. This leads to cyanosis (a bluish-purple color to the skin).

Coarctation of Aorta: It is a narrowing of part of the aorta (the major artery leading out of the heart). It is a type of birth defect. Aortic coarctation is more common in persons with certain genetic disorders, such as Turner syndrome. However, it can also be due to birth defects of the aortic valves.

1.1.2 Types of cries in infants

In relevant prior works, different kind of cry signals as a database is observed such as hunger cry, pain cry, and normal cry. Crying due to pass 3 to 3.5 hours after last feeding of infants has been referred as the hunger cry (Newman, 1985). Some studies have elicited pain cry based on use of a stimuli such as rubber band snap, heel stick with a blood lancet, skin pinch on the arm or ear, or removal of electrodes from infant's body (Cacace et al., 1995). The pleasure cry is produced by an infant who has been fed and changed and who shows clear indications of being comfortable (Sagi, 1981).

Crying rate varies from 50 to 70 utterances per minutes, and duration of the each cry unit ranges from 0.4 to 0.9 seconds. Figure 1.1 depicts a typical cry sequence which follows a rhythmic pattern that is noticed 30 minutes after birth. The normal cry starts with a cry coupled with a briefer silence, which is followed by a short high-pitched inspiratory whistle. Next, there is a brief silence followed by another cry. Hunger is a main stimulant of the basic cry. Greater variability in some cry parameters appears after the end of the second month. Crying may continue in this manner during a period of 40 seconds to more than 4 minutes (Newman, 1985).

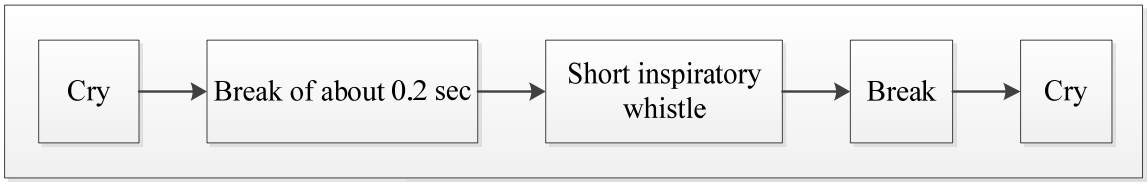


Figure 1.1 Rhythmic pattern of a typical infant cry

Crying following a painful experience is called “Pain Cry” and a typical example of such cry has a length of approximately 3 seconds. The pattern of such a cry is shown in Figure 1.2.

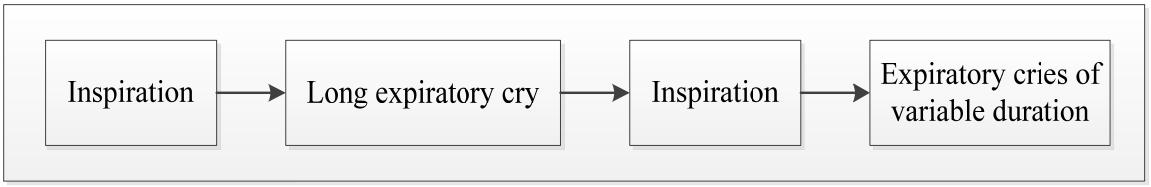


Figure 1.2 Pattern of Pain Cry

Although among the first three cry signals after the pain stimulus there were no marked differences in cry characteristics (see Table 1.1), study on infants’ cries during the first six months had shown few changes in the cry characteristics (Wasz-Hockert, Michelsson et Lind, 1985).

Table 1.1 Comparison of the first three cry signals after pain stimulus

	Max/Min pitch	**Shift**	**Duration**	**Glottal roll**
1st Cry signal	like the other ones	more often	longer and often interrupted	more common
2nd Cry Signal	like the other ones	-	shorter and often continuous	-
3th Cry Signal	like the other ones	-	shorter and often continuous	-

Investigators studying cry characteristics have found diagnostic value in pain cry analysis. For example, compared to normal infants’ cry, pain cries of infants with Down’s syndrome are lower in pitch, longer, and flatter in melody contour (Wasz-Hockert et al., 1968).

1.2 Background

This section briefly presents some birth prevalence rates of selected birth defects and causes of infant death. Moreover, some previous research studies that are related to ours are reviewed.

1.2.1 Mortality rate and birth defects

Statistics reports by World Health Organization (Congenital anomalies, 2014) and Center for Disease Control and prevention (Rynn, 2008) present that the congenital anomalies or birth defects affect about 1 in 33 born infants every year. In an article published by the New Brunswick Beacon (Silverthorne, 2014), it was reported that according to press released from the CDC and the Public Health Agency of Canada, the risk of birth defects in Canadian babies is higher than American. Moreover, based on the Factbook published by Central Intelligence Agency (The World factbook, 2013-14), United States' infant mortality rate is 6.17 per 1,000 live birth which is higher than at Canada of 4.71 rate. In Table 1.2 the leading causes of infant death in the U.S. in 2010 are listed (Heron, 2013).

Heart defect, neural tube defects and Down syndrome are especially prevalent among infants (Congenital anomalies, 2014). Down syndrome, also known as trisomy 21, is a genetic disorder which is fairly common chromosomal abnormality among infants (about 1 in 800 (Lobo et Zhaurova, 2008)). This genetic disorder can often infect other parts of the body and bring on other diseases such as heart defects, leukemia and Alzheimer's disease. There are a lot of maternal and environmental issues which can raise the risks of several complications and associated anomalies, such as gestational age, birth weight, consanguinity (relationship by blood), maternal age, multiple gestations, and maternal infection during pregnancy, socioeconomic factors and maternal nutritional status. For example, the risk of having a baby with DS (Lobo et Zhaurova, 2008) increases as she gets older (see Table 1.3).

Table 1.2 Deaths and percentage of total deaths for the 11 leading causes of infant death: United States, 2010
Adapted from Heron (2013)

Cause of death	Rank	Deaths	Percent of total deaths
All causes	…	24,586	100.0
Congenital malformations, deformations and chromosomal abnormalities	1	5,107	20.8
Disorders related to short gestation and low birth weight, not elsewhere classified	2	4,148	16.9
Sudden infant death syndrome	3	2,063	8.4
Newborn affected by maternal complications of pregnancy	4	1,561	6.3
Accidents (unintentional injuries)	5	1,110	4.5
Newborn affected by complications of placenta, cord and membranes	6	1,030	4.2
Bacterial sepsis of newborn	7	583	2.4
Respiratory distress of newborn	8	514	2.1
Diseases of the circulatory system	9	507	2.1
Neonatal hemorrhage	11	458	1.8
Necrotizing enter colitis of newborn	10	472	1.9

Table 1.3 Maternal age versus risk of DS
Adapted from Lobo (2008)

Age	Risk
Age < 35	0.05 % (or 1 in 2,000)
Age 40	1 % (or 1 in 100)
Age 50	8.3 % (or 1 in 12)

Gestational age is the noteworthy predictor of infant's health condition with the normal range of 37-41 weeks for babies which are fully developed (full-term). Any live birth before

completing of 37 weeks is called preterm birth (Cunningham FG et al., 2010). Although most women in their ninth month of pregnancy are exhausted due to shortness of breath, sleeping problems and other symptoms, these last weeks are to crucial to have completed fetal development. Some vital organs such as lungs, brain, and liver develop at the last weeks (Cunningham FG et al., 2010), so the premature birth, even only a few weeks early, increases the chance of birth defects or infant death in a way that in the U.S. in 2010 mortality rate for very early preterm (under 32 weeks) was 74 times worse than that of full-term infants (see Figure 1.3).

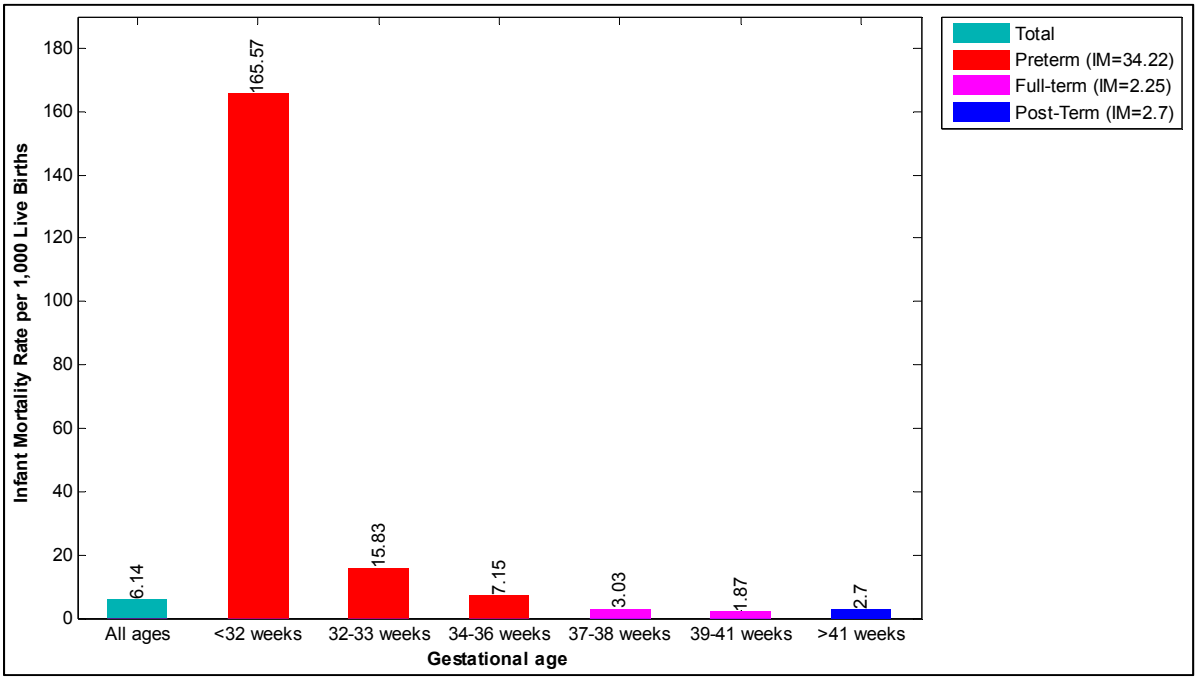


Figure 1.3 Infant mortality by gestational age in the U.S. in 2010
Adapted from T.J (2013)

Birth-weight is another important predictor of infant's health. Figure 1.4 indicates the 3rd, 5th, 10th, 50th (median), 90th, 95th, and 97th percentile birth weights for both male and female infants. Newborns with birth-weights below the 10th and above the 90th percentiles are conventionally considered respectively as small-for-gestational-age (SGA) and large-for-gestational-age (LGA). Infants with weights between these two thresholds are considered as appropriate-for-gestational-age (AGA). Filled areas with borders in Figure 1.4 depict full-

term infants (38-42 weeks) with AGA weights. Although weight gain during pregnancy occurs incrementally, it is not the only factor related to infant's weight at the time of birth, for example SGA or low birth weight (LBW) can be due to prematurity or slow prenatal growth rate. In the U.S. in 2010, more than 80% of infants with less than 0.5 kg weren't able to survive the first year of their life. The mortality rate for infants with less than the weight of 2.5 kg (50.98 per 1,000) was about 24 times larger than that of infants with birth weights of 2.5 kg or more (2.13 per 1,000) (T.J. et F. MacDorman, 2013).

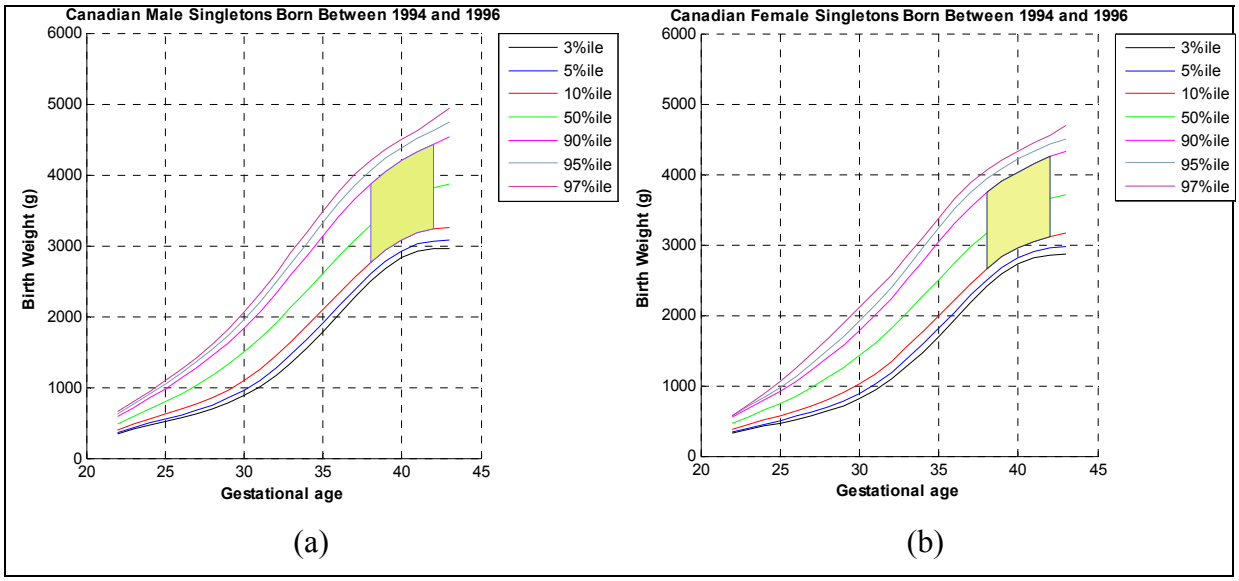


Figure 1.4 Relation of weight and gestational age for (a) male and (b) female singletons

As we mentioned it earlier, approximately 1 percent of the world's infant deaths happen in developed countries and the situation is worse for many developing countries. Therefore, we believe that by providing inexpensive health care system, with no need of complex and advanced technology for poor mothers with newborn babies in low-income countries, more babies can be survived beyond the first months of life.

Birth defects may have different causes such as genetic, maternal nutritional status, maternal age, infectious or environmental but it is hard to get an accurate diagnosis of their causes in

origin. However, for some known risk factors there are some primary prevention solutions such as adequate use of antenatal care and vaccination. Congenital anomalies can affect any part of the body such as brain, ears, and heart. However, it is easier to identify a baby with structural problems such as cleft lip, but on the other hand, symptoms of other defects might be invisible and hidden from sight.

These official statistics can provide more information about the chance of infants born with specific congenital disease which is completely independent of the information inside infant cries. Moreover, there are other independent sources of information related to the physiological condition of newborn infants that can be useful like in a similar way in multimodal biometric systems. However, in this article we are curious to examine only the ability of information embedded in infant cries.

1.2.2 Primary research

Some of prior works have focused on analyzing different kinds of cries and trying to find differences between them. A preliminary report of infant cry analysis in 1963, researchers could distinguish 4 types of infant cry, namely the first birth cry, the hunger cry, the pain cry, and the pleasure cry from each other both auditorily and by using of sound spectrography (Wasz-Hockert et al., 1963).

Another group of researchers were interested in auditory identification of cry types by training people who had had past experience with infant cries, such as midwives (Wasz-Hockert, Michelsson et Lind, 1985). Additionally, in 1967 they found that cries of sick infants could be distinguished auditorily as basic cry types, namely birth, hunger, pain, and pleasure. Infants with asphyxia, brain damage, hyperbilirubinemia and, Down's syndrome were used in the research work (Partanen et al., 1967). Table 1.4 compares the results for the hunger, birth, and pleasure cry. In these methods training phase plays a vital role in improving the ability to recognize the cries.

Table 1.4 Similarities between hunger, first birth, and pleasure cry

	Max Pitch (Hz)	**Min Pitch (Hz)**	**Shift (occurred in %)**	**Melody Type**	**Glottal Roll (occurred in %)**	**Mean Duration**
Hunger Cry	550	390	2%	falling, rising / falling in 80%	24%	-
First Birth Cry	550	450	18%	-	-	Short (1.1 sec)
Pleasure Cry	650	360	19%	flat in 46%	26%	-

Many experiments on sick infants with various diseases have been done in order to make a general assessment of the effect on cry characteristics. Table 1.5 depicts some cry characteristics, such as pitch, melody type and the occurrence of biphonation and glide change in sick infants (Wasz-Hockert, Michelsson et Lind, 1985).

Normal range of fundamental frequencies has been mentioned in papers between 400 and 600 Hz for healthy infants' cries (Lind et Wermke, 2002). In addition, three cry features, namely biphonation, glide, and shift, have been rarely found in the crying of healthy infants. In contrast, abnormal high mean value of fundamental frequencies (F_0>600 Hz) has been reflected in crying of infant who suffer from CNS-disorders (Michelsson, 1971; Michelsson et Michelsson, 1999).

The changes in cry characteristics in newborn infants with asphyxia were so apparent and the results indicate that cry analysis has diagnostic value as well as prognostic value when analyzing cries of infants with meningitis. As you can see in the Table 1.6 (Wasz-Hockert, Michelsson et Lind, 1985), it is observed that the pitch and some other cry characteristics change when the child is sick, especially the ones with central nervous system diseases. For example, the latency of normal infants is less than that of infants with diffuse brain damage. It means that healthy infants respond more quickly than others to stimuli.

Table 1.5 Comparison table between cry characteristics of several diseases

	Pitch	**Melody Type**	**Biphonation**	**Glide**	**Noise Concentration**
Affected CNS	high pitched	rising, falling and rising	more common	more common	-
Bacterial Meningitis	high pitched	rising, falling and rising	more common	more common	-
Herpes simplex virus encephalitis	high pitched		more common	more common	occurred in 2-3 khz
Hydrocephalus	high pitched	flat	more common	more common	-
Abnormalities of chromosomal 4 or 5	high pitched	more flat in Cri du chat	Not observed	Not observed	-
13 & 18 trisomy, Down's syndrome	low pitched	monotonous (flat)	Not observed	Not observed	-
Hyperbilirubinemia	high pitched		common in 50%	-	-
Asphyxia	high pitched	rising in more than 30%	more than 20%	more than 10%	-

Table 1.6 Comparison table between cry characteristics of healthy and sick infants

Cry characteristics	Healthy	Sick	Brain damage	Meningitis	CNS disorders
latency	1.2 s	-	2.6 s	-	-
Duration	2.6-5.2 s	-	-	1.7 s	-
Maximum Pitch	570-680 Hz , 650	greater	-	-	-
Minimum Pitch	330-420 Hz	greater	-	-	-
Shift	every third pain cry 1-2 kHz	-	-	-	high-pitched shift
Melody Type	falling or rising / falling	-	-	-	rising and falling/rising
Glottal Roll	relatively common at the end of the phonations,18% to 73% of cries	less common due to shorter cry and end abruptly	-	-	-
Biphonation	extremely rare	-	-	-	especially present in this disease
Glide	extremely rare	Mostly	-	-	present in this disease
Noise concentration	extremely rare	-	-	-	-

1.2.3 Early-infant medical researches

Here, we will very briefly define some standard measure as specificity and sensitivity. These measures are computed from true positive (TP), true negative (TN), false positive (FP), and false negative (FN) as presented in Table 1.7.

$$Sensitivity = \frac{TP}{(TP + FN)} \tag{1.1}$$

$$Specificity = \frac{TN}{(TN + FP)} \tag{1.2}$$

$$Overall\ accuracy = \frac{TP + TN}{(TP + TN + FP + FN)} \tag{1.3}$$

and:

- TP = true positive, the classifier classified as pathology when pathological samples were present;
- TN = true negative, the classifier classified as normal when normal samples were present;
- FN = false negative, the classifier classified as normal when pathological samples were present;
- FP = false positive, the classifier classified as pathological when normal samples were present.

Table 1.7 Confusion matrix

Actual classification	**Predicted classification**	
	Pathological	**Normal**
Pathological	TP	FN
Normal	FP	TN

The medical research into infant cry signals is divided into three main areas:

1. Severe pathology and medical problems such as Asphyxia which may be identified by existing techniques and tests (see Table 1.8, (Benson et Haith, 2009));

2. Diseases and medical problems such as SIDS that are currently undetectable until it is too late for treatment (see Table 1.9, (Benson et Haith, 2009));

3. Medical conditions which place the infants at risk for poor outcome but the prognosis is not clear such as prenatal exposure to illegal drugs or premature infants (see Table 1.9, (Benson et Haith, 2009)).

Table 1.8 Cry features of infants with severe pathologies

Medical Condition	Cry Characteristic
Asphyxia	↑F0, ↑ F0 instability, biphonation, ↑sub-harmonic break, ↓ duration
Brain damage	↑F0, ↑ F0 instability, biphonation , ↑ threshorld, ↓ duration, ↑ latency, ↑ short utterances.
Cri du chat	↑F0
Down Syndrome	↑F0, ↑ F0 instability , ↓ intensity (amplitude)
Hydrocéphalus	↑F0, ↑ F0 instability , ↓ latence
Hypothyroïdism	↓F0
Krabbe's disease	↑F0
Meningitis bacterial	↑F0, F0 instability, biphonation , ↓ duration
Trisomie 13,18, 21	↓F0

For diagnosis of medical syndromes or damage to the CNS, the most common changes in cry characteristics are higher f_0 and more variability in it. In case of one of these significant medical problems, there are often other clinical signs. Nonetheless there is no doubt that this

sort of help could be valuable for infants already diagnosed with CNS damages. For example, in some cases with severe asphyxia or bacterial meningitis infants had the poorest prognoses. For health problems that are not detectable by available medical examinations such as SIDS, it is worthwhile to look for some cry characteristics associated with medical problems. Limited previous works has shown that infants with vocal constriction (high F_1) and poor control over the vocal tract (increased cry mode changes) are more likely to die of SIDS. Briefly Table 1.9depicts cry characteristics observed in infants who are at-risk (Benson et Haith, 2009).

Some experiments have been carried out on infants of mothers who abused a variety of substances, namely alcohol, tobacco, and cocaine during pregnancy (Corwin, Lester et Golub, 1996). The cry characteristics of these infants also have been shown to be abnormal in comparison to healthy infants.

172 healthy infants have been under studied according to their gender separately in (Michelsson et al., 2002) and no significant differences between cry characteristics such as melody type, and mean value of maximum/minimum of the fundamental frequency have been noted. The same result has been achieved for babies in different ages (1-7 days old) or the gestational age when they were born. On the contrary of former studies (Gilbert et Robb, 1996; Prescott, 1975), no significant weekly changes were found in (Lind et Wermke, 2002) during the first three months of life. As you can see in Figure 1.5, there is no marked increase or decrease in f_0.

Table 1.9 Cry features of infants with undetectable disease with not clear prognosis

Medical Condition	Cry Characteristic
Low birth weight (<2500g) small for gestation	↑duration , ↓f_0, ↑f_0 variability (biphonation)
Preterm infants	↑F0, ↑ F0 variability, F1 variability, ↓amplitude associated with ↓ BSID(18 months), ↓duration, ↑F1, ↓amplitude with ↓ cognitive scores (McCarthy, 60 months), ↑short cry utterances with ↓ developmental outcome (30 months)
Hyperbilirubinemia	↑F0), ↓duration, ↓latency, ↑F0 variability, unstable glottic function (mode changes), ↑F1variability, ↑Phonation
Lead exposure	Low % nasalization, ↓number of cries, ↑F0
Prenatal opiate exposure	↑hyperphonation, ↑short utterance, ↑F0, ↑duration of 1st cry utterance associated with withdrawal symptoms, increased likelihood of abnormal cries
Prenatal cocaine exposure	Direct effects (excitation) ↑duration, ↑F0, ↑F1, ↑F1 variability, indirect effect via growth retardation (depression) ↑latency, ↓amplitude, ↑dysphonation, ↓cry utterances, ↑short cry utterances, ↓hyperphonation, ↓F2, 2nd utterance
Prenatal marijuana exposure	Shorter cries, ↑dysphonation, ↑F0, ↑F0 variability, ↓F1, ↑mode changes, ↑F2
Prenatal alcohol exposure	↑dysphonation, ↑F1, ↓threshold, ↑hyperphonation, ↓F1
Prenatal tobacco exposure	↑F0, ↑F2, ↑F2 variability
Prenatal methamphetamine exposure	↓threshold, ↑variability in F0, ↑variability in amplitude, ↑mode changes, ↑dysphonation, ↑short utterances, ↑variability in dysphonation

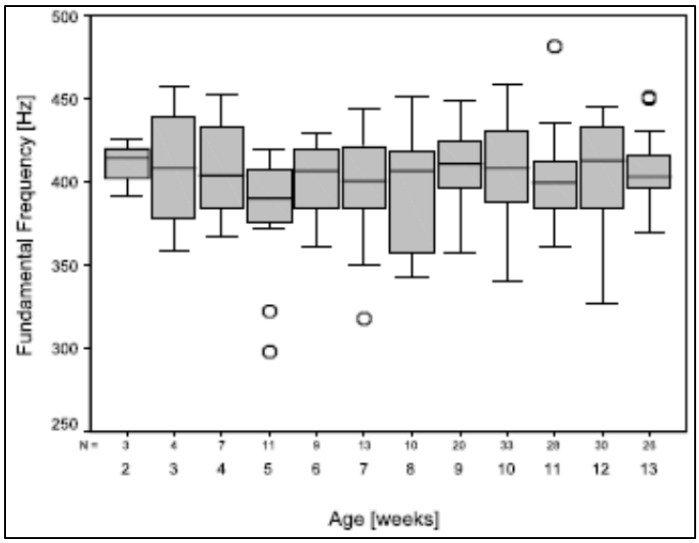


Figure 1.5 Median values, the 25th and 75th percentiles of the F_0 as well as the extreme values across the 13 weeks of study

1.2.4 Review of studies on machine learning and classification problems

In recent years, several machine learning algorithms have demonstrated their ability to recognize cry patterns and make intelligent decision based on available training database. Therefore, the pattern recognition is an absolutely necessary phase to auto-classify infants' cries. Generally, the diagnostic system can be shown by a general block diagram depicted in Figure 1.6.

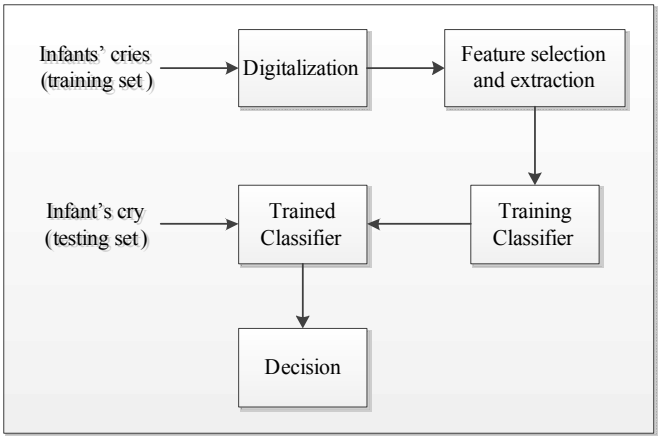


Figure 1.6 Block diagram of auto diagnostic system by using pattern recognition

An Artificial Neural Network (ANN) is a learning algorithm that may be used to solve artificial intelligence problems without necessarily creating a model of system. Generally, neural network has two parts, namely nodes and links instead of neurons and their connections respectively. It is usually used to model complicated relation between input vectors and desired output vectors. In the learning phase with a training example, the weights of connections are iteratively adjusted in order to achieve the minimum possible error between the output and the desired output.

In (Orozco et Garcia, 2003) neural network was used in order to classify the cries into healthy and deaf infants. Moreover, linear prediction coefficients (LPC) were used as a feature vector to feed the neural network. The LP analysis on one second of cry signal is shown in Figure 1.7. Principle Component Analysis (PCA) was used due to eliminate the correlation between coefficients and reduce the size of input vectors from 320 parameters per second to 30 parameters per second. The prime objective of data reduction methods such as PCA is to eliminate redundant data and preserve the most relevant information.

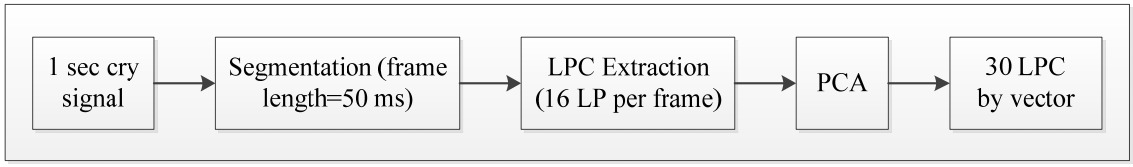


Figure 1.7 Linear prediction analysis on 1 second of cry signal

Gradient descent algorithm is a popular method in optimization methods. Scaled Conjugate Gradient (SCG) algorithm from the class of Conjugate Gradient Methods was used to minimize the error function that depends on the weights in the network. This method for training phase was reported to get better result than back-propagation and cascade neural network (Orozco et Garcia, 2003). Table 1.10 indicates the confusion matrix of the classification results.

Table 1.10 Confusion matrix of Neural Network with SCG algorithm

		Confusion Matrix		
Kind of crying	**Samples**	**Normal**	**Pathological**	**Accuracy**
Normal	157	142	15	
Pathological	879	128	751	
Total	1036			86.20%

Combinations of acoustical characteristics such as, melody, biphonation, pitch, and cepstral coefficients can be used as the input vectors in the neural networks or other learning methods. In (Cano Ortiz, Escobedo Beceiro et Ekkel, 2004a) the authors used such this idea to select a feature vector. Searching through the 25 primary features with a fast non-linear classification procedure was employed to find the winning combination of them with the best results. The authors used a special type of neural network called Radial Basis Function (RBF) network. Briefly, it usually has three layers namely an input layer, a hidden layer, and an output layer (see Figure 1.8).

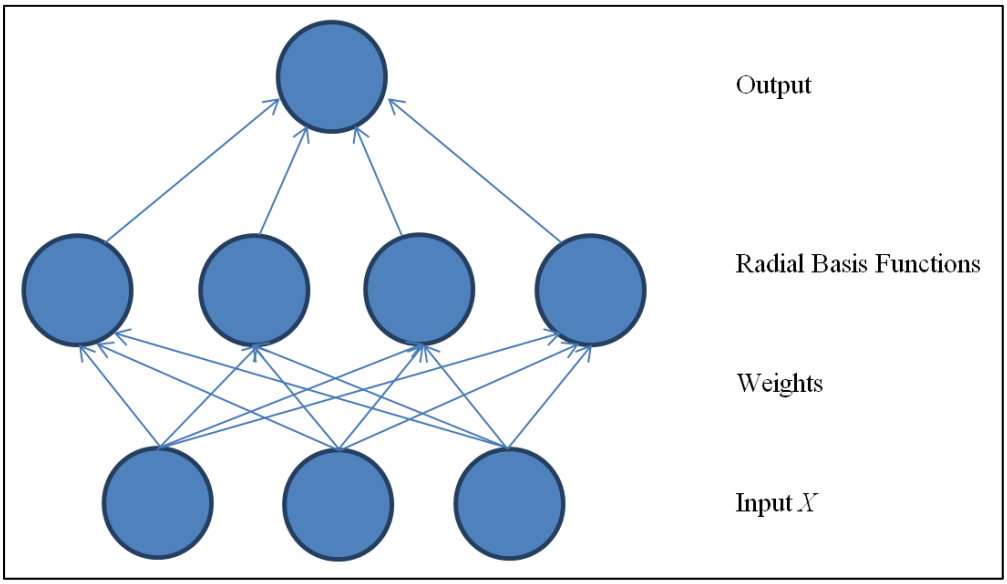


Figure 1.8 Structure of a basic RBF network

The mapping function $\varphi : \mathbb{R}^n \longrightarrow \mathbb{R}$ is constructed by linear combination of the basic functions.

$$\varphi(X) = \sum_{i=1}^{N} w_i \, \phi(\|X - C_i\|) \tag{1.4}$$

Where W_i are the weights of the linear output neuron, C_i is the center vector for neuron i, and N is the number of neurons in the hidden layer. The basis function typically is taken to be Gaussian, and norm is taken to be the Euclidean distance

$$\phi(X) = \exp[-\beta \|X - C_i\|^2] \tag{1.5}$$

where the β is a parameter which controls the smoothness of the total approximation $\varphi(X)$. The winning combination of 10 cry features depicted in Table 1.11 had the accuracy rate of 85% to distinguish between normal infants and infants who suffer from hypoxia (see Table 1.12).

Table 1.11 The winning combination with 10 features

F_1 minimum	F_1 mean	F_0 maximum	F_0 mean	First latency
Voicedness mean	Voicedness variability	Energy maximum	Energy minimum	Energy mean

Table 1.12 Confusion matrix of RBF network

	Confusion Matrix		
Actual Class	**Normal**	**Hypoxia**	**Accuracy**
Normal	79%	21%	
Hypoxia	12%	88%	
Total			85%

The evolutionary strategies were applied in (Galaviz et García, 2005) to introduce a new method to find the feature set with the best possible classification results. The method was

examined using Mel Frequency Cepstral Coefficients (MFCC) and Linear Prediction Coefficients (LPC) and due to improvement in its learning phase it obtained better classification results in comparison with those achieved by PCA to reduce the features vector. The results of experiments on the introduced evolutionary-neural hybrid system depicted that the MFCC were the most successful features with 96.79% classification accuracy. However, there is a design flaw with this hybrid system, because there was no clean method to optimize the parameters.

According to the primary results mentioned in Table 1.5 and Table 1.6, pitch and melody type offer a good ability to make a distinction between healthy and sick infant. These distinguishing characteristics with two more features namely stridor and voicedness have been used in introduced combined classifier in (Cano et al., 2006) which contained a threshold-based classifier and a supervised neural network classifier with scaled conjugate gradient learning algorithm. The two marks obtained from the output of each classification method, called FN1 and FN2, have been used to make a decision on two classes, normal infants or infants who suffer from CNS disorders. In brief, FN1 was computed with the following gradation:

Table 1.13 Determination of FN1

Parameters	Stridor, Voicedness, Melody type, and Pitch
Output of threshold-based classifier	**Number of parameters that are out of the threshold boundary for normality**
FN1 = 0.25	1
FN1= 0.5	2
FN1= 0.75	3
FN1= 1	4
FN1= 0	0

The input vectors of neural network were reduced from 500 MFCC to 50 MFCC by using of PCA. The output of this classifier, FN2, was assigned to 0 or 1 for normal infant and

pathological infant respectively. Finally, the mean of FN1 and FN2 makes the final decision based on the Table 1.14. The confusion matrix of the combined classifier is shown in Table 1.15.

Table 1.14 Determination of decision parameter

Levels	D = (FN1+FN2)/2
Normal	$D \leq 0.5$
Moderately-pathologic	$0.5 < D \leq 0.75$
pathologic	$0.75 < D$

Table 1.15 Confusion matrix of the ensemble method

Classes	**Number of samples**	**Confusion Matrix**		**D index**			**Accuracy**
		P	**N**	**$X \leq 0.5$**	**$0.5 < X \leq 0.75$**	**$0.75 < X$**	**%**
Normal	10	10	0	10	0	0	100
Sick	10	2	8	2	7	1	80
Total	20			12	7	1	90

The idea of combining an ensemble of classifiers for reducing classification error rates has been employed in (Amaro-Camargo et Reyes-García, 2007). Feed-forward Neural Networks (FFNN) with Backpropagation, Sequential Minimal Optimization on SVM, J48, Naïve Bayes and Random Forest as classification methods were chosen to be combined under several approaches like Bagging (Bauer et Kohavi, 1999a), Boosting (Bauer et Kohavi, 1999a), Majority Vote, and Staking. Original acoustical feature vectors which contained a total of 304 MFCC for every one second cry signal were reduced by means of 5 statistical operations namely minimum, maximum, average, standard deviation, and variance. Using these statistical operations instead of PCA for either MFCC or LPC obtained better results for

neural network classifier (see Table 1.16). In addition, the more components it has, the more training time network requires.

Table 1.16 Comparison accuracies of FFNN with PCA and statistic reduction

	PCA reduction 50 principal components	**Statistic reduction 5 statistics characteristics**
FFNN	90.12%	91.86%

Several experiments have been conducted on single classifiers and their ensembles with three separate sets of data named A, B and C. According to Table 1.17, it is apparent that ensembles achieved better results except for data set C which is used input vectors without reduction.

Table 1.17 Comparison table between best results of classifiers and their ensembles

Set	**A**	**B**	**C**
Classifier	**Neural N**	**Neural N**	**SMO**
	91.67%	91.86%	91.67%
Ensemble	**Staking: NN, SMO, R. Forest**	**Vote: Neural N, R. Forest**	**Staking: SMO, J48 - Vote: SMO, R. Forest**
	91.83%	93.23%	91.66%

Although time and memory are not the criteria for comparison among the different automatic classification of infants' cry, taking a quick look at the size of input matrices for each case could be a good idea. Ensembles of classifiers usually require more processing time than a single classifier. Therefore, training and testing the ensembles with feature vectors without dimension reduction requires more memory space and time.

Recently probabilistic neural network introduced by Specht in (Donald F, 1990) was used for classifying normal and infants with Asphyxia via wavelet packet transform based features (Hariharan, Yaacob et Awang, 2011). In contrast with Discrete Wavelet Transform (DWT),

both lower and higher frequency bands are decomposed into 2 sub-bands in wavelet packet transform. The decomposition coefficient of the *i*-th depth was computed and frequency ranges of subspaces in each level of decomposition can be calculated as below:

$$\left[0, \frac{f_s}{2^{i+1}}\right], \left[\frac{f_s}{2^{i+1}}, \frac{2f_s}{2^{i+1}}, \right], \dots, \left[\frac{(2^{i-1}-1)f_s}{2^{i+1}}, \frac{f_s}{2}, \right] \tag{1.6}$$

After 5 levels of decomposition, the sub-band energy and entropy were computed from wavelet packet coefficients by the following equations.

$$Energy_n = \sum_{i=1}^{n} \left|C_{n,k}^P\right|^2 \quad n = 1,2, \dots, N, k = 0,1, \dots, 2^N - 1 \tag{1.7}$$

$$Entropy_n = \sum_{i=1}^{n} \left|C_{n,k}^P\right|^2 log\left|C_{n,k}^P\right|^2, n = 1,2, \dots, N, k = 0,1, \dots, 2N - 1 \tag{1.8}$$

where *P* is the scale index, *n* is number of decomposition level. Several experiments have been done with different level of wavelet packet decomposition, and the results in Table 1.18 depicted that the highest achievable classification accuracy of 99% was obtained at the fifth level of decomposition.

1.3 Cry pattern classification

This section discusses briefly the idea behind choosing the proposed machine learning methodology and other related issues from different point of views.

Generally we can consider the solution of our classification problem in two different ways: Set up a multi-class classification problem or treat each classification problem independently like a one-class or binary classification. One is not necessarily better, there are trade-offs. First of all, many good classifiers like logistic regression can only handle binary classification problem. So if we want to use it for multi-class problems, we have to turn it into a set of binary classification problems.

Table 1.18 Obtained accuracy rate in each decomposition level for PNN classification

Decomposition Level	Sensitivity	Specificity	Overall Accuracy
1	88.71	88.68	88.60
2	98.33	98.10	98.20
3	99.19	98.48	98.82
4	99.63	99.34	99.49
5	99.85	98.48	99.15
A: Results for energy feature			
Decomposition Level	**Sensitivity**	**Specificity**	**Overall Accuracy**
1	84.08	84.12	84.04
2	97.89	98.24	98.05
3	98.39	98.31	98.35
4	98.91	99.12	99.01
5	99.63	99.20	99.41
B: Results for entropy feature			

Secondly, multi-class classifiers tend to be more complex, and less well-understood from the theoretical standpoint. On the other hand, taking the outputs of bunch of binary classifiers and turning them into a single multi-class output is not straightforward, as there maybe ties, or the numbers that binary classifiers output might not be comparable. Sometimes the outputs of binary classifiers are confidence score, and these cannot be directly compared for example 0.6 confidence from classifier “A” might not be more confidence than 0.5 from classifier “B”.

Another problem happens if there are lots of classes, and we choose to train multiple one-class or binary classifiers instead of one multi-class classifier. If we assume that there are K classes, it leads to K classifiers each comparing one class with all the others namely ‘target class’ and ‘outlier class’ respectively. Therefore, we a have large class imbalance in each training set. For example if classes evenly distributed over the training set, the outlier class

will have K-1 times as many samples as the target class. We should be well aware of class imbalance, since it would have an adverse impact on the performance of many classifiers.

So finally, neither one is necessarily better. It is a better idea to try both practically and see which performance is better for our particular case.

1.3.1 Brief description on various classifiers

A brief description and comparison of the various classifiers that have been used in past studies like Artificial Neural Network (ANN), Support Vector Machine (SVM) are given below.

1.3.1.1 ANN and SVM

We have a fairly similar case in ANN in which two options are presented; separate networks for each binary classification or train one network with one output for each binary classification, but with a shared hidden layer. Using a shared hidden layer could be a clever idea to have all scores on a same scale and solve comparability of classifiers score. Nevertheless, having some networks is not always preferable over the one network with shared hidden layer. In the case with shared hidden layer and more output nodes, the network needs a larger hidden layer, as the learning function gets more complex. A larger hidden layer means we are more prone to overfitting, so we'll need more training data. However, as above, figuring out how to turn the output of k networks into a single k-class output is not an easy task.

The development of ANN followed a heuristic path, with applications and extensive experimentation preceding theory. In contrast, the development of SVMs involved sound theory first, then implementation and experiments. A significant advantage of SVMs is that whilst neural networks can suffer from multiple local minima, the solution to an SVM is global and unique. Two more advantages of SVMs are simple geometric interpretation and

sparse solution. Moreover, unlike neural networks, the computational complexity of SVMs does not depend on the dimensionality of the input space. Neural networks use empirical risk minimization, whilst SVMs use structural risk minimization. The reason that SVMs often outperform neural networks in practice is that the SVMs are less prone to overfitting. The key features of SVMs are the use of kernels, the absence of local minima, the sparseness of the solution and the capacity control obtained by optimizing the margin.

A common disadvantage of non-parametric techniques such as SVMs is the lack of transparency of results. SVMs cannot represent the score of all companies as a simple parametric function of the financial ratios, since its dimension may be very high. It is neither a linear combination of single financial ratios nor has it another simple functional form. The weights of the financial ratios are not constant. Thus the marginal contribution of each financial ratio to the score is variable. Using a Gaussian kernel each company has its own weights according to the difference between the value of their own financial ratios and those of the support vectors of the training data sample. An important practical question that is not entirely solved is the selection of the kernel function parameters. The most serious problem with SVMs is the high algorithmic complexity and extensive memory requirements of the required quadratic programming in large-scale tasks. Here are some disadvantages of SVM:

1. Computationally demanding to train and run;

2. Sensitive to noisy data;

3. Prone to over fitting and thus bad generalization;

4. Choice of kernel function and the parameters have to be set manually and can greatly impact the results.

Here are some advantages and disadvantages of Neural Network classifiers.

Advantages:

1. Powerful non-linear classifier;

2. Elegant solutions built of continuous basis-functions;

3. Handles noisy data well;

4. Fast to run.

Disadvantages:

1. Computationally demanding to train;

2. With difficulty when there is complex boundary.

1.3.1.2 Decision tree

The decision tree is a class discriminator that recursively partitions the training set until each partition consists entirely or dominantly of examples from one class. Each non-leaf node of the tree contains a split point that is a test on one or more attributes and determines how the data is partitioned. The decision trees are easy to understand and modify, and the model developed can be expressed as a set of decision rules. This algorithm scales well, even where there are varying numbers of training examples and considerable numbers of attributes in large databases. The decision tree model contains rules to predict the target variable and it provides an easy-to-understand description of the underlying distribution of the data. It can be constructed relatively quickly, compared to other methods. Moreover it can process both numerical and categorical data. The process of pruning the initial tree consists of removing small, deep nodes of the tree resulting from 'noise' contained in the training data, thus

reducing the risk of overfitting, and resulting in a more accurate classification of unknown data. Some disadvantages of the decision tree classifier are mentioned in below:

1. Categorical output attribute;

2. Limited to one output attribute;

3. Unstable algorithms;

4. Complex trees created from numeric datasets;

5. Over-sensitivity to the training set, irrelevant attributes and noise.

1.3.1.3 Naïve Bayes

A Naïve Bayes classifier is a simple probabilistic classifier based on applying Bayes' theorem with strong (naive) independence assumptions. In simple terms, the Naïve Bayes classifier assumes that the presence (or absence) of a particular feature of a class is unrelated to the presence (or absence) of any other feature, given the class variable. Depending on the precise nature of the probability model, naive Bayes classifiers can be trained very efficiently in a supervised learning setting. In many practical applications, parameter estimation for naive Bayes models uses the method of maximum likelihood. An advantage of the naive Bayes classifier is that it only requires a small amount of training data to estimate the parameters necessary for classification. Since variables are assumed to be independent, only the variances of the variables for each class need are determined not the entire covariance matrix. However, it is not capable of solving complex classification problems.

1.3.1.4 K-nearest neighbor

K-Nearest Neighbor (K-NN) is very simple to understand and easy to implement. So it should be considered in seeking a solution to any classification problem. The process is transparent, it is easy to implement and debug. There are some noise reduction techniques that work only for k-NN that can be effective in improving the accuracy of the classifier.
Most important disadvantages of KNN are as follows:

1. Because all the work is done at run-time, K-NN can have poor run-time performance if the training set is large;

2. K-NN is very sensitive to irrelevant or redundant features because all features contribute to the similarity and thus to the classification. This can be ameliorated by careful feature selection or feature weighting;

3. On very difficult classification tasks, K-NN may be outperformed by more exotic techniques such as SVMs or Neural Networks.

1.3.2 Why Gaussian Mixture Models?

The classical uni-modal Gaussian model represents feature distributions by a position (mean vector) and an elliptic shape (covariance matrix) and a vector quantization (VQ) or nearest neighbor model represents a distribution by a discrete set of characteristic templates. The GMM acts as a hybrid between these two models by using a discrete set of Gaussian functions, each with their own mean and covariance matrix, to allow a better modeling capability. Figure 1.9 compares the densities obtained using a uni-modal Gaussian model, the GMM and VQ model. Plot (a) shows the histogram of a single feature from a speaker recognition system (a single cepstral value from a 25 second utterance by a male speaker); plot (b) shows a uni-modal Gaussian model of this feature distribution; plot (c) shows the

GMM and its ten underlying component densities; and plot (d) shows a histogram of the data assigned to the VQ centroid locations of a 10 element codebook. The GMM not only provides a smooth overall distribution fit, its components also clearly detail the multi-modal nature of the density.

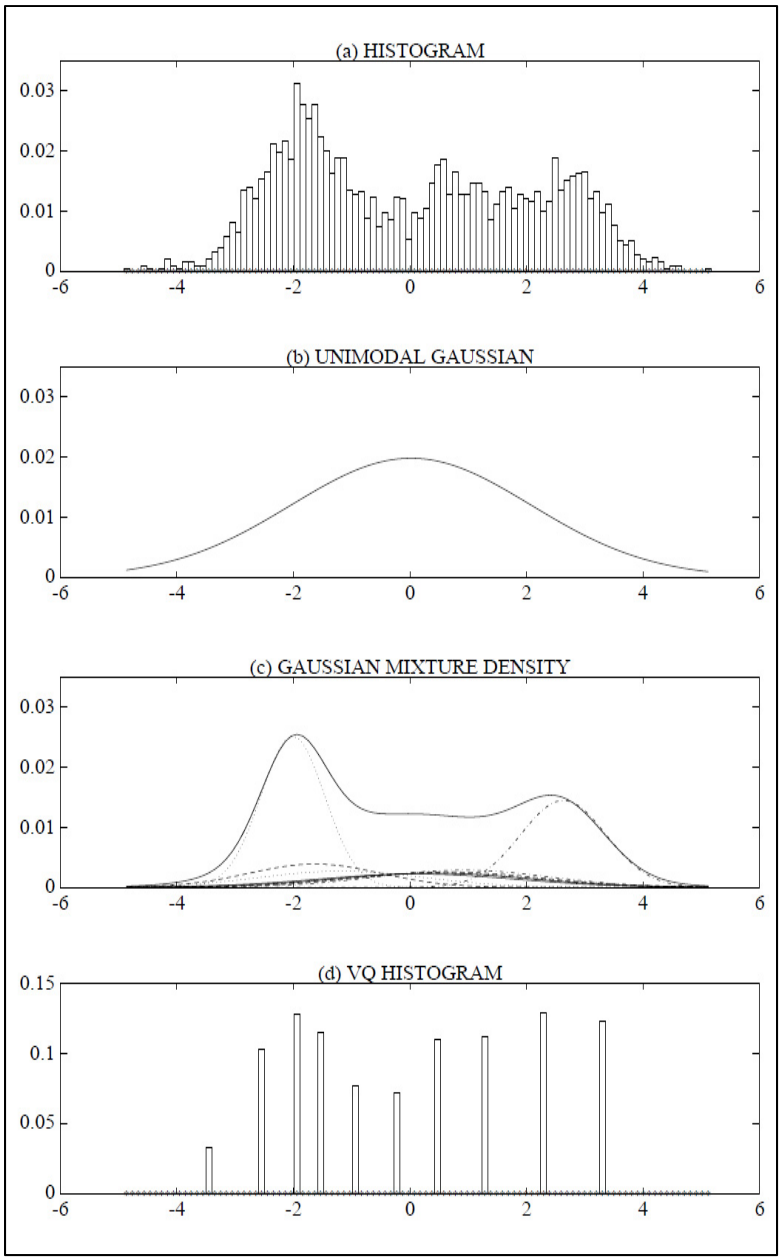


Figure 1.9 Obtained densities for uni-modal Gaussian model, GMM, and VQ

Experimental results of the GMM have shown that its accuracy is higher than those obtained by the VQ approach, the Radial Basis Function network model (RBF), and also the learning Vector Quantization (LVQ) approach. Moreover, the training time of the GMM is less than that of Multilayer Perceptron (MLP) (Ma et Gao, 1998). The GMM trained with the EM learning algorithm has comparable flexibility with the multilayer perceptron in modeling non-stationary, multimodal machine signal characteristics, but has significantly fewer parameters to train (Heck et Chou, 1994).

Moreover, the GMM has the capability to form smooth approximations to arbitrarily shaped densities and it has proved to be an effective probabilistic model for a lot of application such as biometric systems, most notably in speaker recognition systems and speaker identification (Reynolds et Rose, 1995) due to their capability of representing a large class of sample distributions. The GMM represents a statistical pattern recognition approach that enables optimal processing of data both for training the classifier (the EM algorithm) and for performing on-line classification. In addition, while the GMMs possess many discriminant surface-modeling capabilities of more complex nonparametric classifiers (e.g., multilayered perceptrons), the GMM is parametric, making it more robust to the effects of a limited amount of training data (Heck et Chou, 1994).

1.3.2.1 Introduction to GMMs

Gaussian Mixture Model as a parametric probability density function is chosen to model infants' cry under available pathological states. A complete GMM for a D dimensional continuous value data vector called X can be represented by $\lambda = \{w_i, \mu_i, \Sigma_i\}\ i = 1, \dots, M$ as a weighted sum of M Gaussian component densities as follow:

$$F_M(X|\lambda) = \sum_{i=1}^{M} w_i f_i(X|\mu_i, \Sigma_i)\ ,\ \sum_{i=1}^{M} w_i = 1 \qquad (1.9)$$

where w_i, μ_i, Σ_i are the mixture weights, mean vector and covariance matrix respectively. Since GMMs is used usually in unsupervised learning and clustering problem which the

number of mixtures and parameter vectors μ_i, Σ_i are unknown, the choice of model configuration is almost determined by the amount of data available for estimating the GMM parameters in a particular application.

The GMM can also be viewed as a single-state HMM with a Gaussian mixture observation density, or an ergodic Gaussian observation HMM with fixed, equal transition probabilities. Assuming independent feature vectors, the observation density of feature vectors drawn from these hidden acoustic classes is a Gaussian mixture. It is also important to note that in case of statistically dependent features, the effect of using a set of M full covariance matrix Gaussians can be equally obtained by using a larger set of diagonal covariance Gaussians, due largely to that the linear combination of diagonal covariance basis Gaussians is capable of modeling the correlations between feature vector elements. Therefore, there is significant difference between Supervised Learning GMM (SLGMM) (Ma et Gao, 1998) and unsupervised learning GMMs.

1.3.2.2 Learning of GMMs

Given training data and a GMM configuration, we wish to estimate the parameters of the GMM, λ, which in some sense best matches the distribution of the training feature vectors. The GMM parameters $\lambda = \{w_i, \mu_i, \Sigma_i\}$ are usually estimated from training data using the iterative Expectation-Maximization (EM) algorithm or Maximum a-Posteriori (MAP) estimation from a well-trained prior model. There are several techniques available for estimating the parameters of the GMM but by far the most popular and well-established method is maximum likelihood (ML) estimation. The aim of ML estimation is to find the model parameters which maximize the likelihood of the GMM given the training data. For a sequence of T training vectors $X = (x_1, \ldots, x_T)$, the GMM likelihood, assuming independence between the vectors, can be written as,

$$P(X|\lambda) = \prod_{t=1}^{T} P(x_t|\lambda) \tag{1.10}$$

Unfortunately, this expression is a non-linear function of the parameters λ and direct maximization is not possible. However, ML parameter estimates can be obtained iteratively using a special case of the EM algorithm. The iterative procedure in the EM algorithm ensures that likelihood function doesn't decrease per iteration. Consequently it yields locally optimal, maximum likelihood parameter estimates. The EM begins with an initial model called λ_0. Next, a new model λ_1 is created after updating all parameters in such a way that $P(X|\lambda_1) \geq P(X|\lambda_0)$. This process is repeated until convergence.

If all goes well, the algorithm converges to local maximum (Heck et Chou, 1994), but there are still some problems when increasing model complexity. Firstly, there is no guarantee that the newly added mixture from random splitting always increases the likelihood function prior to re-estimation. Secondly, convergence to the optimum point in EM-based re-estimation is not be guaranteed due to sensitivity to initial parameters of the randomly split Gaussians. So it is not the optimal manner of the model estimation (Jun, Yu et Hui, 2011).

A new method based on combination of Genetic Algorithm and the EM algorithm introduced which has a better performance in the practical Brain Computer Interface (BCI) application, due to reduce the negative effect of noisy data or outliers available in database (Boyu et al., 2010).

In ASR system usually Gaussian mixtures HMMs are used as acoustic models in order to model basic speech units. To deal with data sparseness problem in model training, the mixing-up step is used to little by little increase the number of mixtures in each tied HMM state to achieve the optimum performance. In such this ASR system, like HTK, the mixing-up process is conducted in two steps (Young et al., 2006b) First of all, all existing Gaussians or the most dominant Gaussian mixtures component in a HMM state is split up based on some random or heuristic strategies. Second, all of these split Gaussians are re-estimated based on the EM algorithm. Although it is a good strategy to learn models without getting trapped in any bad local optimum, there are still some aforementioned problems when increasing model complexity.

Recently another new method called Boosted Mixture Learning (BML) to learn Gaussian mixture HMM is introduced (Jun, Yu et Hui, 2011). The new method called Boosted Mixture Learning (BML) could be used as a successful candidate for training a GMM with some adaptation in our case, due in part to its ability to rectify and overcome the aforementioned problems in available techniques for estimating the GMM parameters.

1.3.2.3 Boosting algorithm

Generally, boosting method combines weak learners in a weighted majority voting scheme to improve the overall classification accuracy for almost any type of learning algorithm. The base classifiers, known also as weak learners, are trained using a weighted form of data set in which the weighting coefficients associated with each data point depends on the performance of the previous classifier. Therefore base classifiers are trained in sequence and the points that are misclassified by one of the base classifiers are given greater weight when used to train the next classifiers in the sequence. Using the updated training weights, a new classifier is trained to concentrate more on these hard examples.

The main idea of boosting is that instead of always treating all data points as equal, component classifiers should specialize on certain examples. In particular, if an example is hard-to-classify and problematic for existing classifier, more components should focus on it. According to the boosting theory, upper bound on training error rate is analytically minimized. Moreover, some recent work has shown that boosting method can effectively increase the margin of all training samples that can be explained by a theoretical view related to functional gradient techniques (Jun, Yu et Hui, 2011). More recently, the traditional boosting method has been used to solve some problems of mixture models (Kim et Pavlovic, 2007; Pavlovic, 2004).

1.4 Brief objectives, methodologies and contributions

Our general objective is to design a non-invasive cry-based diagnostic tool using computer acoustical analysis of newborn cries to detect serious medical conditions such as heart defects and infections. The diagram demonstrating the proposed system is shown below (see Figure 1.10). It can interpret recorded cries to help neonatologists detect specific pathologies affecting newborns since cry production in newborns can be influenced by neurological and physiological states.

Our research team in the Multimodal-Modelisation-Specification (MMS) laboratory, located at École de technologie supérieure (ÉTS), consists of three members. Their roles on the research problem are explained briefly in below.

Mrs. Yasmina Kheddache, a PhD graduate from ÉTS, has worked on spectrographic analysis of newborn infant cry signals to model newborn infant cry signals by parameters that describe vocal cords and vocal tract. To achieve this objective, she proceeded to a qualitative characterization of the cries of sick and healthy infants. For this purpose she used predefined characteristics from literature that describe the behavior of cords and vocal tract during the cry. For extraction of selected features, she implemented the methods of effective measures to overcome the overestimation and underestimation of characteristics.

Mrs. Lina Abou-Abbas, pursuing a PhD degree, is working on the automatic segmentation of newborn's cry signals recorded in real conditions based on Hidden Markov Models using the HTK (Hidden Markov Model Toolkit). The purpose of signal segmentation is to differentiate the important acoustic parts of the cry recordings from the unimportant acoustic activities that compose the audio signals.

In order to make a high accuracy decision in our diagnostic system, we should have had a good understanding of different methods to create a pattern for cry signals. During my PhD

program, I was part of MMS team where I created a model-based approach to detect the health conditions of the infants based on the features extracted from their cry signals.

At this point, it would be good to clarify on the origin of the cry database corpus. First, cry signals are collected from hospitals by trained nurses during a specific period of time. Then upon receiving recorded signals in the laboratory, all team members are responsible for manual segmentation of recorded cry signals into different predefined labels.

Combination of imbalanced data and small sample size hinders learning leading to convergence difficulties and presents new challenge to the domain. We proposed a solution to mitigate the multi-pathology imbalanced classification in which individual binary classifiers through hierarchical scheme are combined to narrow down the health condition of the infant.

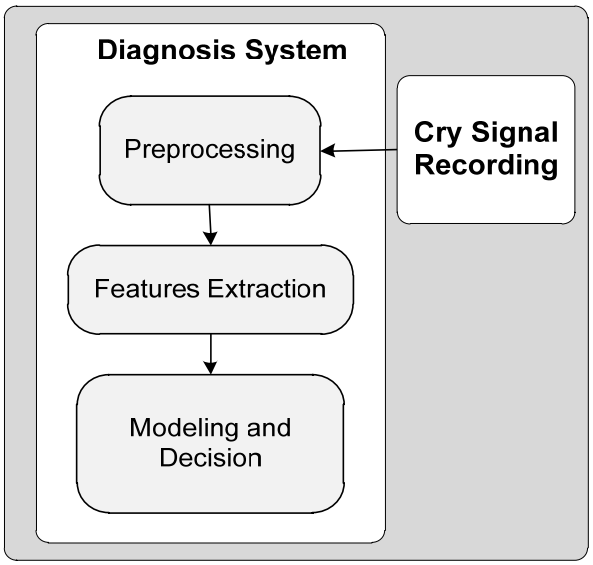


Figure 1.10 The general system diagram

In non-static data like time series data, characteristics of the data may change gradually over time. Cry data are not a static and have a dynamical behavior. It means that any cry sample at any moment in time depends on crying pattern before and after that time. Consequently, using a classifier which is not capable of temporal processing is a pointless exercise.

Moreover length of time series data can changes over time, so using discriminative classifier like Support Vector Machine for non-static or time series data is very hard. In other hand, Hidden Markov Models are a class of stochastic process and can be used as a powerful generative classifier for modeling time series data. It also has a good performance in some application like ASR or handwritten word recognition. Gaussian Mixture Model (GMM) is a special case of Hidden Markov Models with one state that is chosen as a prototype in our health care application.

Towards this end, we have proposed a finite Gaussian mixture learning algorithm which will concentrate more on the hard example in the growing process. It can bear a striking resemblance to log-likelihood value of GMM trained traditional EM algorithm and estimate the optimum number of mixture components as well as some benefits to support system in general such as adding a new component in an incremental and recursive manner and reducing sensitivity to initial parameters (see Figure 1.11).

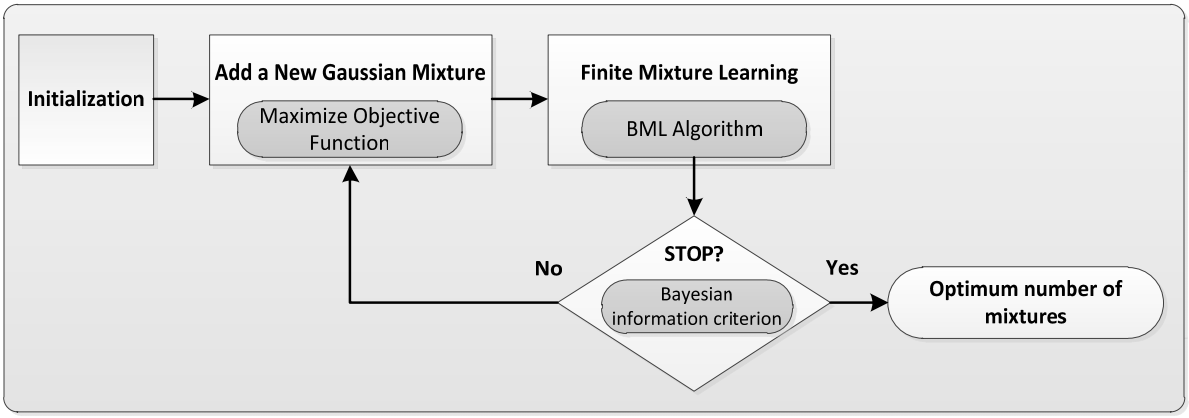


Figure 1.11 The growing process of finite mixture model

Then, a variant of boosted mixture learning (BML) method is presented in order to derive a unique cry-pattern for each enrolled disease from the trained GMM-UBM by adaptation of GMM parameters. We will show how this boosting-based approach can enhance common maximum a-posterior (MAP) method of adaptation of the parameters of GMM.

Both expiratory and inspiratory vocalizations of infant cry signals are analyzed separately in this study. Fusion of two subsystems that are based on above-mentioned vocalizations, into a single effective system is being sought in order to make a reliable decision (see Figure 1.12). We present log-likelihood ratio score fusion to stop worrying on the feature compatibility and rigid fusion. The concept of Log-likelihood ratio (LLR) was used for a test sequence of feature vector. Both fast scoring method and score normalization for a sequence of feature vector were employed to reduce the computational complexity.

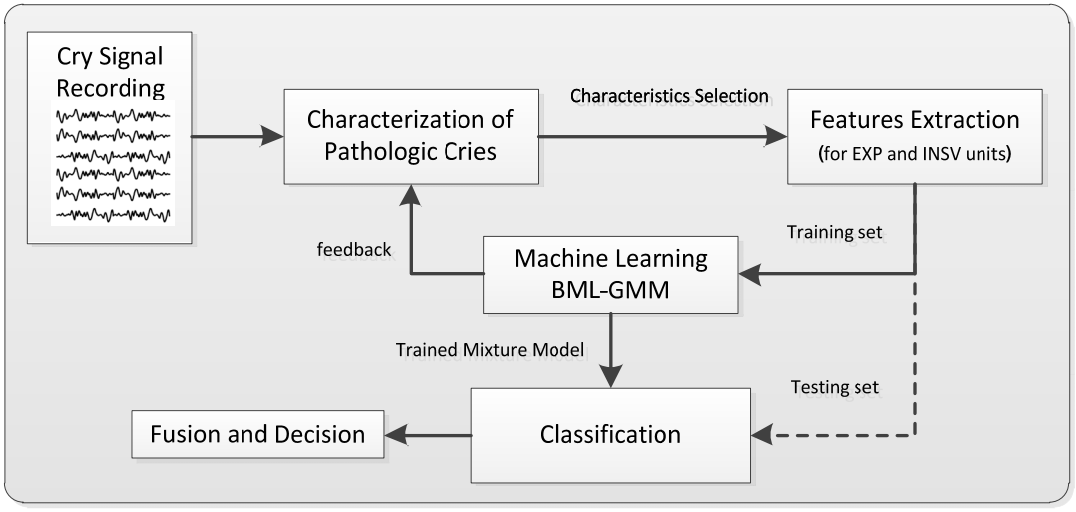


Figure 1.12 Modeling and decision

1.5 Summary

In this chapter, initiation and motivation for the research project is explained. The background and previous research studies correlated to this research problem were presented. Scope and outlines of this study are also mentioned. Then, with our objectives on hand, we demonstrate different parts of our desire diagnosis system.

In this thesis, we specify two main contributions – an algorithm for learning statistical Gaussian mixture models and another algorithm which enhance maximum a-Posterior (MAP) adaptation of the parameters of the GMM. In summary, here is what we have contributed to the domain:

1. A design and implementation of a non-invasive cry-based diagnostic tool using computer acoustical analysis of newborn cries to detect enrolled medical conditions such as heart defects and infections. It is implemented using MATLAB software;

2. A boosted mixture learning algorithm for learning if statistical Gaussian mixture models - This pertains to finding optimal number of mixture component and Gaussian parameters;
3. A boosting-based adaptation algorithm to derive the hypothesized health-condition model by adapting the parameters of UBM;

4. Separate analysis of both expiratory and inspiratory cry vocalizations and employing valuable information that comes from the fusion of the two independent subsystems in decision making process;

5. Various experiments that demonstrate that our idea of proposed classification system is possible and feasible. Moreover, it can be extended to represent more disease and syndromes, providing enough corresponding infant cry data.

CHAPITRE 2

CRY-BASED CLASSIFICATION OF HEALTHY AND SICK INFANTS USING ADAPTED BOOSTED MIXTURE LEARNING METHOD FOR GAUSSIAN MIXTURE MODELS

Hesam Farsaie Alaie, Chakib Tadj
Department of Electrical Engineering, École de Technologie Supérieure,
1100 Notre Dame West, Montréal, Québec, H3C 1K3, Canada

This article is published in "Journal of Modeling and Simulation in Engineering", volume 2012 (2012), Article ID 983147, 10 pages, Accepted 30 November 2012

Résumé

Nous utilisons de l'information présente dans le signal cri des nourrissons afin de déterminer l'état psychologique de l'enfant. Un mélange de gaussiennes (GMMs) est utilisé afin de distinguer entre les nourrissons nés à termes en bonne santés, les prématurés, et ceux qui ont des problèmes médicaux spécifiques. Des modèles de cri pour chaque état pathologique sont créés en utilisant la méthode adapted boosted mixture learning (BML) pour estimer les paramètres du modèle de mixture. Dans nos expériences, nous comparons la méthode proposée à un système de référence utilisant un algorithme EM, pour Expectation-Maximisation, pour la classification multi-pathologique. Les résultats des tests ont démontré que la méthode BML adaptée pour l'apprentissage de GMM a une meilleure performance que celle utilisant l'algorithme EM. Le system de diagnostic proposé, extrait des coefficients de Fourier (MFCC) comme un vecteur de caractéristiques des modèles de cri des nouveau-nés. Dans l'expérience de classification binaire, le système identifie le cri comme appartenant à l'un des deux groupes, sains ou pathologique. Le classificateur binaire a réalisé un taux réel positif de 80,77% et un taux réel négatif de 86,96%, ce qui montre la capacité du système à identifier correctement les nourrissons en bonne santé et malades, respectivement.

2.1 Abstract

We make use of information inside infant's cry signal in order to identify the infant's psychological condition. Gaussian mixture models (GMMs) are applied to distinguish between healthy full-term and premature infants, and those with specific medical problems available in our cry database. Cry pattern for each pathological condition is created by using adapted boosted mixture learning (BML) method to estimate mixture model parameters. In the first experiment, test results demonstrate that the introduced adapted BML method for learning of GMMs has a better performance than conventional EM-based reestimation algorithm as a reference system in multipathological classification task. This newborn cry-based diagnostic system (NCDS) extracted Mel-frequency cepstral coefficients (MFCCs) as a feature vector for cry patterns of newborn infants. In binary classification experiment, the system discriminated a test infant's cry signal into one of two groups, namely, healthy and pathological based on MFCCs. The binary classifier achieved a true positive rate of 80.77% and a true negative rate of 86.96% which show the ability of the system to correctly identify healthy and diseased infants, respectively.

2.2 Introduction

Crying is the first sound the baby makes when he enters the world outside of his mother's womb, which is a very positive sign of a new healthy life. Infants cry for the same reason that adults talk i.e. to let others know about their needs or problems. Since crying is all a baby can do to express any discomfort, it seems that this multimodal signal carries a lot of information about him. In early studies of the infant cry analysis, the acoustic structure of infant crying was analyzed and some of the important variables controlling the production of their cries were described (Wasz-Hockert, Michelsson et Lind, 1985). After cry analysis on infants with various diseases, in some cases it has been noticed that there are fixed cry attributes, which are rarely seen in cries of healthy infants. Instead, these attributes occur frequently in cries of infants with diseases (Benson, 2009; Wasz-Hockert et al., 1968; Wasz-Hockert, Michelsson et Lind, 1985). Therefore the concealed information contained within a cry signal could clarify the infant's present psychological condition. Acoustic analysis of the infants' cry

signal helps to measure these parameters quantitatively to perform a comparison between healthy and ill states. Since infants' cry could be changed from normal to abnormal by diseases or deformities which have the ability to produce a ill effect on the central nervous system, the oral cavities, or respiratory organs, our goal is to develop a NCDS to classify infants with different kind of physiological conditions.

Generally, sounds can be represented in multiple ways. In feature representation method, the features selection step relies heavily on good understanding of the problem. There are some literatures on defining and using different cry characteristics and frequency features which distinguish between a healthy infant's cry and that of infants with asphyxia, brain damage, Hyperbilirubinemia, Down's syndrome, and mothers who were drug-abused abused during pregnancy (Corwin, Lester et Golub, 1996; Wasz-Hockert, Michelsson et Lind, 1985). Human speech features characteristics such as linear prediction coefficients (LPCs), MFCCs, fundamental frequency and formants are studied in previous works (Amaro-Camargo et Reyes-García, 2007; Benson, 2009; Cano et al., 2006; Galaviz et García, 2005; Lind et Wermke, 2002; Orozco et Garcia, 2003). The work presented by Hariharan, et al, employed wavelet packet transform (WPT) to compute sub-band energy and entropy features from wavelet packet coefficients (Hariharan, Yaacob et Awang, 2011). The goal is given a set of exemplary patterns for C different pathological infant's cry classes, to construct a function such that when presented with a new feature from an infant's cry belonging to class i the function will recognize the correct index pathology class. In recent years, several machine learning algorithms such as artificial neural network (ANN), radial basis function (RBF), probabilistic neural network (PNN) have demonstrated their ability to recognize cry patterns and make intelligent decision based on available training database (Cano Ortiz, Escobedo Beceiro et Ekkel, 2004a; Hariharan, Yaacob et Awang, 2011; Orozco et Garcia, 2003). Furthermore, hybrid systems in which classification methods are combined under several approaches like bagging (Bauer et Kohavi, 1999a), boosting (Bauer et Kohavi, 1999a), majority voting, staking were examined in order to achieve better final results than the case where a single classifier is run (Amaro-Camargo et Reyes-García, 2007; Cano et al., 2006; Galaviz et García, 2005).

In this paper we make use of extracted MFCCs from an infant's cry signal to diagnose pathological conditions and specific diseases which have not been previously studied such as "Coarctation of Aorta" and "Tetralogy of Fallot" by drawing support from collected cry database. As we mentioned earlier, there exists a large number of approaches to do the modeling and the classification tasks. We will focus on GMMs, which is the most successful classifiers in use for audio data when their temporal structure is not important (Divakaran, 2009). This paper employs GMMs to introduce a classification technique in the field of statistical learning theory which uses adapted BML method to train mixture models for modeling of infants' cry signals. The BML method (Jun, Yu et Hui, 2011) presents three key advantages: (1) Add new components into the direction that largely increases the objective function, (2) Decrease sensitivity to initial parameters and (3) Estimate the optimum number of components, unlike the conventional EM-based re-estimation algorithm. Partial and global updating methods were used in model parameters estimation processes in order to speed learning process up and converge to more robust and reliable estimation of a new mixture component. Another advantage of the adapted BML method was that it used Bayesian Information Criterion (BIC) (Schwarz, 1978) for model selection. It is partially based on the likelihood function but to avoid overfitting there is also a penalty term.

This paper is organized as follows: In section 2.3 we give a brief review of GMM, its role in cry-pattern classifier, and advantages of adapted BML method. Section 2.4 explains the different parts of the NCDS and how it identified infants. In section 2.5, results of experiments in both multi-pathological and binary classification tasks are reported, and in section 2.6 a follow up analysis of the results and conclusion are presented to finalize the paper.

2.3 GMMs for Cry-Pattern Classification

GMMs are a special case of Hidden Markov Models (HMMs) which pay more attention to the temporal structure of a sound and have proven to be invaluable tools in areas such as speech recognition (Divakaran, 2009). Compared to the human speech which is modeled by Hidden Markov Models with finite states, cry signal has just a single state to be considered.

Moreover, GMM has the ability to form smooth approximations from arbitrarily shaped densities and it has proved to be an effective probabilistic model for applications such as biometric systems, most notably in speaker recognition systems and speaker identification (Reynolds et Rose, 1995) due to its capability of representing a large class of sample distributions. In a cry-based diagnosis system there is no chance to train the classifier with a specific individual compared to what happens in speaker dependent automatic speech recognition (ASR) systems. Therefore we should use our available cry database to create a more general model for each available pathological condition in order to fine tune the pathology detection of test infants. Like ASR systems in learning phase, there are two main parts(O'Shaughnessy, 2008): first, some cry features are selected and then patterns are created from these features. Second, the cry-pattern classifier works according to the just created cry-patterns to recognize physiological conditions on the newborn infants. The proposed cry-modeling method trained the GMM classifier from feature streams. It means that cry signals coming from either healthy or pathological classes were modeled by a separate pool of Gaussians using extracted feature vectors. Adapted BML was used to learn mixture models in an incremental and recursive manner in which unlike EM-based re-estimation algorithm, the final model was less sensitive to initial parameters. It might, therefore, converge to a better optimal point. According to the boosting theory, upper bound on training error rate is analytically minimized and the margin of all training samples is increased. Moreover, in the preceding paper (Jun, Yu et Hui, 2011) the strong point of BML method shows that a new Gaussian component is estimated in each step according to the functional gradient of the objective function. Therefore each new component is always added to the direction that increases the objective function the most. In this paper adapted BML has been described for the log-likelihood function of the mixture model over training data as our objective function.

2.4 Newborn Cry-Based Diagnosis System (NCDS)

2.4.1 Cry Database

The number of labeled data used during training phase has a leading role in performance of the classifier. For example in case of having small number of cry samples for the pathologies of interest, the resulting trained classifier may be too specific to be generalized to unseen infant's cry signal. Cry database collecting is still in progress and up to now, the following two kinds of newborn infants are considered in the database:

1- Healthy newborn infants, both full-term and premature;

2- Sick newborn infants, both full-term and premature, with specific selected pathologies.

The imbalanced learning problem (He, 2011) is concerned with the performance of learning algorithms. In the presence of underrepresented data and skewed class distribution this problem arises, which is direct result of the nature of the data space present in the cry database. Table 2.1 shows the list of different pathologies and the number of available samples in each class.

2.4.2 Pre-processing and feature extraction

In data collection step we have used 2-channel recorder with 44.1 kHz sampling rate. The time domain representation of one cry signal in two channels is shown in Figure 2.1. In pre-processing step it converted into one channel signal using mean value function.

Table 2.1 Cry database

Infants	State	Pathologies	Numbers
Fullterm	**Healthy**	N/A	38
	Pathologies	Bovine protein allergy	13
		Tetralogy of Fallot	5
		Thrombosis in the vena cava	13
Premature	**Healthy**	N/A	25
	Pathologies	Tetralogy of Fallot	9
		Cardio Complex	14
		X-chromosomal abnormalities	9
		Coarctation of Aorta	10

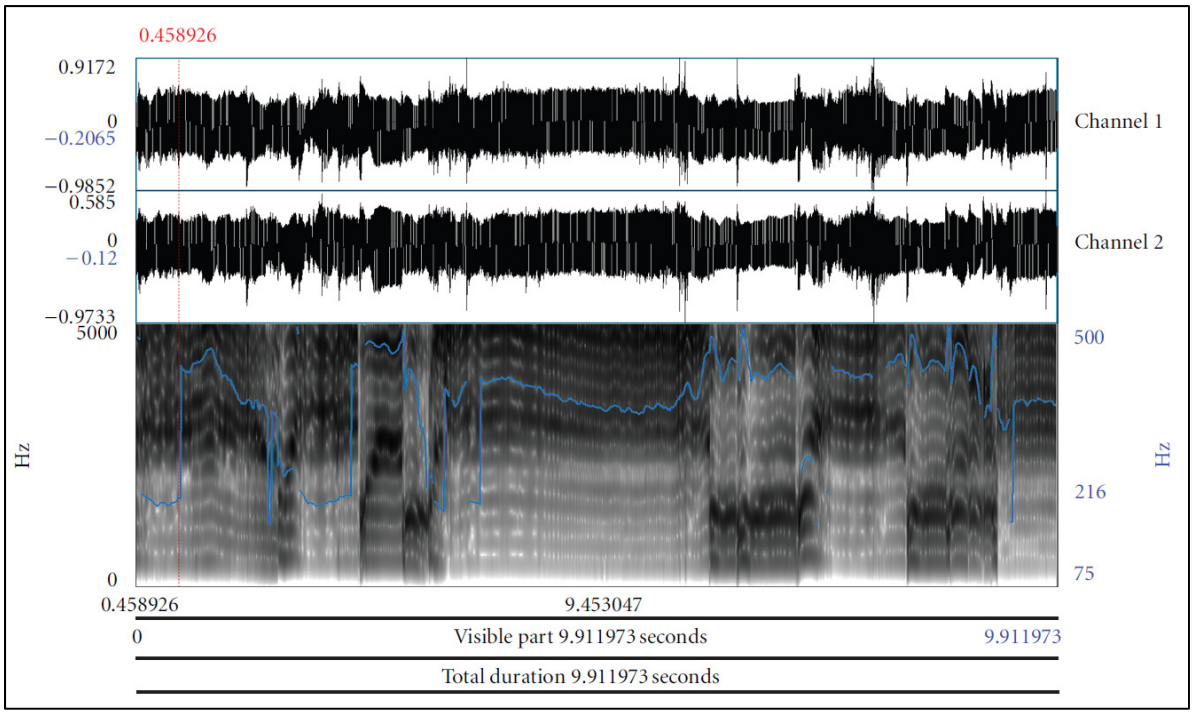


Figure 2.1 Time domain representation of a cry signal

In the acoustical analysis step, the resulting wave was cleared of any silence region or external unwanted sounds as for the nurse or pediatrician voices, then normalized and split into frames. Next, MFCCs were extracted. The vocal tract shape generally changes slowly with time and tends to be constant over short intervals. A reasonable approximation to guarantee reproducibility is to analyze the signal into a sequence of millisecond-time frames, where each frame is represented by a single feature vector describing the average spectrum for a short time interval (Holmes, 2001). In reading about application of frequency feature analysis of speech signals, it is common practice to pre-emphasis the signal prior to computing the parameters by applying the first order difference equation $s'(n) = s(n) - \alpha\, s(n-1)$ to the sample sequence $[s(n), n = 1, \dots, N]$ in each window of length N. The z-transform of the filter is $P(z) = 1 - \alpha z^{-1}$. Deller (John R. Deller, Proakis et Hansen, 1993) had earlier referred to the reasons behind employing a pre-emphasis filter which are twofold: First, it is due to cancel spectral effects of one of the glottal poles and the second reason is to prevent numerical instability. Gray (Gray et Markel, 1974) and Makhoul (Makhoul et Viswanathan, 1974) have worked with an optimal value of α given by $\alpha = \frac{r_s(1;m)}{r_s(0;m)}$ in the sense of MSE, where $r_s(\eta; m)$ is the usual short-term autocorrelation sequence for the frame ending at m with the parameter η corresponding to the autocorrelation lag. One estimator is given by (John R. Deller, Proakis et Hansen, 1993):

$$r_s(\eta; m) = \frac{1}{N} \sum_{n=-\infty}^{\infty} s(n)w(m-n)\, s(n-|\eta|)w(m-n+|\eta|) \qquad (2.1)$$

where $w(n)$ is a window of length N. For voiced frames the optimal value is near unity, whereas for unvoiced frames it is small ($\alpha \approx 0$). Therefore it should not performed on unvoiced speech and in voiced frames it is taken in the range $0.9 \leq \alpha \leq 1$ which introduces a zero near $\omega = 0$, and a $6 - db$ per octave shift on the spectrum. We use a common value for this factor which is 0.97 (Akande et Murphy, 2005; Flynn et Jones, 2008; Mporas et al., 2011; Young et al., 2006c). In the next step, L MFCCs per frame were extracted just for those voiced frames. The sequence of feature vectors describing the average spectrum for a

short time interval can be presented as a matrix which acts like a pattern in the classification phase.

In all related practical applications, the short terms or frames should be utilized which implies that the signal characteristics are uniform in the region. Therefore the selected portion of the signal has to be short enough to be stationary. Temporal properties can be assumed fixed over time intervals on the order of 10-30 msec (Rabiner et Schafer, 1978). Prior to any frequency analysis, the Hamming windowing is necessary to reduce any discontinuities at the edges of the selected region. Generally a longer window will tend to produce a better spectral picture of the signal while the window is completely within a stationary region, whereas a shorter window will tend to resolve events in the signal better in time. This trade-off is sometimes called the spectral temporal resolution trade-off (John R. Deller, Proakis et Hansen, 1993). A common choice for the value of the window length (10-30 msec) (Benzeghiba et al., 2007; Huang, Acero et Hon, 2001a; O'Shaughnessy, 2008; Rabiner et Schafer, 1978) is normally larger than the frame rate. For example, the typical values for the window length in HTK (Young et al., 2006c) is 25ms. MFCCs are obtained by applying the Discrete Cosine Transform (DCT) to the output of the Mel-filters. The difference from the real cepstrum is that a nonlinear frequency scale is used, which approximates the behavior of the auditory system (Rabiner et Schafer, 1978). A filterbank with K filter is defined, where all these triangular filters compute the average spectrum around each center frequency with increasing bandwidth. An acoustic representation using MFCCs is often referred as a "mel cepstrum". After performing fast Fourier Transform (FFT) on each windowed frame, MFCCs are calculated using the following DCT (Divakaran, 2009):

$$c_n = \sqrt{\frac{2}{K}} \sum_{i=1}^{K} log\, S_i \times \cos\left(n\left(i - \frac{1}{2}\right)\pi/K\right), n = 1,2, \dots L \tag{2.2}$$

where K is the number of sub-bands, L is the desired length of cepstrum and $S_i, i = 1,2, \dots K$ $(1 \leq i \leq K)$, represents the filter bank energy after passing through the triangular

band pass filters. We use a set of 20 triangular windows ($K = 20$) which is utilized in a common approach to simulate critical-band filtering (Davis et Mermelstein, 1980; O'Shaughnessy, 2000b), whose energy outputs are designed $S_i, i = 1,2,\dots,20$. We will discuss the choice of the parameter$L$ later. Figure 2.2 shows all the pre-processing steps from the cry recording step until the extraction of the MFCCs.

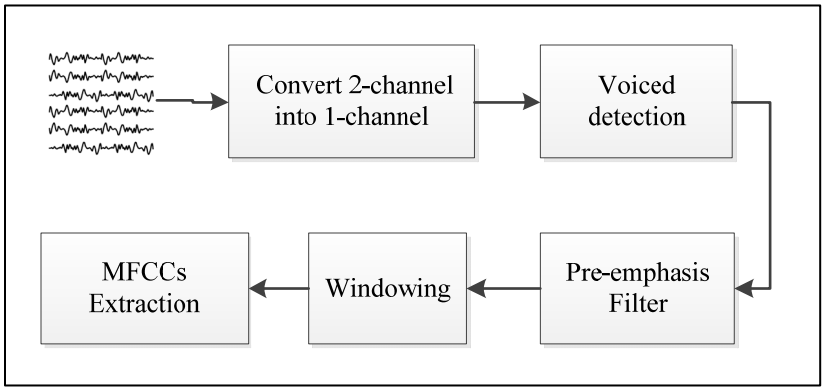


Figure 2.2 Pre-processing steps

2.4.3 Adapted BML method for GMMs

The main idea of boosting method in machine learning is that instead of always treating all data points as equal, component classifiers should specialize on certain samples. In particular, if a sample is hard-to-classify and problematic for the existing classifier, more components should focus on it. Compared to other learning mixture models (Berlinet et Roland, 2007; Ng et McLachlan, 2004; Redner et Walker, 1984), BML method (Jun, Yu et Hui, 2011) has a great privilege to add new mixture components in such a way that has the greatest improvement in the predefined objective function, $\mathcal{C}(F_k)$. Moreover, this method is less sensitive to initial parameters, resulting in better optimal point in the convergence process. The whole cry-pattern classification approach comprised a classification scheme using GMMs that classify patterns created by extracted real-valued frequency domain features. A GMM, $F_K(X)$ with K Gaussian components and given feature vector Xcan be represented as:

$$F_K(X) = \sum_{k=1}^{K} \pi_k f_k(X) \tag{2.3}$$

with the restriction that $0 \leq \pi_k \leq 1$ for $k = 1, \ldots, K$ and

$$\sum_{k=1}^{K} \pi_k = 1 \tag{2.4}$$

where $\pi_k$and $f_k(X)$ are mixture proportions and distributions of the k^{th} component respectively. The k^{th} multivariate Gaussian component of a D-dimensional feature vector X can be written in the following notation:

$$\begin{aligned} f_k(X|\Phi_k) &= \mathcal{N}(X; \mu_k, \Sigma_k) \\ &= \frac{1}{(2\pi)^{\frac{D}{2}}|\Sigma_k|^{\frac{1}{2}}} \times exp\left(-\frac{1}{2}(X-\mu_k)^{Tr}{\Sigma_k}^{-1}(X-\mu_k)\right) \end{aligned} \tag{2.5}$$

where $\Phi_k = [\,\mu_k\,, \Sigma_k]$ are the mean and covariance parameters for the k^{th} component and A^{Tr} represents the transpose of matrix A. The model commences with one mixture and learns gradually by adding a new mixture component on each step. According to the defined objective function $\mathcal{C}(.)$, each adding component process should satisfy the inequality $\mathcal{C}(F_k) > C(F_{k-1})$.All the re-estimation formulas to update Gaussian distribution parameters can be computed afterwards. Log-likelihood function of the mixture model over all training feature data has a vital role in aforementioned formulas. For example, the pre-defined objective function of the mixture model over all training feature can be computed using equation below:

$$\mathcal{C}(F_j) = \sum_{t=1}^{T_j} log\, F_j(X_t) \tag{2.6}$$

where T_j is the number of training feature vectors X in j^{th} pathology class. Iterative re-estimation formulas 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:

$$w^n(X_t) = \frac{f_k\left(X_t \middle| \Phi_k^{(n)}\right)}{F_{k-1}(X_t|\Psi_{k-1})} \tag{2.7}$$

$$\mu_k{}^{n+1} = \frac{\sum_{t=1}^{T_j} w^n(X_t).X_t}{\sum_{t=1}^{T} w^n(X_t)} = \sum_{t=1}^{T_j} \gamma_t\left(\Phi_k^{(n)}\right).X_t \tag{2.8}$$

$$\Sigma_k{}^{n+1} = \frac{1}{\sum_{t=1}^{T_j} w^n(X_t)} \times \sum_{t=1}^{T_j} w^n(X_t)(X_t - \mu_k{}^{n+1})(X_t - \mu_k{}^{n+1})^{Tr} \tag{2.9}$$

where $\Phi_k^{(n)} = [\mu_k{}^n, \Sigma_k{}^n\ ]$ denotes the mean vector and covariance matrix for k^{th} Gaussian component at the n^{th}iteration, and $\Psi_k = [\Phi_k, \Psi_{k-1}\ ]$. Note how $w^n(X_t)$ represents a weight assigned to feature vector X_t after n^{th} iteration. As you can see according to this weighting function it is clear to understand that feature vector with lower probability by current model are given larger weights than those with more probability. Therefore, the new Gaussian component f_k focuses on those features which are poorly modeled by the current model F_{k-1}, in much the same way as other boosting algorithms (Freund et Schapire, 1997; Friedman, 2001).

2.4.4 Initialization of sample weights

There is a problem with the initialization values of weights based on boosting theory which can be computed by using equation below:

$$w^0(X_t) = 1/F_{k-1}(X_t|\Psi_{k-1}) \tag{2.10}$$

where $\Psi_{k-1} = [\Phi_{k-1}, \Psi_{k-2}\ ]$. The dynamic range of F_{k-1} is large in a way that it could be dominated by only a few number of samples with low probability or outliers. We use the so-called 'Weight decay' method (Rosset, 2005) to overcompensate for the low probability by smoothing sample weights based on power scaling.

$$w^0(X_t) = (1/F_{k-1}(X_t|\Psi_{k-1}))^p\ , 0 < p < 1 \tag{2.11}$$

where p is a decay parameter or an exponential scaling factor. In the second method the idea of sampling boosting in (Freund et Schapire, 1997) 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 just created subset are utilized with equal weights to estimate the new component parameters. Assume $\bar{M}$ and σ^2 denote the mean and variance of weights calculated in Equation (10) as defined below:

$$\bar{M} = mean\,[log\ w^0(X_t)] \tag{2.12}$$

$$\sigma^2 = variance\,[log\ w^0(X_t)] \tag{2.13}$$

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

$$X_{sub} = \{X_t | log\,[w^0(X_t)] > \bar{M} + \beta\sigma\} \tag{2.14}$$

where β is a linear scaling factor to control the size of subset X_{sub}.

2.4.5 Process of adding a new component

In the adding process the part of training vectors in which $f_k(X)$ had a higher value than the reminder of the mixture model, denoted by $F_k - [f_k]$, was selected. Then this subset of data X_{sub} should be modeled by a small GMM consisting in two Gaussian components called f_k^* and f_{K+1}.The initial component came from the EM-based re-estimation, and then the second component and its weight were estimated based on BML method and line search respectively. We considered the estimated component –the second one– as an initial component and ran BML method 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 f_{K+1} and f_k^* continued for $k = 1, \dots, K$. Amongst all the created K mixture models, denoted by F_{K+1}, the one that gave the highest value of the objective function (same as log-likelihood value) was selected and added to the mixture by adjusting its weight.

2.4.6 Partial and global updating

During previous step, instead of finding the new mixture weight from the line search below:

$$\pi_k{}^* = \underset{\pi_k \in [0,1]}{argmax}\ \mathcal{C}\big((1-\pi_k)F_{k-1} + \pi_k f_k^*\big) \tag{2.15}$$

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.

$$\{f_k^*, \pi_k^*\} = \underset{\pi_{k,} f_k}{argmax}\ \mathcal{C}\ (\ (1-\pi_k\ )F_{k-1} +\ \pi_k f_k\ ) \tag{2.16}$$

All the equations for updating weight assigned to feature vector X_t, mixture weight value, mean and covariance matrix are estimated as follows (Jun, Yu et Hui, 2011):

$$w^n(X_t) = \frac{f_k\left(X_t \middle| \Phi_k^{(n)}\right)}{\pi_k{}^n f_k\left(X_t \middle| \Phi_k^{(n)}\right) + (1-\pi_k{}^n)F_{k-1}(X_t|\Psi_{k-1})} \tag{2.17}$$

$$\gamma_t\left(\Phi_k^{(n)}\right) = \frac{w^n(X_t)}{\sum_{t=1}^{T_j} w^n(X_t)} \tag{2.18}$$

$$\pi_k{}^{n+1} = \frac{1}{T}\sum_{t=1}^{T_j} \pi_k{}^n\, w^n(X_t) \tag{2.19}$$

$$\mu_k{}^{n+1} = \sum_{t=1}^{T_j} \gamma_t\left(\Phi_k^{(n)}\right).X_t \tag{2.20}$$

$$\Sigma_k{}^{n+1} = \sum_{t=1}^{T_j} \gamma_t\left(\Phi_k^{(n)}\right).(X_t - \mu_k{}^{n+1}) \times\ (X_t - \mu_k{}^{n+1})^{Tr} \tag{2.21}$$

Moreover, in order to speed converging process up and finding the minimum number of Gaussian component in the final mixture, 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 $k = 1, \dots, K$ when the reminder of the mixture mode is assumed to be fixed. This procedure continues iteratively until the objective function value reaches a local maximum. It means that after obtaining a mixture model F_K, we could update each component f_k and its weight over all training feature vectors by using the same updating equations.

2.4.7 Criterion for model selection

The process of adding new mixture component to previous mixture model 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 Information Criterion (BIC). It can be represented as the following (Schwarz, 1978):

$$BIC(k) = -2 \times \mathcal{C}(F_k) + M_k \, log(T_j) \tag{2.22}$$

where $\mathcal{C}(F_k)$ 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_j denotes total number of training data for the j^{th} pathology class. The second term in BIC equation is a penalty term for the number of parameters in the model. BIC is closely related to Akaike Information Criterion (AIC) (Akaike, 1974; Bengtsson et Cavanaugh, 2006) but the penalty term is larger in BIC than in AIC. Figure 2.3 shows brief review of all mentioned processes to train a GMM for each available pathological condition in order.

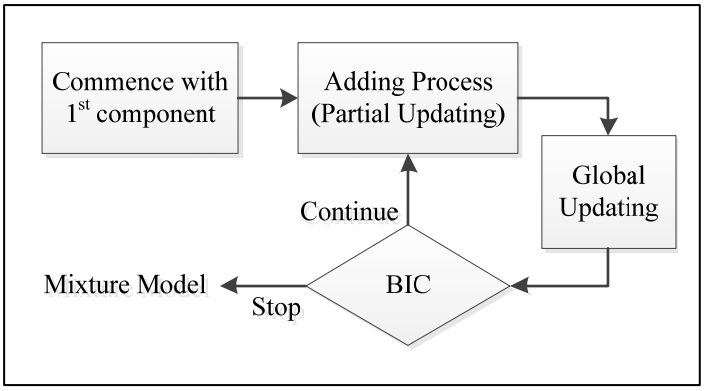


Figure 2.3 Block diagram of learning GMM using adapted BML technique

2.4.8 Decision rule

The likelihood of a feature vector X given a Gaussian model $\mathcal{L}$ is defined as:

$$\mathcal{L}(X) = \sum_{k=1}^{K} \pi_k \mathcal{N}(X|\mu_k, \Sigma_k) \tag{2.23}$$

where μ_k and $\Sigma_k$are mean and covariance parameters for a set of K Gaussians, and π_k is a normalizing factor that also weights them appropriately and constrained such that $0 \leq \pi_k \leq 1$ and $\sum_{k=1}^{K} \pi_k = 1$. Each of the trained mixture models $\mathcal{L}_j$ approximates the distribution of the features of one class only. There is significant structural difference between cry signals of infants with different pathologies. Therefore we can assume that the distributions of the features of each cry signal are different. As a result, when classifying a feature vector X_i belonging to pathology class i we will expect $\mathcal{L}_i(X_i) > \mathcal{L}_j(X_i), \forall j \neq i$. One of the common decision rules is to select the hypothesis that has the highest likelihood value called the Maximum Likelihood (ML) decision criterion.

$$Pathology\ Class\ \# = max_j\ [\mathcal{L}_j(X)] \tag{2.24}$$

Likelihood values of under-test infant's cry signal were computed according to generated Gaussian mixture model for each $Class_j, j = 1, \ldots, C$, then by use of the ML rule the decision

was made. Figure 2.4 shows how mixture models trained on the MFCCs are associated with different pathological conditions. NHF and NHP are the total number of Gaussian components which can describe models of healthy full-term and premature infants respectively. Similarly, NSF_i and NSP_i are the numbers of Gaussian components for full-term and premature infants with pathology i respectively.

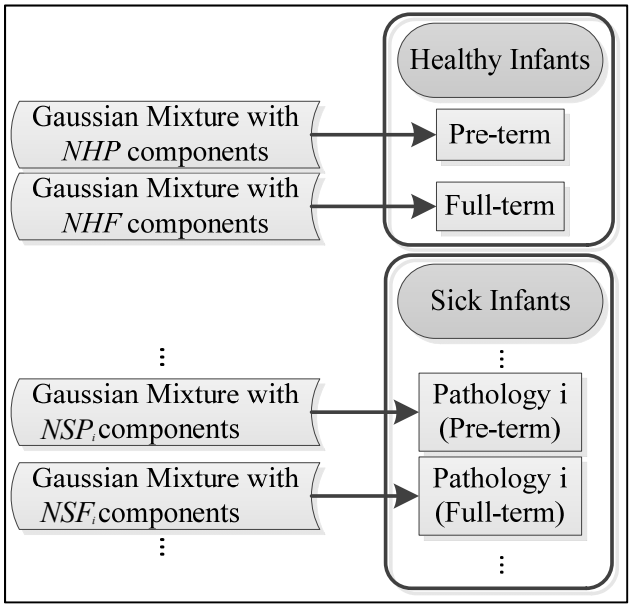


Figure 2.4 Mapping of estimated GMMs to pathological conditions

2.5 Experiments

For implementation the cry database was split into two disjoint subsets for training and testing. Almost 63% of total cry signals were utilized for the training phase and the rest for testing phase. After creating GMMs for each available pathological condition in the cry database using adapted BML method, we can assess what accuracy rate it may have. The MFCC order has also been studied experimentally for speech recognition. A total number of 12 MFCCs are common in speech processing (John R. Deller, Proakis et Hansen, 1993; Young et al., 2006c) and they are computed directly from the data. It is that same number

which is used in (Nwe, Foo et De Silva, 2003) to recognize speech emotion via HMMs. The energy within a frame is also an important feature that can be easily obtained. For better performance, the 0^{th}cepstral coefficient $[c_0]$ is appended to the feature vector as the 13rd feature. The initial coefficient represents the average energy (weighting with a zero-frequency cosine) same as role of the log energy $[E = log \sum_{n=1}^{N} S_n^2]$ a (Huang, Acero et Hon, 2001b; O'Shaughnessy, 2000a). Therefore, used feature vectors are composed of first 13 MFCCs $[c_n, n = 0,1,2, \dots, L = 12]$. As we defined earlier, L is the desired length of cepstrum and it is a fixed parameter. The higher-order MFCC does not further reduce the relative error rate with a typical speech recognition system in comparison with the 13th-order MFCC, which indicates that the first 13 coefficients already contain most salient information needed for speech recognition (Huang, Acero et Hon, 2001a). We made full use of both initialization methods with decay parameter $p = 0.05$ and linear scaling factor $\beta = -0.5$ values for the parameters to overcome overfitting and the small covariance matrix which was created after several iterations. It is those same parameter values which are set and designed for BML algorithm in large-vocabulary continuous speech recognition tasks in (Jun, Yu et Hui, 2011). After that only samples in subset with equal sample weights were used to estimate the mean and covariance matrix of Gaussian components. The presented method had a vital role to achieve good performance and avoid the overfitting problem in the learning step.

In the first experiment, the NCDS was tested on several multi-pathology classification tasks. It consisted of all aforementioned conditions in the cry database. It could be difficult to evaluate the effectiveness of the created GMMs for modeling and adapted BML method for learning the mixture model by extracting a single feature from a small cry database. Nevertheless our results show that it had a better accuracy rate compared with conventional EM-based method for GMMs as our reference system. It is worth mentioning that the GMMs created by the EM-based re-estimation method for each class were trained by setting the number of components equal to that of mixture model learned by adapted BML method. Here, we address the question of the classification performance with respect to the frame length by evaluating the system with different frame durations but same overlap percentages (30%) between two consecutive windows. In order to extract MFCCs, frames with different

durations are used while 30% overlap was introduced between two consecutive windows. Table 2.2 shows the obtained accuracy rate for all 9 different groups of infants in the order they are shown in Table 2.1 for frame durations 20msec, 25msec and 30msec. It can be seen that both methods delivered great performances for most pathology classes, but the presented method had better final outcomes. For the premature infants with "Coarctation of Aorta" it seemed that the learned pattern was not well-defined enough to be capable of accurately classify them. We believe this was due to either small number of training samples (6 and 4 samples of infants' cry for training and testing respectively) or used pathologically-non-informed features for this disease.

Table 2.2 Obtained accuracy rate for multi-pathology classification (%)

Frame duration	**20msec**		**25msec**		**30msec**	
Method	**EM-Based**	**ABML**	**EM-Based**	**ABML**	**EM-Based**	**ABML**
1	100	100	100	100	100	100
2	100	100	100	100	100	100
3	100	100	0	50	0	50
4	75	100	75	100	75	50
5	100	88.9	100	100	100	100
6	100	100	100	100	100	100
7	80	60	40	60	20	40
8	100	100	100	100	100	100
9	0	0	0	0	0	0

To better understand the effect of frame duration on the performance, the mean values of classification accuracy rates are computed from frequency distribution over 9 pathology classes and it is given by (Zill, wright et Cullen, 2011)

$$Mean = \frac{\sum_{i=1}^{9} f_i m_i}{\sum_{i=1}^{9} f_i} \tag{2.25}$$

Where f_i and m_i show the frequency and obtained accuracy rate for i^{th} pathology class. The results in Figure 2.5 show that, the performance of both EM-Based and Adaptive BML methods degrade when the frame duration increase. Therefore, the system performance is the best when using 20msec frame length to extract MFCCs. In addition, Figure 2.5 says that the presented adaptive BML method, on the average, works better than the EM-Based method when frame duration varies.

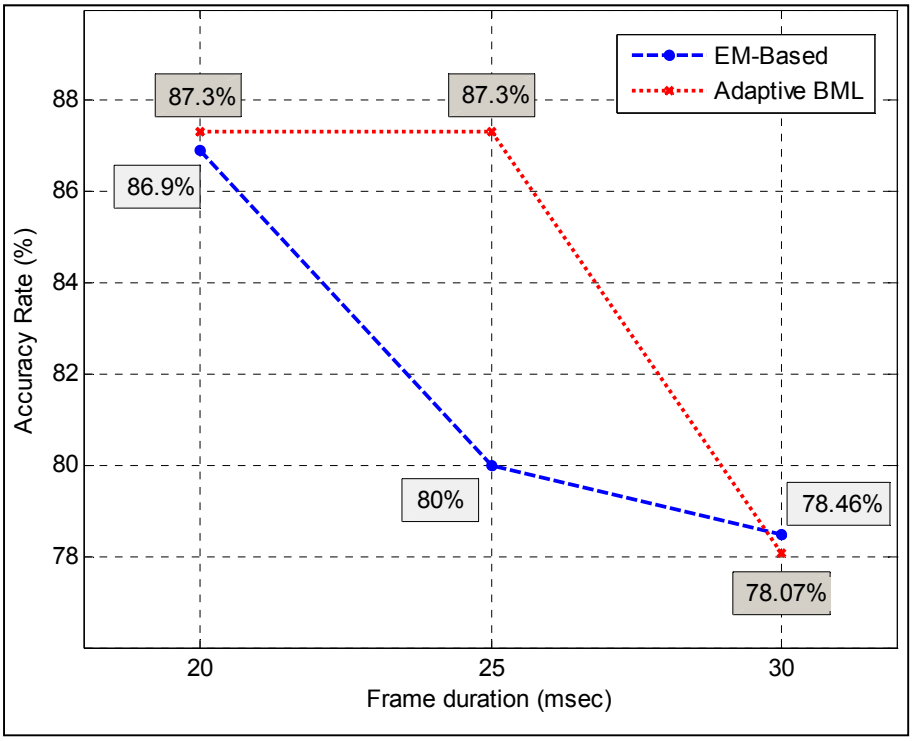


Figure 2.5 Mean classification accuracy rates

The coefficient of variation (CV) is particularly useful for representing the reliability of performance tests which is the coefficient of dispersion based on standard deviation. It gives the standard deviation as a percentage of the mean values as follows (Zill, wright et Cullen, 2011):

$$StandardDeviation = \sqrt{\frac{\sum f_i m_i{}^2 - \frac{(\sum f_i m_i)^2}{\sum f}}{\sum f_i - 1}} \tag{2.26}$$

$$CV = \frac{StandardDeviation}{Mean} \times 100\% \tag{2.27}$$

In Figure 2.6 we present this coefficient of dispersion for both techniques with different frame durations. The larger the CV, the more the performance varies. Since the coefficient of variation is less for shorter segments, theirs performances are therefore more consistent. The CV values for adaptive BML method are much less than those of EM-Based method for frame length 25-30 msec, although they are so close to each other for frame length 20 msec.

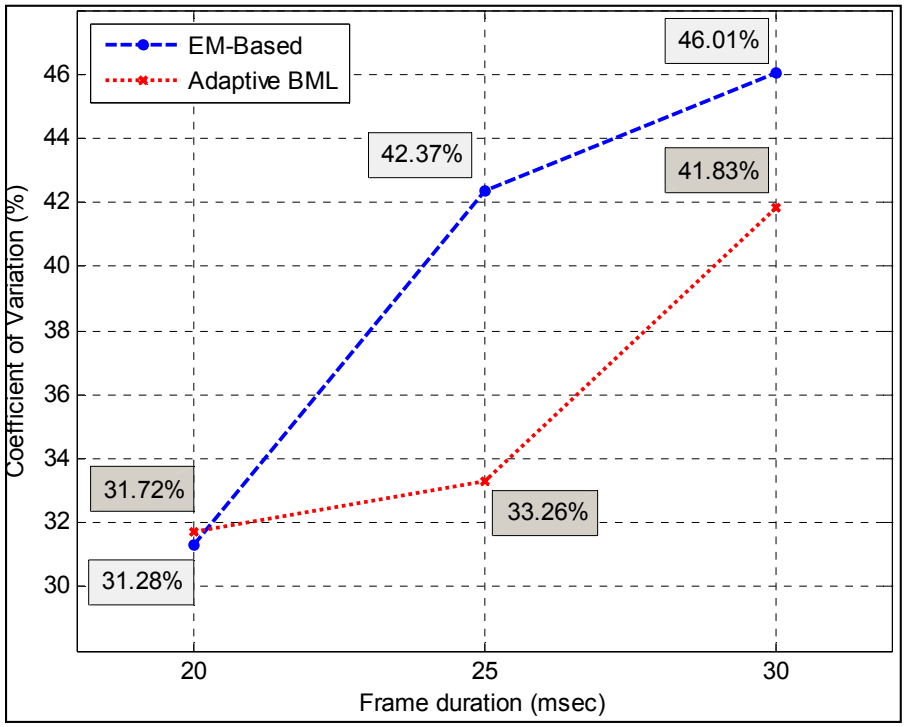


Figure 2.6 Coefficient of variation

The large cry signal database is required to make well-defined mixture model to keep the number of components as small as possible. As we said earlier, in large cry signal samples, small number of outliers is to be expected. The numbers of components that minimize BIC in the each mixture models are shown in Figure 2.7.

The second experiment was designed to test the diagnostic system for Binary classification task in which all cry data in database were organized into two separate groups namely healthy and pathological. Note that, here the frame length of 30 msec with 30% overlap has been used. In this experiment for each defined infant's class, a GMM which fitted extracted data from cry signals is trained by utilizing adapted BML technique. The number of components in the mixture models for healthy and pathological classes was estimated 9 and 12 respectively. These numbers of components were employed in learning steps of mixture models by conventional EM-Based method just like in the previous experiment. Table 2.3 displays two confusion matrices that allow visualization of the performance of each method in the binary classification problem. These two matrices, for (a) the proposed method and (b) conventional EM-Based method, are provided for comparison which makes it easy to see if the system is confusing two predefined classes by containing the number of healthy and pathological infants that were correctly classified or mistakenly classified.

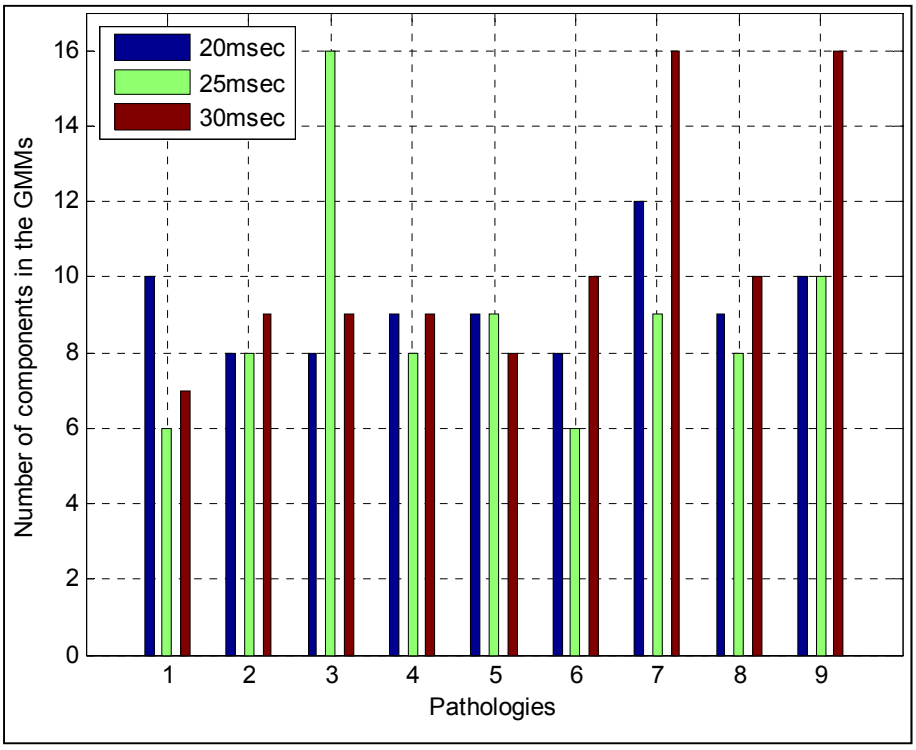


Figure 2.7 Number of components

Table 2.3 Confusion Matrix for defined
Binary classification task

	Predicted Classes	
Actual Classes	**Pathological**	**Healthy**
Pathological	21	5
Healthy	3	20
(a) Proposed ABML-GMM method		
	Predicted Classes	
Actual Classes	**Pathological**	**Healthy**
Pathological	26	0
Healthy	6	17
(b) Conventional EM-GMM method		

True positive (TP) and True negative (TN) rates are defined for a two by two confusion matrix, as calculated using the following equations (Kohavi et Provost, 1998):

$$TP = \frac{d}{c+d} \tag{2.28}$$

$$TN = \frac{a}{a+b} \tag{2.29}$$

where “a” and “d” are the numbers of correct predictions that an instance is negative or positive respectively. The other parameters, “b” and “c” are defined in a similar way by counting the number of incorrect predictions that an instance is positive or negative accordingly. In the pathology diagnostics system, true positive rate or test sensitivity shows the ability of the system to correctly detect infants with disease, whereas true negative rate or test specificity demonstrate the ability of the system to correctly identify those without disease. Both these statistical measures of the two methods are summarized in Table 2.4.

Table 2.4 Obtained two statistical measures for Binary-classification problem

	EM-GMM	**ABML-GMM**
Test Sensitivity	100 %	80.77 %
Test Specificity	73.91 %	86.96 %

The ramification of false positive (Type I error) and false negative (Type II error) in some cases especially medical examinations are not the same (He, 2011). One can be more costly and irrecoverable than the reverse situation. Preferably, the classifier should be able to provide a balanced degree of predictive accuracy (ideally 100%) for both the minority and majority classes in our imbalanced data which is direct result of the nature of the cry database.

2.6 Conclusion

A newborn cry-based diagnostic system (NCDS) based on extracting Mel frequency cepstral coefficients (MFCCs) from infant's cry signal is presented in this paper. For all cry samples which belong to the healthy infant class or pathological infant classes with different physiology conditions, a mixture model with separate Gaussian pool was estimated as a cry-pattern. Adapted boosted mixture learning (BML) method was introduced to train mixture models. Some advanced techniques of signal processing, and machine learning were employed in different part of the learning process such as adding new component, weighting function for samples, model selection, and global re-estimation of parameters. In multi-pathological classification tasks, results show that, on the average, presented method achieved a higher classification accuracy rate to identify infants' diseases than EM-based re-estimation algorithm for Gaussian mixture models (GMMs). The performance and reliability of adaptive BML-GMMs is the best when using 20msec as a frame duration and gradually degrade when the length increase further. The results demonstrate that the adaptive BML method can provide better classification accuracy rate than EM-Based method with higher

system reliability. For binary classification problem, with 30msec frame duration (the worst-case scenario), adapted BML can identify full-term and pre-mature healthy infants better than EM-Based, but on the other hand it deliver a little lower performance than EM-Based method for sick infants. However, adapted BML provides better balanced degree of predictive accuracy for both the minority and majority classes (test sensitivity 80.77% and test specificity 86.96%).

2.7 Acknowledgment

We would like to thank Dr. Barrington and members of neonatology group of Mother and Child University Hospital Center in Montreal (QC) for their dedication of the collection of the Infant's cry data base. This research work has been funded by a grant from the Bill & Melinda Gates Foundation through the Grand Challenges Explorations Initiative.

CHAPITRE 3

SPLITTING OF GAUSSIAN MODELS VIA ADAPTED BML METHOD PERTAINING TO CRY-BASED DIAGNOSTIC SYSTEM

Hesam Farsaie Alaie, Chakib Tadj
Department of Electrical Engineering, École de Technologie Supérieure,
1100 Notre Dame West, Montréal, Québec, H3C 1K3, Canada

This article is published in "Journal of Engineering", volume 5, Pages 277-283
Received June 2013

Résumé

Dans cet article, nous utilisons la méthode boosting afin d'introduire un nouvel algorithme d'apprentissage pour GMM (Gaussian Mixture Models), appelé adapted Boosted Mixture Learning (BML). La méthode possède la capacité de corriger les problèmes existants dans d'autres techniques classiques pour estimer les paramètres GMM, due en partie à une nouvelle stratégie de mélange pour augmenter le nombre de gaussiennes. L'idée de la séparation discriminatoire est employée pour des densités de mélange de gaussiennes. Celle-ci est suivie par une étape d'apprentissage selon la méthode proposée. Ensuite, le classificateur de GMM est appliqué afin de différencier entre les nourrissons en bonne santé et ceux qui présentent une des pathologies étudiées. Chacun des deux groupes comprend à la fois des bébés prématurés et à terme. Chaque état pathologique est représenté par un modèle créé en utilisant la méthode adaptée BML et des vecteurs de 13 coefficients MFCC. Les résultats des tests démontrent que la méthode proposée pour entrainer les GGM a une meilleure performance que le système de référence utilisant un algorithme EM, (Expectation-Maximisation) pour la classification multi-pathologique.

3.1 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 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.

3.2 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 (Reynolds et Rose, 1995). The GMMs are estimated from available training data using a special case of the Expectation-Maximization (EM) algorithm based on the maximum-likelihood (ML) (Dempster, Laird et Rubin, 1977).A finite amount of sample data produces 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 (Heck et Chou, 1994). Performance degradation due to parameter estimation errors is a function of the number of free parameters in the classifier (Heck et Chou, 1994), 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 (Jun, Yu et Hui, 2011): 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 (Kim et Pavlovic, 2007; Pavlovic, 2004). 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 (Jun, Yu et Hui, 2011). In (Boyu et al., 2010) 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 (Heigold et al., 2011; Heigold et al., 2008), 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 (Bauer et Kohavi, 1999b) were examined for discriminating between normal and sick infant's cry signals (Amaro-Camargo et Reyes-García, 2007; Cano et al., 2006; Galaviz et García, 2005; Hariharan, Sindhu et Yaacob, 2012; Hariharan, Yaacob et Awang, 2011; Orozco et Garcia, 2003; Ortiz, Beceiro et Ekkel, 2004). In our previous work (Farsaie Alaie et Tadj, 2012), we

made use of cry signals to distinguish between healthy and sick infants both full-term and premature. Most of the previous studies (Amaro-Camargo et Reyes-García, 2007; Cano et al., 2006; Galaviz et García, 2005; Hariharan, Sindhu et Yaacob, 2012; Hariharan, Yaacob et Awang, 2011; Orozco et Garcia, 2003; Ortiz, Beceiro et Ekkel, 2004; Wasz-Hockert, Michelsson et Lind, 1985) 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 3.3 we give a brief review of GMM. Section 3.4 explains the different parts of introduced learning algorithm. In section 3.5, preprocessing steps and experiments are reported, and in section 3.6 a follow-up analysis of the results and a conclusion are presented at the end to finalize this paper.

3.3 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 $\lambda = [c_k, \mu_k, \Sigma_k]$ $k = 1, \dots, M$ as follows:

$$F_M(X|\lambda) = \sum_{k=1}^{M} c_k \mathcal{N}_k(X; \mu_k, \Sigma_k) \, , \sum_{k=1}^{M} c_k = 1 \tag{3.1}$$

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.

3.4 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 (Bishop, 2006; Duda, Hart et Stork, 2001). 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 (Jun, Yu et Hui, 2011). 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 c_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.

$$F_k(X) = (1 - c_k)F_{k-1}(X) + c_k\mathcal{N}_k(X) \tag{3.2}$$

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

$$\mathcal{C}(F_k) = \sum_{t=1}^{T} \log F_k(X_t) \tag{3.3}$$

where c_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.

$$\mathcal{C}((1-\varepsilon)F_k + \varepsilon\mathcal{N}_k) > \mathcal{C}(F_{k-1}) \tag{3.4}$$

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,

$$\langle P, Q\rangle = \frac{1}{T}\sum_{t=1}^{T} P(X_t)Q(X_t) \tag{3.5}$$

the optimal new component can be obtained by:

$$\mathcal{N}_k^* = \text{argmax}_{\mathcal{N}_k}\langle\nabla\mathcal{C}(F_{k-1}), (\mathcal{N}_k - F_{k-1})\rangle = \text{argmax}_{\mathcal{N}_k}\sum_{t=1}^{T}\frac{\mathcal{N}_k(X_t)}{F_{k-1}(X_t)} \tag{3.6}$$

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 (Jun, Yu et Hui, 2011). After estimating $\mathcal{N}_k^*$, the mixture weight c_k^* can be obtained by using the following line search:

$$c_k^* = \text{argmax}_{c_k\in[0,1]}\,\mathcal{C}((1-c_k)F_{k-1} + c_k\mathcal{N}_k^*) \tag{3.7}$$

3.4.1 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 $k = 1, \dots, K$. 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 framework is repeated as long as the added component causes an increase in the predefined objective function.

3.4.2 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.

$$\{\mathcal{N}_k^*, c_k^*\} = \underset{\mathcal{N}_k, c_k}{argmax}\ \mathcal{C}\left((1 - c_k)F_{k-1} + c_k\mathcal{N}_k\right) \tag{3.8}$$

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 (Jun, Yu et Hui, 2011):

$$w^n(X_t) = \frac{\mathcal{N}_k\left(X_t \middle| \Phi_k^{(n)}\right)}{{c_k}^n \mathcal{N}_k\left(X_t \middle| \Phi_k^{(n)}\right) + (1 - {c_k}^n)F_{k-1}(X_t|\Psi_{k-1})} \tag{3.9}$$

$$\gamma_t\left(\Phi_k^{(n)}\right) = \frac{w^n(X_t)}{\sum_{t=1}^{T} w^n(X_t)} \tag{3.10}$$

$${c_k}^{n+1} = \frac{1}{T}\sum_{t=1}^{T} {c_k}^n\, w^n(X_t) \tag{3.11}$$

$$\mu_k{}^{n+1} = \sum_{t=1}^{T} \gamma_t\left(\Phi_k^{(n)}\right).X_t \tag{3.12}$$

$$\Sigma_k{}^{n+1} = \sum_{t=1}^{T} \gamma_t\left(\Phi_k^{(n)}\right).(X_t - \mu_k{}^{n+1}) \times (X_t - \mu_k{}^{n+1})^{Tr} \tag{3.13}$$

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 $k = 1, \dots, K$ 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.

3.4.3 Initialization of sample weights

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

$$w^0(X_t) = 1/F_{k-1}(X_t|\Psi_{k-1}) \tag{3.14}$$

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 (Rosset, 2005) to overcompensate for the low probability by smoothing sample weights based on power scaling.

$$w^0(X_t) = (1/F_{k-1}(X_t|\Psi_{k-1}))^p, 0 < p < 1 \quad (3.15)$$

where p is a decay parameter or an exponential scaling factor. In the second method the idea of sampling boosting in (Freund et Schapire, 1997) 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 $\bar{M}$ and σ^2 denote the mean and variance of weights calculated in equation (3-15) as defined below.

$$\bar{M} = mean[log\, w^0(X_t)] \quad (3.16)$$

$$\sigma^2 = variance[log\, w^0(X_t)] \quad (3.17)$$

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

$$X_{sub} = \{X_t |\, log\, w^0(X_t) > \bar{M} + \beta\sigma\} \quad (3.18)$$

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 overfitting and these same parameter values which utilized for BML algorithm in (Jun, Yu et Hui, 2011).

3.4.4 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 Information Criterion (BIC). It can be represented as the following (Schwarz, 1978):

$$BIC(k) = -2 \times \mathcal{C}\,(F_k) + M_k\, log\, T \quad (3.19)$$

where $\mathcal{C}\ (F_k)$ 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 3.1 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.

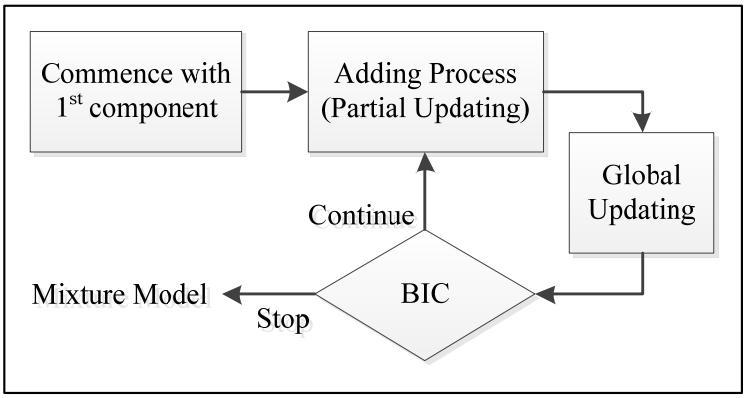
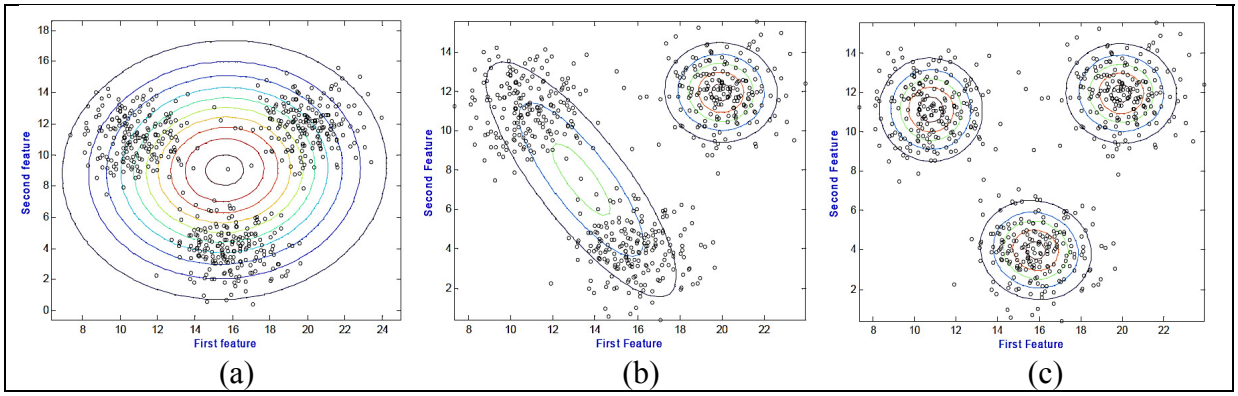


Figure 3.1 Block diagram of adapted BML technique

Figure 3.2 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 $2.7682 \times 10^3$and 2.7684×10^3 respectively.



(a) (b) (c)

Figure 3.2 Estimated contour (a) of the first Gaussian component, (b) after splitting GMM into 2 components, (c) of final GMM

3.5 Experiments

3.5.1 Preprocessing and feature 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 (Corwin, Lester et Golub, 1996; Wasz-Hockert, Michelsson et Lind, 1985) 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 3.1 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.

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 (Plumpe, Quatieri et Reynolds, 1999). This type of excitation source characteristics is one of the popular schemes in speaker recognition and identification systems (Longbiao et al., 2010; Murty et Yegnanarayana, 2006; Nengheng, Tan et Ching, 2007; Plumpe, Quatieri et Reynolds, 1999). It is common practice to pre-emphasis the signal prior to computing the speech parameters by applying the filter $P(z) = 1 - 0.97z^{-1}$ (Rabiner et Schafer, 1978; Young et al., 2006a). 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 msec (Benzeghiba et al., 2007; Huang, Acero et Hon, 2001a; Rabiner et Schafer, 1978).

Table 3.1 Cry database

Infants	State	Pathologies	Number
Fullterm	**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

3.5.2 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.

$$Pathology\ Class\ \# = \text{argmax}_j\ \mathcal{L}_j(X) \tag{3.20}$$

where $\mathcal{L}_j(X)$ shows the likelihood of a feature vector X given a Gaussian model λ_i for i^{th} pathology class. 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 (Zill, wright et Cullen, 2011):

$$CV = \frac{Standard\ Deviation}{Mean} \times 100\% \tag{3.21}$$

Due to space limitation, Table 3.2 shows only the results for two frame length (10 msec and 20 msec) as the most reliable results. Note that the states correspond to the order given in Table 3.1. 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 msec frame size had better final accuracy rate. Moreover, the larger the CV, the more the performance varies.

Table 3.2 Obtained accuracy rate (%) for multi-pathology classification 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

3.6 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 serves 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.

3.7 Acknowledgment

We would like to thank Dr. Barrington and members of neonatology group of Mother and Child University Hospital Center in Montreal (QC) for their dedication of the collection of the Infant's cry data base. This research work has been funded by a grant from the Bill & Melinda Gates Foundation through the Grand Challenges Explorations Initiative.

CHAPITRE 4

CRY-BASED INFANT PATHOLOGY CLASSIFICATION USING GMMS

Hesam Farsaie Alaie, Lina Abou-Abbas, Chakib Tadj
MMS Lab, Department of Electrical Engineering, École de Technologie Supérieure
1100 Notre Dame West, Montréal, Québec, H3C 1K3, Canada

This article is submitted to "Journal of Speech Communication" in January 2015

Résumé

Les études traditionnelles sur le cri des nourrissons se concentrent plutôt sur la classification basée sur des signaux non-pathologiques. Dans cet article, nous proposons un système non invasif, pouvant être intégré dans un système de soins de santé. Le système effectue l'analyse acoustique des signaux de cris bruités des nourrissons pour en extraire et mesurer quantitativement certaines caractéristiques et les classer comme étant en bonne santé ou pathologiques. Les coefficients MFCC, statiques et dynamiques sont extraits pour les deux vocalisations du cri : expiratoire et inspiratoire. Cette procédure a pour but de produire un vecteur caractéristique le plus discriminant et informatif. Ensuite, nous créons un modèle de cri unique selon le type de vocalisation et l'état pathologique. Ceci est réalisé en introduisant une nouvelle idée utilisant le méthode BML (Boosted Mixture Learning) pour obtenir des modèles de cris sains et pathologiques à partir d'un modèle universel GMM-UBM. Le système de diagnostic basé sur le cri du nouveau-né (NCDS) que nous proposons, fonctionne selon un système hiérarchique correspondant à une combinaison arborescente de classificateurs individuels. En plus, une fusion au niveau du score des sous-systèmes expiratoire et inspiratoire est réalisée rendant la prise de décision plus fiable. Les résultats expérimentaux indiquent que la méthode adaptée BML a des taux d'erreur inférieurs à ceux de l'approche bayésienne ou l'estimateur du maximum a posteriori (MAP).

Highlights

- We characterize the distributions of the acoustic features of infant cry signals with GMMs as a universal background model;
- An adapted BML method is presented to derive either healthy or pathology subclass models from the GMM-UBM;
- A score level fusion of obtained log-likelihood ratio scores from both expiratory and inspiratory sounds is performed;
- The proposed cry-based diagnostic system is used to classify healthy and sick infants;
- Subjective results indicated that the proposed method can perform better than Bayesian adaptation.

4.1 Abstract

Traditional studies of infant cry signals focus more on non-pathology-based classification of infants. In this article, we introduce a non-invasive health care system that performs acoustic analysis of unclean noisy infants' cry signals to extract and measure certain cry characteristics quantitatively and classify healthy and sick newborn infants according to only their cries. In the conduct of this newborn cry-based diagnostic system, the dynamic Mel-Frequency Cepstral Coefficients (MFCC) features along with static MFCCs are selected and extracted for both expiratory and inspiratory cry vocalizations to produce the most discriminative and informative feature vector. Next, we create a unique cry pattern for each cry vocalization type and pathological condition by introducing a novel idea using the Boosted Mixture Learning (BML) method to derive either healthy or pathology subclass models separately from the Gaussian Mixture Model-Universal Background Model (GMM-UBM). Our newborn cry-based diagnostic system (NCDS) has a hierarchical scheme that is a treelike combination of individual classifiers. Moreover, a score-level fusion of the proposed expiratory and inspiratory cry-based subsystems is performed to make a reliable decision. The experimental results indicate that the adapted BML method has lower error rates than the Bayesian approach or the maximum a posteriori probability (MAP) adaptation approach when considered as a reference method.

Keywords: Gaussian mixture model; Universal background model; Mel-frequency Cepstral Coefficient; Likelihood ratio scores; Newborn infant cries; Expiratory sound; Inspiratory sound.

4.2 Introduction

Crying is the first clear sign of life that is observed shortly after a baby's live birth. Although there have been some books and products that were created through the years to unlock the secret language of babies, their potential for use in the early diagnosis and treatment of newborns remains largely in an open and undeveloped state. The results of these studies highlight the existence of some cry attributes in sick infants that are rarely observed in the cries of healthy infants (Benson et Haith, 2009; Wasz-Hockert et al., 1968; Wasz-Hockert, Michelsson et Lind, 1985). Instead, these attributes occur frequently in the cries of sick infants who suffer from different medical diseases and conditions. Therefore, infant cry characteristics reflect the integrity of the central nervous system.

4.2.1 Early studies and birth defects

Many early researchers defined several cry characteristics and presented their common values, such as the fundamental frequency, formants, cry modes, cry latency, phonation, hyperphonation, and dysphonation (LaGasse, Neal et Lester, 2005; Lederman, 2002; Newman, 1985; Wasz-Hockert, Michelsson et Lind, 1985). Gradually, detailed acoustic analysis, which measures and compares the acoustical characteristics of newborn infant cry signals, shows hidden diagnostic potential of cry signals for the basic cry types and the cries of infants in pathological conditions such as with brain damage, central nervous system diseases and Down's syndrome (Michelsson, 1971; Michelsson et Michelsson, 1999; Partanen et al., 1967; Wasz-Hockert et al., 1968; Wasz-Hockert, Michelsson et Lind, 1985). It appears that some of the symptoms are not always recognized or even do not appear for months or years; thus, it might be too late for treatment after clinical symptoms start,

especially in countries that do not have well-established health services. As Figure 4.1 shows, congenital anomalies and preterm births were the dominant causes of approximately 2.7 million infants deaths in 193 countries in 2010 (Congenital anomalies, 2014). Statistical reports by the World Health Organization (WHO) (Congenital anomalies, 2014) and Center for Disease Control and prevention (CDC) (Update on overall prevalence of major birth defects—atlanta, georgia, 1978-2005, 2008) state that congenital anomalies or birth defects affect approximately 1 in 33 infants born every year. Moreover, in spite of the fact that the U.S. and Canada are highly developed countries, the results of an investigation of early infant mortality rates in 176 countries indicate that the U.S. and Canada had the 1st and 2nd worst rates in the developed world, respectively, by 2.6 and 2.4 first-day deaths per 1,000 births (SaveTheChildren, 2013). It is worthwhile mentioning that approximately 1 percent of the world's infant deaths occur in developed countries, and the situation is worse for many developing countries. However, it is easier to identify a baby who has structural problems such as cleft lip; on the other hand, symptoms of some defects might be invisible and hidden from sight. Therefore, we believe that by providing an inexpensive health care system that does not have complex and advanced technology for poor mothers with newborn babies in low-income countries, more babies can survive beyond the first months of life.

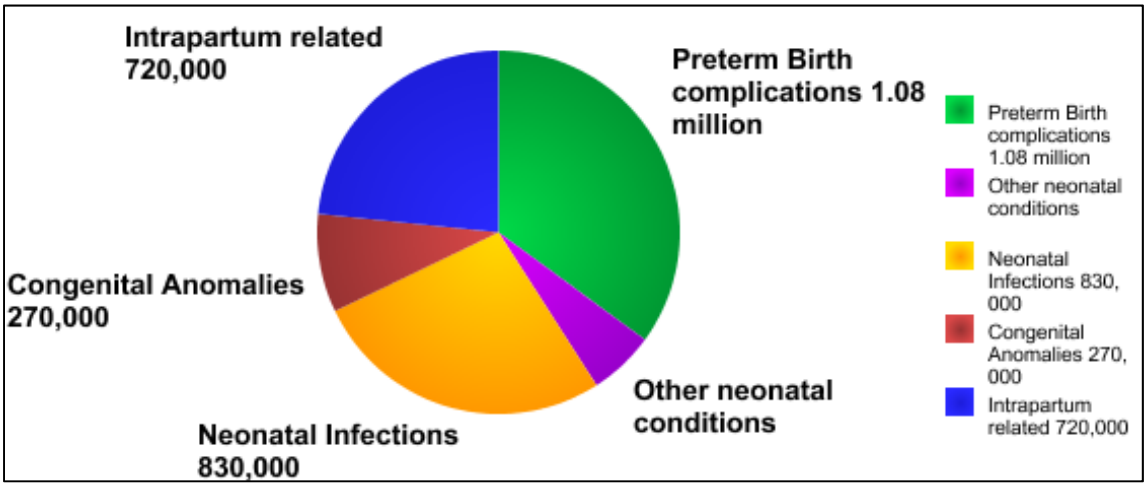


Figure 4.1 Leading causes of infant deaths in 193 countries in 2010
Adapted from Congenital anomalies (2014)

There are a substantial number of maternal and environmental issues that can raise the risks of several complications and associated anomalies, such as the gestational age, birth weight, consanguinity, maternal age, multiple gestations, and maternal infection during pregnancy, socioeconomic factors and maternal nutritional status. For example, the gestational age is a noteworthy predictor of infant health conditions within the normal range of 37-41 weeks for babies who are fully developed (full term). Premature birth, even only a few weeks early, increases the chance of birth defects or infant death in such a way that in the U.S., the 2010 mortality rate for very early preterm (under 32 weeks) births was 74 times worse than that of full-term infants (T.J. et F. MacDorman, 2013).

These official statistics can provide more information about the chance that an infant is born with a specific congenital disease, which is completely independent of the information in the infant cries. Moreover, there are other independent sources of information that are related to the physiological condition of the newborn infants that can be useful in a similar way in multimodal biometric systems, which use multiple independent sources of information and indeed provide a reliable system. However, in this article, we are curious about examining only the ability of information that is embedded in infant cries to differentiate between several pathologies in spite of the other sources.

This approach encouraged us to be ambitious and develop a newborn cry-based diagnostic system for the care of birth defects after birth by identifying some possible physiological disorders and birth defects. This early intervention can definitely save the lives of many infants and protect them from some physical, intellectual, visual or auditory impairment before severe disabilities might be caused.

4.2.2 Related studies

The leading role in the classification of the infant cry is how to scientifically discriminate between different neonatal health statuses, only on the basis of their cry signals besides the health examination of infants and other predictors of child health. In recent years, several machine learning and classification algorithms, such as artificial neural networks (Cano et al., 2006; Hariharan, Yaacob et Awang, 2011; Orozco et Garcia, 2003), radial basis function (RBF) networks (Cano Ortiz, Escobedo Beceiro et Ekkel, 2004b), support vector machines (SVMs) (Amaro-Camargo et Reyes-García, 2007), Naïve Bayes (Amaro-Camargo et Reyes-García, 2007), Genetic Selection of a Fuzzy Model (GSFM) (Rosales-Pérez et al., 2012) have demonstrated the ability to recognize cry patterns and make intelligent decisions based on the available training databases. It is worthwhile mentioning that it is sometimes not easy to collect a large number of samples to represent a general cry pattern. The failure to achieve the lowest possible error rate is the main drawback of having no acceptable cry database. For this reason, learning from a small, incomplete set of samples is of practical interest.

Finite mixture models is a flexible and powerful probabilistic tool for modeling univariate and multivariate data to perform modeling and classification tasks (McLachlan et Peel, 2004). In this article, we employ the Gaussian mixture model (GMM), which is a powerful model for representing almost any distribution. The Gaussian mixture model is computationally inexpensive and is based on a well-understood statistical model that can be viewed as a hybrid between a parametric and nonparametric density model. Moreover, there are many advantages that are claimed when using GMM as the likelihood function (Reynolds, Quatieri et Dunn, 2000). The expectation-maximization (EM) algorithm is a common method for maximum likelihood learning of finite GMMs; this approach has some advantages over other learning methods, such as a gradient-based approach (Xu et Jordan, 1996). In our previous studies (Farsaie Alaie et Tadj, 2012; 2013), we have introduced a working prototype to train a GMM in an incremental and recursive manner; this method is called the adapted boosted mixture learning Method (BML). The proposed method trains finite mixture models by a pool of Gaussian components using an extracted Mel-frequency

Cepstral Coefficients (MFCCs) feature stream, which includes both static and dynamic features. Partial and global updating methods are used in model parameter estimation processes to speed up the learning process and converge to a more robust and reliable estimation of a new mixture component. The selected strategy to stop the adding process is a criterion-based approach called Bayesian Information Criterion (BIC). We have shown that the proposed method has better performance than the traditional EM-based re-estimation algorithm as a reference system for the classification of the infant cry. In a binary classification task, the system discriminated a test infant's cry signal into one of two groups, namely, healthy and sick groups, based on MFCCs.

In this paper, we describe the development and evaluation of a Gaussian Mixture Model-Universal Background Model (GMM-UBM) system that is applied to an infant cry expiration and inspiration corpora for the enrolled health conditions. This newborn cry-based diagnostic system can be referred to as the GMM-UBM health-condition detection system. The remainder of this paper is organized as follows: In section 2, we present our cry database (CDB). Next, in section 3, the feature extraction procedure is explained. Section 4 presents our classification approach, and section 5 describes experiments and the results of each health-condition detector using our cry database. Finally, conclusions and future directions are presented in section 4.7.

4.3 Recording procedure and cry data base

The recordings were made in the neonatology departments of several hospitals in Canada and Lebanon. We performed the recording process by converting the analog cry signal to an uncompressed digital audio format that is suitable for storing an original recording in a wav file. Each infant's cry was recorded by an Olympus hand-held digital 2-channel recorder at a sampling frequency of 44.1 kHz and a sample resolution of 16 bits, placed 10-30 cm away from the infant's mouth. A neonatal intensive-care unit (NICU) is a special system of care for newborn infants who are sick or premature or generally need more medical attention due to

suffering from some congenital abnormalities. Occasionally, the cry recording process was performed with background noise or even with a constant noise from the care unit and from medical equipment that is connected to the infants who are in the NICU due to their prematurity or defects. Although the NICU should be a quiet environment for sleeping babies, in reality there is a large amount of unwanted noise from infusion pumps, monitors, ventilators, telephones and doors. Because we want to develop a system that does not need complex and advanced technology and, thus, can be used by poor mothers with newborn babies in low-income countries, soundproof rooms or units were not used to record the cry signal to obtain the best signal-to-noise ratio that could otherwise be achieved. Each recorded infant's cry signal, even a healthy infant who is not completely clean, is manually segmented into 13 units or classes, which are defined and labeled in Table 4.1.

Table 4.1 Different units available in the CDB

Labels	Definitions
EXP	Voiced expiration segment during a period of cry
EXPN	Unvoiced expiration segment during a period of cry
INS	Unvoiced inspiration segment during a period of cry
INSV	Voiced inspiration segment during a period of cry
EXP2	Voiced expiration segment during a period of pseudo cry
INS2	Voiced inspiration segment during a period of pseudo cry
PSEUDOCRY	Any sound generated by the baby and it is not a cry
Speech	Sound of the nurse or parents talking around
Background	Kind of noise so low, it is characterized by a very low power-silence affected with little noise.
Noisy Cry	Any sound heard with the cry e.g. machine's bip, water, diaper etc….
Noisy pseudo cry	Any sound heard with the pseudo cry
Noise	Like the sound caused by the mic moved by someone, the diaper, a door sound, speech + background, speech + bip.
BIP	sound of the medical instruments next the baby

The case subjects for this study were infants selected from 1 to 53 days old, comprising healthy and sick full-term babies. For each infant, there are three recording files, with the average duration of 90 seconds for each continuous file. Useful information such as the date of birth were recorded along with the following pertinent information: weight, gender, maturity, race, ethnicity, gestational age, known and detected diseases, APGAR result, date and time of each cry recording and the reason for the crying (such as pain, hunger, diaper change, birth cry, medical exam).

We divided the available health conditions in our CDB into different categories listed in Table 4.2. The reason for the cry is not considered in the selected samples, in contrast to previous studies that used only the pain cry (Partanen et al., 1967).

Table 4.2 List of health-conditions

Categories	Describtion
Healthy infants	Fullterm infants without any major disorder or sickness
Heart problems	Fullterm infants suffering from Tetralogy of Fallot, thrombus, complex cardio or congenital heart diseases.
Neurological	Fullterm infants suffering from Sepsis or Meningitis.
Respiratory distress	Fullterm infants suffering from Respiratory distress or Asphyxia diseases.
Blood abnormalities	Fullterm infants suffering from Hyperbilirubinemia or Hypoglycemia diseases.
Other	Fullterm infants suffering from other abnormalities or physical problems which are not in priority order for our system.

4.4 Feature extraction

Usually, in human speech signals, there are low-level and high-level cues that can be used to recognize different speakers; these cues are related to the acoustic and semantic or linguistic

aspects of speech. The human auditory system uses different levels of information, in contrast to automatic systems, which depend still on low-level acoustic information.

The major challenges of having a higher level of information derived from a cry signal are to find and extract some features in such a way that they convey distinctive information from the cry signal; this approach has been under study in recent years (Kheddache, 2014). In this article, MFCCs are selected to be extracted as features that represent the cry signals because they have good performance among various types of speech applications (Deller, Proakis et Hansen, 1993; Quatieri, 2002). Note that the same basic model of speech production (Deller, Proakis et Hansen, 1993) in adults is used to find these measurements. Thus far, it has been shown that they are also effective in classifying healthy and sick infants based on our primary results (Farsaie Alaie et Tadj, 2012). Moreover, we incorporate context information by adding dynamic features in the second step, but they are not necessarily the most informative features for the intended pathology classification task.

4.4.1 Preprocessing stages

To increase the accuracy and reliability of the MFCC feature extraction process, cry signals are pre-processed in 3 simple steps:

1. Convert stereo channel to mono channel

In the data collection step, because we have used a 2-channel recorder, we must average the channels first and then convert the signal into a single-channel signal using a mean value function.

2. Pre-emphasization

Similar to in a speech recognition system, we used a first-order high-pass FIR filter to pre-emphasize the signal due to the high dynamic range of the digitized cry waveform, such as in

a speech waveform. The main reason for using this filter is to compensate the spectral effect of the glottal source by introducing a zero near $z = 1$ (Deller, Proakis et Hansen, 1993). Therefore, the filter $P(z) = 1 - 0.97z^{-1}$ (Rabiner et Schafer, 1978; Young et al., 2006a) should be applied prior to deriving the features or characteristics that correspond to the vocal tract only.

3. EXP/INSV detection

Although a cry is defined as the expiratory phase of respiration with sound or phonation by the larynx, which contains the vocal cords or folds and the glottis (LaGasse, Neal et Lester, 2005), here the input that is given to our cry-based diagnostic system (cry pathology classifier) represents a processed version of one or more voiced expiration (EXP) or inspiration (INSV) segments of cry utterances called feature vectors. Therefore, after segmentation and labeling, only the EXP and INSV segments of the cry signals are selected for the feature extraction procedures. The system has been built manually by trained experts so far, but we are working on automatic segmentation of recorded cry signals that can act instead of voice activation detection (VAD) in speech recognition systems.

4.4.2 Static and dynamic MFCCs

Briefly, the cry signals are pre-processed to be prepared for short-term processing, and then, the feature extraction procedure is applied, including MFCCs, delta and delta-delta coefficients. Generally, all of the conventional analysis techniques used in the signal processing application work with short-term frames of signals with non-stationary dynamics, such as human speech. Therefore, even in our case in point, it is our duty to select a reasonable portion of the cry signal in such a way that it does not change statistically. Frames are commonly 10-30 msec in duration, to be statistically stationary with a good tradeoff between the frequency and time resolutions in applications that use speech signals. In this article, feature extraction was performed by using two different frame durations, 10 and 30, with the same overlap percentage (30%) between two consecutive windows, to find a good tradeoff between the frequency and time resolution of the cry signals and to assess what

improvements it might have. After framing and prior to any frequency analysis, the hamming windowing has been applied to split the frames to reduce any discontinuities at the edges of the selected region. In human speech signals, there is not much information above 6.8 kHz. The cumulative power spectrum is used here to detect the upper cutoff frequency of the efficient frequency band of the cry signal, where the power almost stops to increase. The results of our experiments depicted in Figure 4.2 demonstrate that the cry signals of full-term healthy and sick infants have almost 94% and 98% of their energies below 4 kHz and 6.8 kHz respectively. The results depicted in Figure 4.2 also indicate that the energies of the inspiration segments for sick infants tend to accumulate at a slower rate than the energies of the expiration segments, especially in cases of RDS disorders. Thus far, information up to a 4 kHz bandwidth has been used, but we plan to conduct pioneering research on the aforementioned upper frequency band.

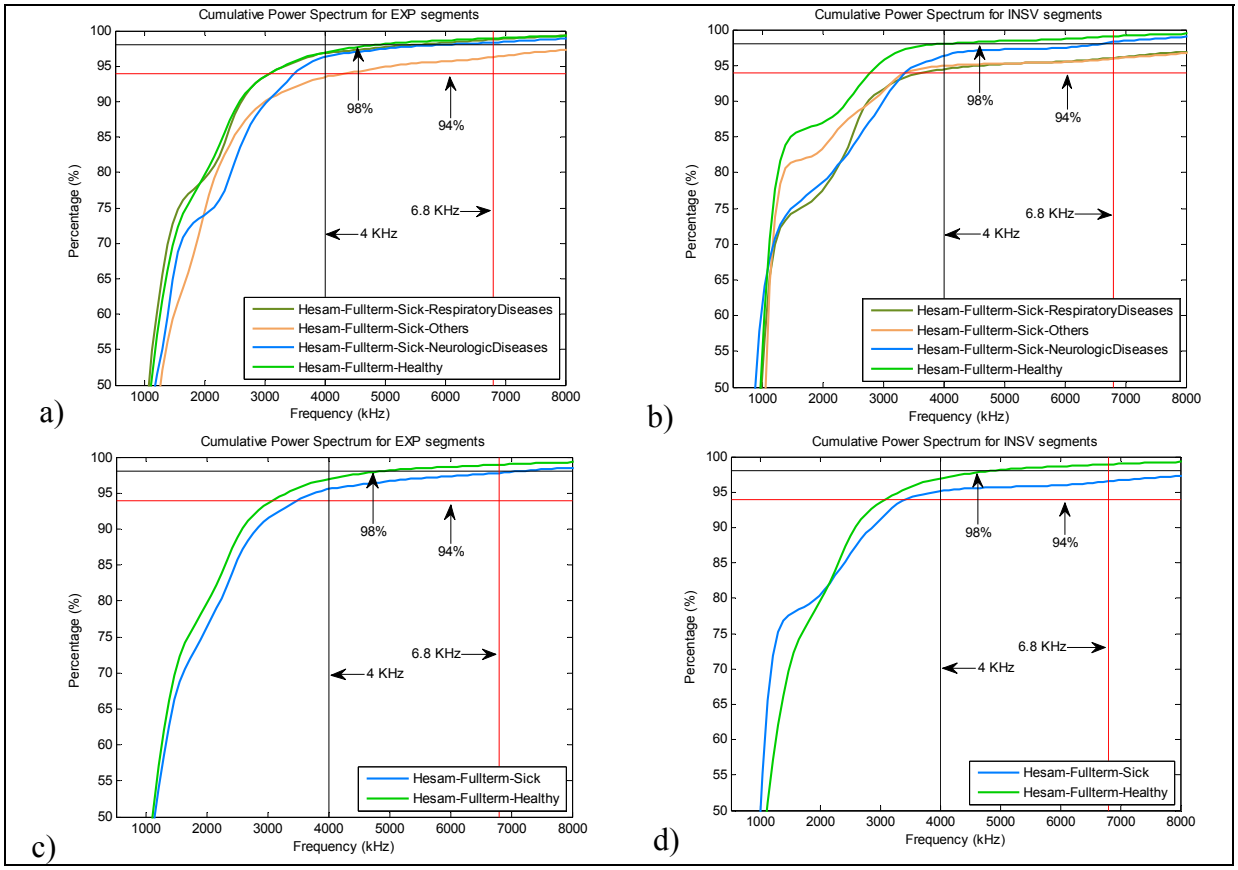


Figure 4.2 Cumulative power spectrum of (a-c) EXP units, (b-d) INSV units for each health condition

In brief, the feature extraction phase for both the INSV and EXP segments can be performed in two stages:

1. Reduce the dimensionality by Cepstral analysis and extract the first 12 MFCCs computed from 24 filter banks plus the energy feature.

MFCCs are introduced by Mermelstein in (Davis et Mermelstein, 1980) as the DCT of the log-energy output of the triangular band pass filters. To extract the MFCCs, first the fast Fourier Transform (FFT) is performed to obtain the magnitude frequency of each windowed frame, and then, the MFCCs are calculated by converting the log Mel spectrum back to the time domain using the discrete cosine transform (DCT):

$$C_i = \sum_{k=1}^{K} S_k \cos[i(k - \tfrac{1}{2})\tfrac{\pi}{K}], i = 1,2, \dots, M \quad (4.1)$$

where K is number of subbands (filter banks) (which is 24 for our selected bandwidth (Reynolds, 1995a)), M is the desired length of the cepstrum, and S_k represents the log-energy output of the kth triangular band pass filter. Figure 4.3 indicates all of the 3 pre-processing steps followed by the aforementioned MFCC extraction procedure in stages.

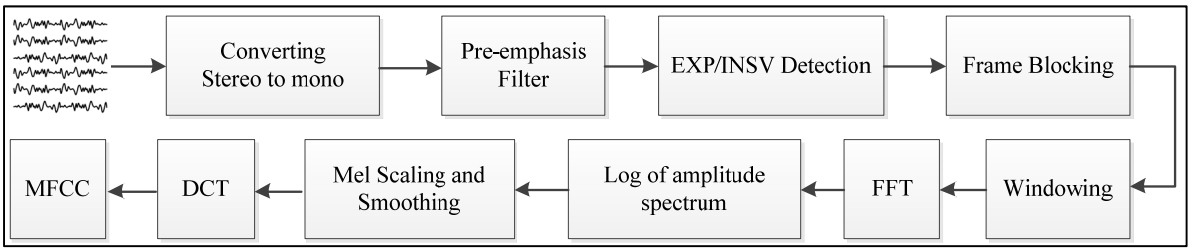


Figure 4.3 Pre-processing and MFCC feature extraction steps

2. Add dynamic features by taking the first and second derivatives of the obtained 13-static features, called the delta and delta-delta (acceleration) coefficients.

The first time derivation of the basic static parameters (referred to as delta coefficients) can be calculated over a limited window, as follows (Young et al., 2006a):

$$D_n = \frac{\sum_{\theta=1}^{\Theta} \theta(C_{n+\theta} - C_{n-\theta})}{2\sum_{\theta=1}^{\Theta} \theta^2} \tag{4.2}$$

where D is a delta coefficient at the discrete time n, and C_i shows the static parameters. Because the equation depends on both the past and future static parameters $C_{n\pm\theta}$, to avoid having a problem with the regression window at the beginning and end of the static parameters, usually replication of the first and last parameters is required. The same formula is applied to the calculated delta coefficients to compute the second derivation of the static parameters (referred to as the acceleration coefficients). After appending the delta and acceleration coefficients to the static MFCC parameters, the set of 39-length feature vectors extracted from each single windowed frame cry is denoted x_t, where t shows the sequence index. Therefore, a cry signal can be displayed by the sequence of feature vectors x_t running up to the end of the signal, with T feature vectors $X = (x_1, \dots, x_t, \dots, x_T)$.

4.5 Statistical modeling and descriptions

There is a minor difference between detection and identification systems in a decision process, while both use the same base of information. It has been shown that identification occurs inside of a detection task in some sense anyway, and their performances change together in the same way (Thomas, 1985). We are seeking to introduce a cry-based identification system to classify the presented infant as having one of the specified health conditions, but in this paper, detection is measured by the ability of our classifier to distinguish between an infant with the specified health condition and an infant with the other conditions listed in Table 4.2 as preliminary stages.

4.5.1 Likelihood ratio detector

In an ideal case and with well-defined models for all newborn infant pathologies and health conditions, the defined classification problem is similar to the canonical language recognition problem (Brummer, 2010) with the closed-set of specified languages. Similar to speaker identification systems that are intended for a 1:N match, the voice is compared against N speaker models $(\lambda_1, \lambda_2, \dots, \lambda_N)$, where λ_i represents the parameters of the i^{th} speaker model. This system can be presented by a maximum likelihood classifier whose objective is to select the speaker model that has the maximum a posteriori probability (MAP) for the observation vector sequence $X = (x_1, \dots, x_t, \dots, x_T)$. The decision can be presented by the minimum-error Bayes' rule, as follows:

$$\text{Matched Speaker Index} = \arg\max_{1 \le i \le N} Pr(\lambda_i|X) = \arg\max_{1 \le i \le N} \frac{p(X|\lambda_i)Pr(\lambda_i)}{p(X)} \qquad (4.3)$$

You can also make an assumption on the prior probability of each speaker to simplify the approach. This assumption is called the assumption of equal prior probabilities of speakers, which results in making the decision formula as follows:

$$\text{Matched Speaker Index} = \arg\max_{1 \le i \le N} \mathrm{p}(\mathrm{X}|\lambda_\mathrm{i}) = \arg\max_{1 \le i \le N} \sum_{t=1}^{T} \log \mathrm{p}(\mathrm{x_t}|\lambda_\mathrm{i}) \qquad (4.4)$$

In verification systems, the task is a 1:1 match, which is in marked contrast to the identification system. For example, in speaker verification systems, the objective is to determine if the observed input X is from the hypothesized speaker (hypothesis H_0) or not (hypothesis H_1). The likelihood ratio detector has been accepted as a general approach in the speaker verification system (Reynolds, Quatieri et Dunn, 2000). Assume that H_0 and H_1 hypotheses are represented by models λ_{Hyp} and $\lambda_{\overline{Hyp}}$, respectively; it calculates the ratio of the posterior probabilities of the two hypotheses:

$$\frac{Pr(\lambda_{Hyp}|X)}{Pr(\lambda_{\overline{Hyp}}|X)} \tag{4.5}$$

Bayes' rule provides a shortcut for calculating the likelihood ratio in the log domain by ignoring constants that result in the log-likelihood ratios of H_0 and H_1, as follows:

$$\Lambda(X) = \log p(X|\lambda_{Hyp}) - \log p\left(X|\lambda_{\overline{Hyp}}\right) \underset{reject\ H_0}{\overset{accept\ H_0}{\gtrless}} \theta \tag{4.6}$$

where θ is a threshold that adjusts the trade-off between two types of error, false acceptance and false rejection. Although the claimed speaker has a well-defined model in such a system, the corresponding alternative models are ill-defined. This issue poses a challenge to create $\lambda_{\overline{Hyp}}$ in such a way that presents the entire space of possible alternatives to the hypothesized speaker. In general, two main approaches have been described in (Reynolds, Quatieri et Dunn, 2000) to model $\lambda_{\overline{Hyp}}$. Because we used both techniques in our cry-based diagnostic pathology system, we describe both of them briefly below.

1. Background Speaker Models

In this approach, the set of speaker models excluding the hypothesized speaker have been selected and combined to model the alternative hypothesis. There has been a large amount of research into background speakers (Higgins, Bahler et Porter, 1991; Matsui et Furui, 1994; Reynolds, 1995b; Rosenberg et al., 1992). Given B equally likely background speakers, which are represented by $(\lambda_1, \lambda_2, \dots, \lambda_B)$, the log-likelihoods of the hypothesized speaker and alternative hypothesis (background speakers) are computed as (Reynolds, 1995b)

$$\log p(X|\lambda_{Hyp}) = \frac{1}{T}\sum_{t=1}^{T} \log p(x_t|\lambda_{Hyp}) \tag{4.7}$$

The $1/T$ factor is used to normalize the duration effect in the log-likelihood. Note that by ignoring the $1/T$ factor, the likelihood of the background speakers can be observed as the joint probability density of the observation X arising from one of the B background speakers:

$$\log p(X|\lambda_{\overline{Hyp}}) = \log(\frac{1}{\mathrm{B}}\sum_{\mathrm{b}=1}^{\mathrm{B}} \mathrm{p}(\mathrm{X}|\lambda_{\mathrm{b}})) \tag{4.8}$$

where $p(X|\lambda_b)$ is computed as in Equation 4.7. The main drawback of this approach is preparing a background speaker set for each hypothesized speaker, which can be a problem for applications that have a large number of hypotheses.

2. Speaker-Independent Model

This technique (Matsui et Furui, 1995; Reynolds, 1997) attempts to pool training samples from a large number of speakers, to represent the population of speakers by a single speaker-independent model; this model is currently known as a universal background model (UBM). A Universal Background Model (UBM) is a world model that is used mostly in biometric verification systems to represent general feature characteristics (Reynolds, 2009). Specifically, the universal-background model-based GMM or GMM-UBM has a large amount of success in statistical modeling techniques for speaker recognition and language recognition systems (Reynolds, Quatieri et Dunn, 2000), and in contrast to previous approaches, a trained UBM can be used for all hypothesized speakers in the task.

4.5.2 Gaussian mixture models

The GMM modeling technique is simple but effective due to its remarkable ability to form smooth approximations from any arbitrarily shaped data distribution. It has been a success as a statistical model in different applications and systems, most notably in speaker recognition and speaker identification systems (Reynolds et Rose, 1995) due to its ability to model the

underlying data classes or distributions of acoustic observations from a speaker. The likelihood function of a GMM used for a *D*-dimensional feature vector, *x*, is a weighted sum of K unimodal Gaussian components, $f_i(x)$, each parameterized by a mean $D \times 1$ mean vector (μ_i) and a $D \times D$ covariance matrix (Σ_i), as given by the equation

$$F(x|\lambda_K) = \sum_{i=1}^{K} c_i f_i(x) = \sum_{i=1}^{K} c_i \mathcal{N}(x|\Phi_i) = \sum_{i=1}^{K} c_i \mathcal{N}(x|\mu_i, \Sigma_i) \tag{4.9}$$

where λ_K represents the GMM parameters and consists of K components with the restriction that the mixture weights must satisfy the following two constraints: $c_i \geq 0$ for $i = 1, \ldots, K$ and $\sum_{i=1}^{K} c_i = 1$. The i^{th} component can be written in the following notation:

$$\begin{aligned} f_i(x) &= \mathcal{N}(x|\Phi_i) = \mathcal{N}(x|\mu_i, \Sigma_i) \\ &= \frac{1}{(2\pi)^{\frac{D}{2}}|\Sigma_i|^{\frac{1}{2}}} \times exp\left(-\frac{1}{2}(x-\mu_i)^{Tr}{\Sigma_i}^{-1}(x-\mu_i)\right) \end{aligned} \tag{4.10}$$

where $\Phi_i = (\mu_i, \Sigma_i)$ are the parameters for the i^{th} Gaussian density, and A^{Tr} represents the transpose of matrix A. Collectively, a GMM can be denoted by its parameters as $\lambda_K = (c_i, \Phi_i, i = 1, .., K)$.

4.5.3 System description

The proposed diagnostic system is built around the likelihood ratio test for detection by using GMMs for likelihood functions and GMM-UBM models to derive speaker models from the related world models. In the related literature, the common method to derive speaker models is called Bayesian learning or the MAP estimation method (Duda et Hart, 1973; Gauvain et Chin-Hui, 1994; Reynolds, Quatieri et Dunn, 2000). In our NCDS, the UBM is a health-independent GMM that is trained with cry samples from the available training CDB that contains full-term healthy and sick infants with specific diseases, to represent the general cry feature characteristics. Then, we employed the adapted BML method to adapt the UBM to a

target or specific class. We will show that this approach improves the performance of our classifier in comparison to our reference system, which uses Bayesian adaptation.

The first part of our system acts as a verification system for healthy infants, while distinguishing between healthy infants and sick infants. The goal here is to determine whether the infant is healthy or not; in the case of unhealthy, the second part should act as an identification system because the cry signals of the sick infants are assumed to be from the predefined set of known sicknesses. The winner sickness best matches the test infant's cry signal model in a known group of diseases. This sickness identification system involves only the aforementioned enrolled sicknesses and not all of the newborn illnesses. In the closed-set case, $(N_1, N_2, \dots, N_L)$ represents L different infant sicknesses, which have well-defined statistical models. In the second scenario, which is called the open-set, the same $(N_1, N_2, \dots, N_{L-1})$ are specified sicknesses, and N_L denotes any of the unseen out-of-set sicknesses. Therefore, we created a class called "others" or "none-of-the-above" in the target set of diseases. The state-of-the-art infant's cry-based health care system has a hierarchical scheme that is composed of two subsystems that are both based on an acoustic approach. Individual scores for expiration-based and inspiration-based experts are fused together to exploit the complementary information that can be represented by our health care system defined over the features extracted from two different types of corpora.

The crux of the design is how we fuse subsystems into a single effective system. Our cry-based multi-class recognition system has a hierarchical scheme that is a treelike combination of individual classifiers in serial and parallel modes. We used the ability of the serial mode to narrow down the health condition of the infants to one of two possibilities, such as the biometric identification system introduced in (Hong et Jain, 1998). This approach means that in the first step, the two-class pattern recognizer should make the decision as to which proposition should be eliminated, healthy or sick infants. For healthy infants, the decision process should be stopped at this stage before using all of the remaining classifiers that can reduce the overall recognition time. Then, in the case of sick infants, two individual pattern

recognizers in a parallel mode of operation should arrive at a final decision on the pathological condition of the test infant. In case the accuracy of the final decision on the most likely disease was called into doubt, there is another class called *others* that corresponds to infants that do not have the considered diseases or those for which we need more recorded cry signals for more examination.

The proposed detection system works in two phases, which are called training and runtime test. In the first phase, labeled cry corpora are analyzed and used to train the corresponding model. Each model should represent some health-dependent characteristics of the training data. In the test phase, the presented cry sample goes through the same process as in the training phase (the preprocessing and feature extraction steps), and then, for both the expiration and inspiration corpora of the sample, the log-likelihood ratio to the hypothesized model is calculated. In the decision stage of the system, we use different methods (SVM, PNN, and MLP) to fuse these scores to improve the performance of the classifier.

4.5.4 Applying the GMM-UBM

In this article, we defined and trained two GMM-UBMs for each corpora (EXP and INSV), based on the health conditions; the first one is a single health-independent background model trained to represent the distribution of the extracted cry features, regardless of what condition the infant might have (healthy or sick), and the second one is a pathology-independent background model that attempts to model cry features from all of the sicknesses that are available in our CDB. Because we focus our attention on full-term healthy and sick newborn infants that have specific diseases, we train the UBM to be used for the classification of healthy and sick infants using only corresponding data that are reflective of the expected alternative cry to be encountered during recognition. For example, in this case, it is known a priori that the cry signal belongs to a full-term infant, and thus, the full-term test infant will only be classified against full-term infant cries. This approach applies to both the gestational age of the infants and the types of diseases that are considered in our case.

For both the EXP and INSV models, the cry signals from subpopulations (healthy and sick infants with selected diseases) are pooled prior to training the UBM. We exploit a portion of each subpopulation within the available data in such a way that we create a balanced training database over the subclasses for each of the predefined UBMs (see Figure 4.4). This approach can help us to avoid obtaining the biased UBM toward the dominant subpopulation which is healthy infants in our CDB.

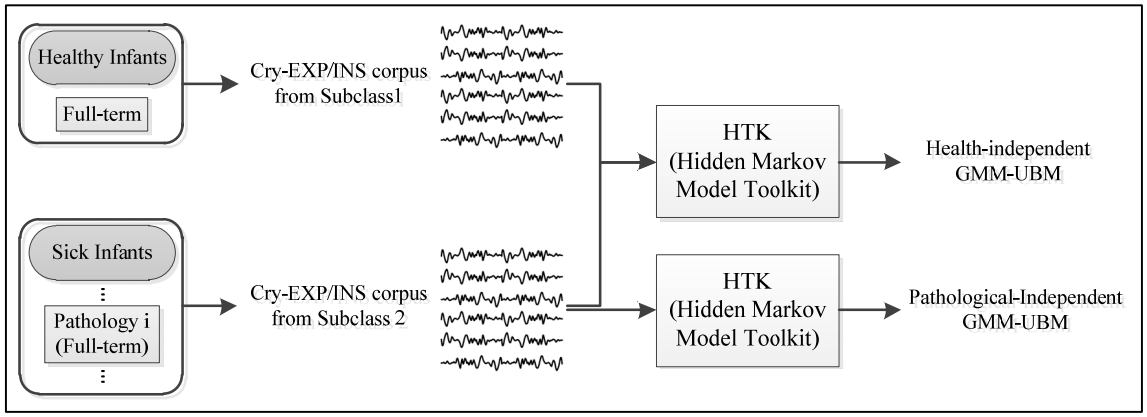


Figure 4.4 Balanced data pooling approaches for two defined GMM-UBM

Table 4.3 provides an overview of the number of recorded cry signals from newborns and the overall data duration within the original and balanced CDB. Note that unused training cry signals available in the CDB within the healthy and sick classes were employed to derive the hypothesized model by adaptation of the infant cry model. Similar to in speaker verification, there is no objective measure to determine the correct number of infants or the duration of the cry signal to train a UBM. It is worthwhile recalling that the procedure for the data collection is still in progress; thus, we used all of the data that was available at the time for training each model and, then, the incoming data for the test and evaluation process.

Prior this work, we introduced the Adapted BML (Farsaie Alaie et Tadj, 2012) method to estimate mixture model parameters; this approach has better performance than the conventional EM-based re-estimation algorithm as a reference system for the GMM training step. The Adapted BML has several advantages over the mentioned reference system, but the

distinct advantage is that it estimates the optimum number of components by iteratively adding new components in the direction that largely increases the predefined objective function. There is no guarantee that increasing the number of components in a GMM trained by HTK provides better system accuracy (Dobrovic et al., 2012), although the EM algorithm (Dempster, Laird et Rubin, 1977) iteratively re-estimates the GMM parameters to monotonically increase the likelihood of the model for the vector of observations, in contrast to the adapted-BML, in which each new added component brings improvement in the predefined objective function. Despite this option, in the preliminary stages of our cry-based diagnostic system, the building or training phase of the defined GMM-UBMs has been performed based on the HTK (Hidden Markov Model Toolkit) software tool, which is an established tool of speech recognition systems based on hidden Markov models (Young et al., 2006a). In the training procedure, we substitute diagonal covariance matrices for the full covariance matrices due to its computational efficiency because a diagonal covariance GMM with order $K > 1$ can model distributions of feature vectors with correlated elements. Then, in the next step, we used the adapted version of the parameter updating procedure described in (Farsaie Alaie et Tadj, 2012) to adapt UBM to create specific health condition models.

4.5.5 BML adaptation of sub-models or health-dependent-infant cry model

As mentioned earlier, there is a common technique called Bayesian adaptation (Duda et Hart, 1973; Gauvain et Chin-Hui, 1994) for deriving the hypothesized speaker model from GMM-UBM. Here, we introduce a new way of updating the GMM-UBM parameters based on the infant cry signals from related subclasses. In fact, a part of this adaptation technique was introduced earlier in (Farsaie Alaie et Tadj, 2012; Jun, Yu et Hui, 2011) as partial and global updating in Boosted mixture learning (BML) of GMM and HMM-based acoustic models. Specifically, we use the concept of boosting to refine the UBM parameters using the training cry signals of a specific health condition.

Table 4.3 Number and duration of the recorded cry signals that were available in the training CDB at the time

Class	Number of Infants	Number of Cry Signals in Training CDB	Overall length of training CDB	
			INSV	EXP
Healthy Infants	58	142	12’4’’	92’3’’
Sick Infants	25	66	3’53’’	41’25’’
Heart	4	12	34’’	5’4’’
Neurological	5	11	51’’	8’2’’
Respiratory	10	27	1’08’’	17’
Blood	3	9	36’’	5’06’’
Others	3	7	43’’	4’5’’
(a) Training cry database (CDB)				
Class	**Number of Infants**	**Number of Cry Signals in balanced Training CDB**	**Overall Length of balanced CDB**	
			INSV	EXP
Healthy Infants	39	53	2’40’’	25’25’’
Sick Infants	22	54	3’03’’	26’06’’
Heart	4	12	34’’	5’40’’
Neurological	5	9	34’’	5’30’’
Respiratory	7	17	35’’	4’49’’
Blood	3	9	36’’	5’06’’
Others	3	7	43’’	4’50’’
(b) Training balanced cry database				

As mentioned earlier, we created the UBMs with a known number of mixtures, K, with the model parameters $\lambda_K = (c_i, \Phi_i, i = 1, .., K)$, using the HTK software tool. To adapt the UBM, the statistics and sample weights, $W(x_t)$, of each subclass training data are calculated for each mixture, f_k, in the UBM. Then, they are used to refine the corresponding mixture parameters, Φ_k, and mixture weights, c_k, iteratively, while F_{K-1} are assumed to be constant.

By applying the EM algorithm to optimize the log-likelihood of the model for the vector of observations only with respect to the mixture component f_k, the iterative formula can be derived to adapt the model parameters. The adapted parameters, $\hat{\lambda}_K = (\hat{c}_i, \hat{\Phi}_i, i = 1, .., K)$, can be estimated in the $(n+1)^{th}$ equation as follows:

$$w^n(X_t) = \frac{f_k\left(X_t \middle| \Phi_k^{(n)}\right)}{c_k{}^n f_k\left(X_t \middle| \Phi_k^{(n)}\right) + \left(1 - c_k{}^n\right) F_{k-1}\left(X_t \middle| \lambda_{k-1}\right)} = \frac{f_k\left(X_t \middle| \Phi_k^{(n)}\right)}{F_k\left(X_t \middle| \lambda_k\right)} \tag{4.11}$$

$$\gamma_t\left(\Phi_k^{(n)}\right) = \frac{w^n(X_t)}{\sum_{t=1}^{T} w^n(X_t)} \tag{4.12}$$

$$\hat{c}_k{}^{n+1} = \frac{1}{T}\sum_{t=1}^{T} \hat{c}_k{}^n w^n(X_t) \tag{4.13}$$

$$\hat{\mu}_k{}^{n+1} = \sum_{t=1}^{T} \gamma_t\left(\Phi_k^{(n)}\right).X_t \tag{4.14}$$

$$\hat{\Sigma}_k{}^{n+1} = \sum_{t=1}^{T} \gamma_t\left(\Phi_k^{(n)}\right).\left(X_t - \hat{\mu}_k{}^{n+1}\right)\left(X_t - \hat{\mu}_k{}^{n+1}\right)^{Tr} \tag{4.15}$$

in which the UBM parameters are used as an initial point. The adaptation procedure is performed in such a way that mixtures with a high count of subclass training data concentrate more on these examples, and vice versa. In other words, due to the existence of f_k in the numerator and F_{K-1} in the denominator of the weight samples equation, the observations that have lower probabilities by the F_{K-1} model are given larger weights than those that have higher probabilities. It is worthwhile mentioning that the first part of the denominator can reduce the probability of the case in which f_k is dominated by a few samples. Moreover, sample weights in the updating mixture weights formula act as a tuning parameter, which helps to rectify the mixture weights iteratively by determining the ability of each mixture component to model the subclass training samples.

In comparison to the clear coupling method presented in Bayesian adaptation (Gauvain et Chin-Hui, 1994; Reynolds, Quatieri et Dunn, 2000), the BML adaptation can be observed as an indirect or hidden coupling between both the mixture weights and the parameters of the

adapted model and UBM. Note that in the Bayesian method, there are relevant factor and adaptation coefficients (Reynolds, Quatieri et Dunn, 2000) that control the balance between the old and new estimates.

4.6 Evaluations and experiments

4.6.1 Defining GMM-UBM and adaptation methods

Specifically, we created two health-independent UBMs by training 875 and 92 mixture GMMs with pooled healthy and sick data, from the balanced database (see Table 4.3) for the EXP and INSV models, called $\lambda_{HI-UBM-EXP}$ and $\lambda_{HI-UBM-INSV}$, respectively. Then, two pathology-independent UBMs that included 443 and 51 mixture GMMs were trained by only sick data for the EXP and INSV models, calle $\lambda_{PI-UBM-EXP}$ and $\lambda_{PI-UBM-INSV}$, respectively. We selected the number of mixtures based on the created UBM in the 1999 NIST SRE, which is a combination of 1024 mixture GMMs from using one hour of speech per gender (Reynolds, Quatieri et Dunn, 2000). Healthy and sick or pathology models are derived from λ_{HI-UBM} health-independent UBMs. Then, for each sickness that was available in CDB, the pathology-dependent model is trained from λ_{PI-UBM}, where the remaining utterances or unused CDBs in training the GMM-UBMs have been exploited to adapt a corresponding dependent model via a different adaptation procedure, as follows:

1. MAP or Bayesian adaptation that adapts only the mean vectors – This approach has the best performance among all of the combinations of parameter adaptations for a speaker verification system (Reynolds, Quatieri et Dunn, 2000). Moreover, it was mentioned that adapting the weights by MAP for known reasons degrades the overall performance.

2. BML adaptation method for refining the mean and variance vectors.

3. Coupling old and BML adaptation estimates over the mean and variance vectors – We compute new statistics for the parameters based on the BML model estimates, and we use a single adaptation coefficient for both the mean and variance parameters $\alpha_i = \frac{n_i}{n_i+r}$ with the relevant factor $r = 16$ to control the balance, which is the same as in Bayesian adaptation.

4. BML adaptation method for refining only the mean vectors.

It is obvious that while adapting λ_{PI-UBM} UBM to derive the GMM models for two pathological conditions namely heart and blood disease, we utilized the same training data as was used in HTK for training λ_{PI-UBM} UBM, while for other diseases we used unseen data that remained in our CDB.

4.6.2 Log-likelihood score computation

We applied the idea of the HNORM score normalization method described in (Reynolds, 1997) for the EXP and INSV cry units separately. In each health-condition detector, we used only non-hypothesized or non-target cry samples (imposter) to estimate the normalization parameters. Therefore, the non-target log-likelihood ratio score distributions have been rescaled to have a mean of zero and a standard deviation of one. Due to different lengths of extracted EXP/INSV segments from each recorded cry signal, more evidence might be needed to make a reliable decision for each test file, especially for the INSV cry type, which has a shorter duration than the EXP type. Therefore, each corpus was split into small cry units of approximately 3 seconds duration to investigate the effect of the EXP/INSV duration length in each recorded file. The results indicate that independent of the frame length, type of cry units (EXP/INSV), adaptation method and task of the detector, recorded files that have more 3 sec-length EXP/INSV cry units have more separable LLR scores (see Figure 4.5). In other words, the more information that is available (EXP/INSV length inside each file), the

more likely that the information leads to more a reliable decision and less uncertainty about the detected pathological condition.

Earlier, we defined an approximately 3-second duration of an EXP/INSV segment as an EXP/INSV cry. In general, cry signals include more expiration cry segments than INSV cry segments, but the situation became worse because finding pure INSV segments was not likely in our noisy CDB. It is worthwhile mentioning that all of the test data (depicted in Table 4.4), except only one test sample, contains at least 1 EXP cry unit, in contrast to INSV cry units, for which Table 4.5 depicts a large reduction in the amount of test data from using a cry unit restriction.

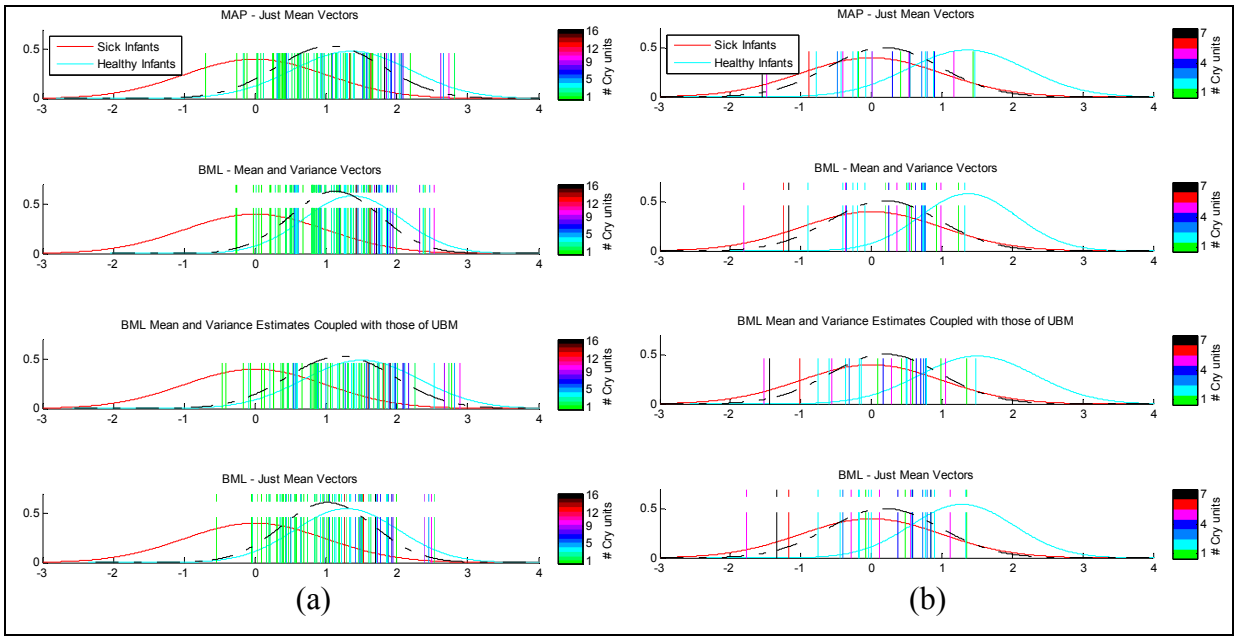


Figure 4.5 Mean of the LLR scores over INSV cry units inside the (a) healthy and (b) sick infants for the healthy infant verification system

Table 4.4 Number of infants and recorded cry signals available in the testing CDB at the time

Class	Number of Infants	Number of Cry Signals in Testing CDB
Healthy Infants	42 (4 male)	89 (11 male)
Sick Infants	40	101
Heart	2 (2 male)	3 (3 male)
Neurological	11 (6 male)	30 (18 male)
Respiratory	18 (12 male)	49 (35 male)
Blood	4 (4 male)	9 (9 male)
Others	4 (2 male)	10 (4 male)

Table 4.5 Number of cry samples that contain EXP/INSV-labeled segments and 3-sec cry units in our test CDB

Number of cry samples in the test cry database											
Class	**Total**	**# Samples with INSV-labeled segments**					**# Samples with at least 1 INSV unit**				
Healthy Infants	89	86					66				
Sick Infants	101	93					62				
		Heart	Neuro	Resp	Blood	Others	Heart	Neuro	Resp	Blood	Others
a/b: a from b		1/3	29/30	45/49	9/9	9/10	1/3	22/30	24/49	7/9	8/10
(a) Inspiratory cry segments											
Number of cry samples in the test cry database											
Class	**Total**	**# Samples with EXP-labeled segments**					**# Samples with at least 1 EXP unit**				
Healthy Infants	89	88					88				
Sick Infants	101	101					101				
		Heart	Neuro	Resp	Blood	Others	Heart	Neuro	Resp	Blood	Others
a/b: a from b		3/3	30/30	49/49	9/9	10/10	3/3	30/30	49/49	9/9	10/10
(b) Expiratory cry segments											

4.6.3 Health-condition detection system

In this section, we present the results of both healthy and sick (with specific diseases) infant detection.

4.6.3.1 Healthy infant detector

We present only the results of our healthy infant detector for a test database using both test EXP and INSV cry units with two different frame lengths (10 msec and 30 msec). Moreover, to describe the entire space of possible alternatives for the healthy class, two explained approaches, called background speaker modes ($\lambda_{\overline{Hyp}} = (\lambda_1, \lambda_2, \ldots, \lambda_B)$) and UBM ($\lambda_{\mathrm{UBM}}$), have been used to compute the LLR scores. Because some of the test data do not have 3-sec INSV cry units, to evaluate the detector based on the INSV models, we performed our experiments on two sets of test data (see Table 4.5): 1) containing INSV-labeled segments with any length and 2) containing at least one 3-sec INSV unit. On the other hand, almost all of the data from the test database contains pure EXP-labeled segments except for one sample, and thus, there are 88 healthy and 101 sick samples with EXP cry units for the evaluation procedure. Here, we only present the results of data that contains 3-sec EXP/INSV cry units, which are more satisfactory, as expected. The miss (false negative) and false alarm (false positive) rates are, respectively, plotted on the x- and y-axis, which are scaled non-linearly (normal deviate scale) as detection error tradeoff (DET) curves (Martin et al., 1997). The DET plots that are depicted in Figure 4.6 and Figure 4.7 distinguish more clearly the performance of the systems that have different adaptation methods, frame lengths, cry unit types and representatives for the alternative health conditions.

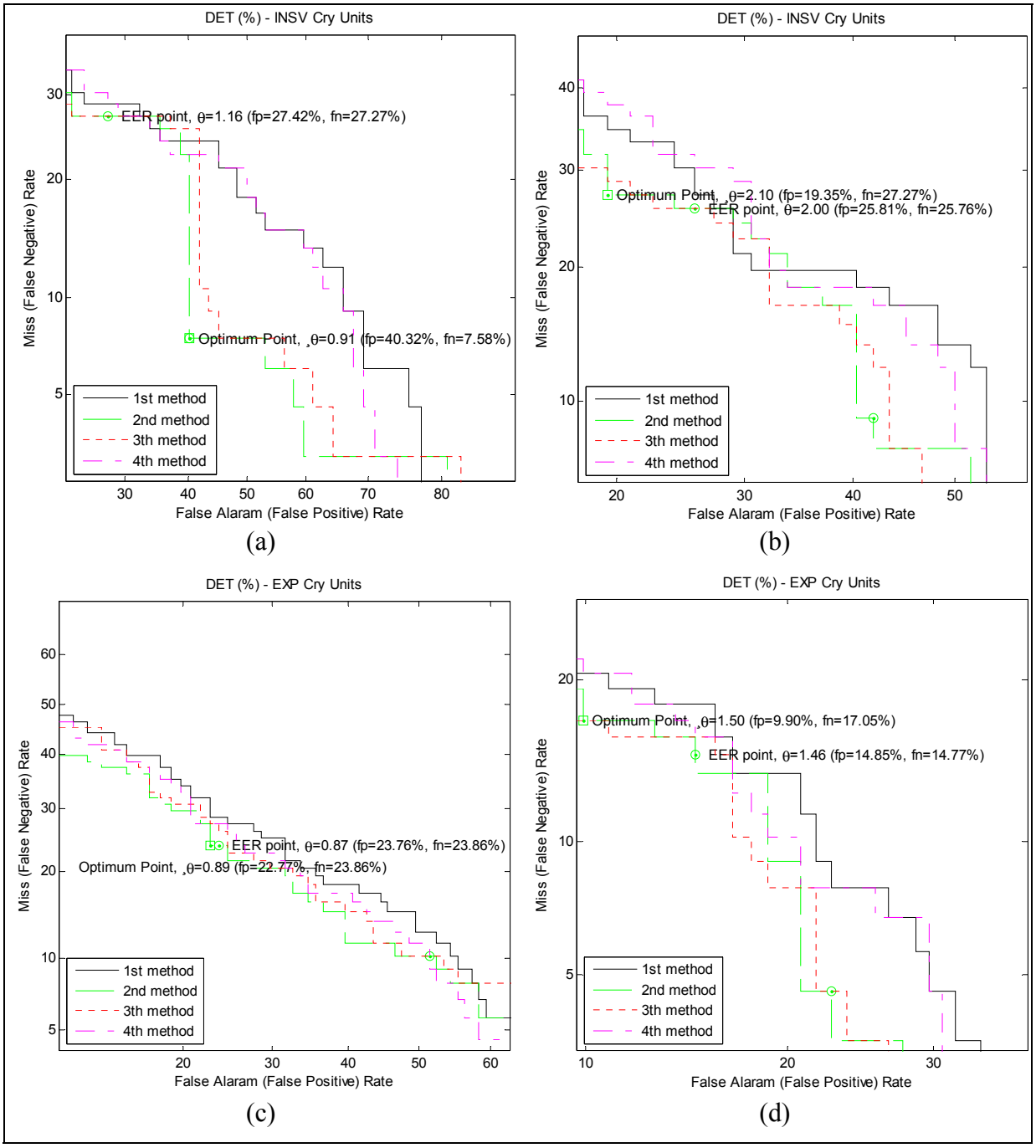


Figure 4.6 DET curves for two alternative hypothesized models $\lambda_{\mathrm{PI-UBM}}$ (a-c) and $\lambda_{\overline{\mathrm{Hyp}}}$ (b-d) and for INSV (a-b) and EXP (c-d) cry units with a 10 ms frame length in the healthy infant verification system

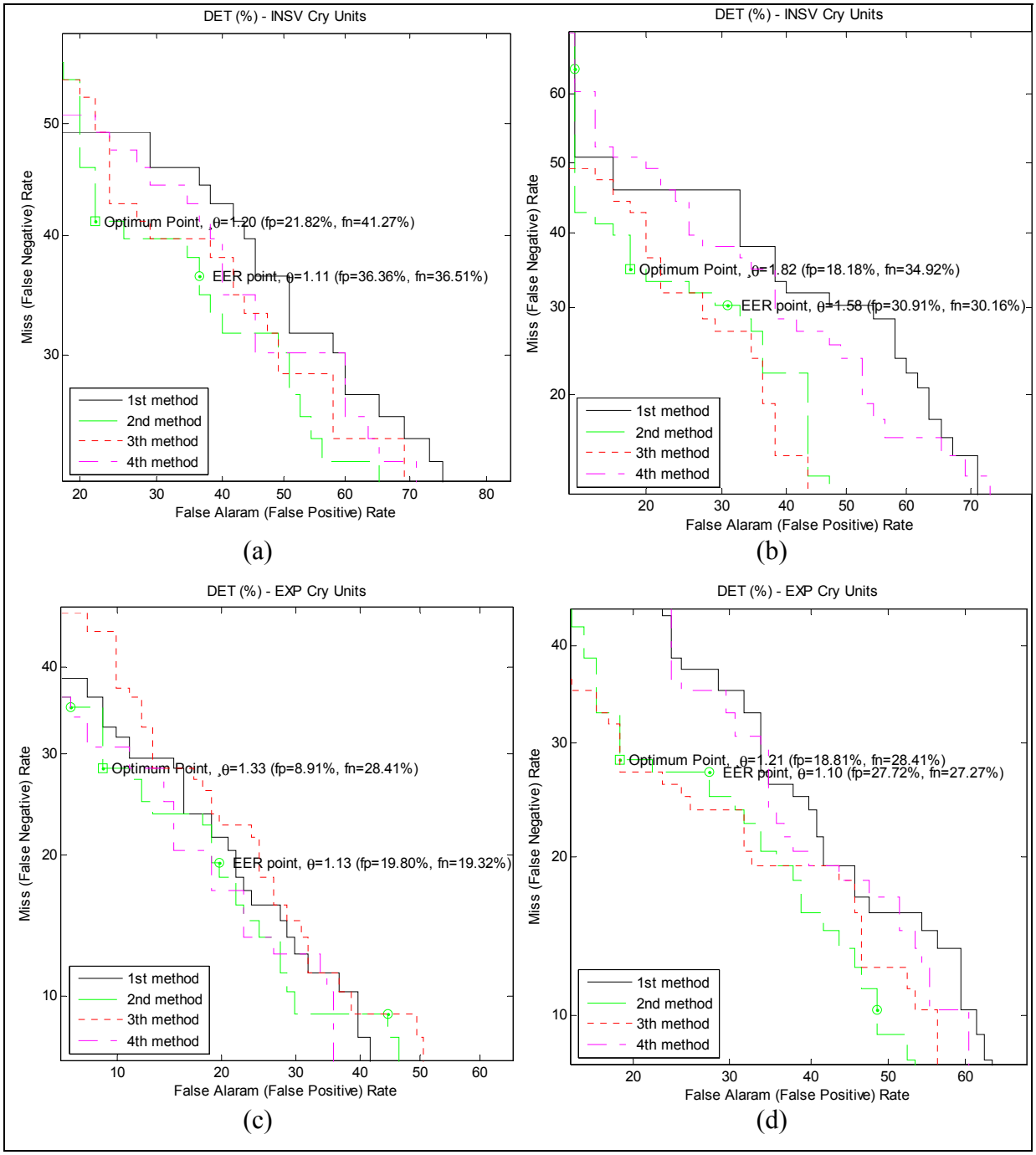


Figure 4.7 DET curves for two alternative hypothesized models $\lambda_{\mathrm{PI-UBM}}$ (a-c) and $\lambda_{\overline{\mathrm{Hyp}}}$ (b-d) and for INSV (a-b) and EXP (c-d) cry units with the 30 msec frame length in the healthy infant verification system

All of the points on the DET curves have different $FAR(\%)$ and $FPR(\%)$, and in practice, the operating point (OP) should be selected based on the task of the system in which all of the application criteria are met. For example, in biometric security systems, the point must have a low FAR. Because finding the best suitable OP in such a diagnostic system is not our concern in this paper, the equal error rate (EER) points are plotted by individual circle-shaped points on curves where $FAR(t) = FPR(t), t \in \mathrm{S}$, and S is the set of thresholds for calculating the OP distribution. Note that an exact EER point might not exist. Moreover, the optimal ROC operating points described in (Metz, 1978) are shown by the square-shaped points on the curves. The decision threshold is selected in a way that minimizes the average cost at this point. The slope of the ROC at this point is given by

$$\mathrm{S} = \frac{\mathrm{C_{FP}} - \mathrm{C_{TN}}}{\mathrm{C_{FN}} - \mathrm{C_{TP}}} \times \frac{\mathrm{P(+D)}}{\mathrm{P(-D)}} \tag{4.16}$$

where $\mathrm{C_{FP}}, \mathrm{C_{TN}}, \mathrm{C_{FN}}, \mathrm{C_{TP}}$ are the costs, and $P(\mp D)$ is equal to the probability that a case from the database is an $\mp$ case.

Here, our predefined costs for computing S are as follows:

$$C_{FP} = C_{FN} = 0.5, C_{TN} = C_{TP} = 0 \tag{4.17}$$

The overall accuracy and error rates depend on the chosen operating point, which is not clear here. Therefore, to compare the systems fairly and independently of the cutpoint, the Area under the ROC curve (AUC) is used as a measure of the performance of the detector, while an ideal classifier has an AUC equal to 1. The value of EER (%) and AUC for the systems plotted in Figure 4.6 and Figure 4.7 are listed in Table 4.6. It is apparent that the experiments on the shorter frame length have better results in most of the cases and the EXP cry units have a more distinctive ability than the INSV cry units in classifying healthy and sick infants independent of the frame length, as we anticipated. Moreover, because in general each cry signal contains more EXP cry units than INSV cry units, the average LLR score computed

over EXP cry units is more reliable than the INSV units due to having a larger number of available EXP units in the samples. To show the impact of the number of cry units on the system performance, especially for the INSV type (the same as in Figure 4.5 except for the values), we apply a criterion to choose only test files that have at least 3 cry units to perform the classification.

Almost all of the cry test samples with EXP-labeled segments have more than 3 units except for one healthy and two sick samples; therefore, the achieved results for the expiratory cry units are the same as the results in Table 4.6 again. However, this condition has a larger effect on the inspiratory segments of the recorded infants' cry signals and reduces the number of test files that contain INSV segments that have any duration (86 healthy and 93 sick to 32 healthy and 23 sick) cry samples. Independent of the frame length, adaptation method and background model, the results given in Table 4.7confirm that there are more INSV cry units inside a test file, with a higher chance at the end of the evaluation to diagnose it correctly.

Among the four adaptation methods defined earlier, our reference system with the Bayesian or MAP adaptation method (method 1) has the lowest AUC, and the other specific methods, both 2-3, which use the BML adaptation estimates, have lower error-detection rates with a higher AUC. The system with the highest AUC for both the EXP and INSV cry units is the system that uses the $\lambda_{\overline{Hyp}}$ background model and the 2nd method of adaptation. Therefore, the minimum achieved equal error rates are 14.85% and 25.8% for the EXP and INSV cry units, respectively.

Table 4.6 Comparison of the different healthy infant detector systems based on the Equal error rate and Area under the curve for all of the test samples

INSV	**10 msec**				**30 msec**			
	EER (%)		**AUC**		**EER (%)**		**AUC**	
	$\boldsymbol{\lambda_{HI-UBM}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$	$\boldsymbol{\lambda_{HI-UB}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$	$\boldsymbol{\lambda_{HI-UBM}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$	$\boldsymbol{\lambda_{HI-UBM}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$
'method1'	29.03	27.41	0.77	0.806	41.81	38.18	0.62	0.68
'method2'	27.41	25.80	0.815	0.8350	36.36	30.90	0.69	0.77
'method3'	27.41	25.80	0.811	0.8355	38.18	29.09	0.68	0.81
'method4'	29.03	29.03	0.78	0.80	40	34.54	0.64	0.71
EXP	**10 msec**				**30 msec**			
	EER (%)		**AUC**		**EER (%)**		**AUC**	
	$\boldsymbol{\lambda_{HI-UBM}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$	$\boldsymbol{\lambda_{HI-UB}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$	$\boldsymbol{\lambda_{HI-UBM}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$	$\boldsymbol{\lambda_{HI-UBM}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$
'method1'	27.72	15.8415	0.81	0.932	20.79	32.67	0.87	0.76
'method2'	23.76	14.8514	0.84	0.951	19.80	27.72	0.89	0.825
'method3'	24.75	15.8415	0.826	0.951	22.77	24.75	0.86	0.824
'method4'	25.74	15.8415	0.827	0.932	18.81	30.69	0.89	0.77

Table 4.7 Comparison of the different healthy infant detector systems based on the EER and AUC for the test samples that have more than 3 INSV units (32 and 23 cry samples of healthy and sick infants respectively)

INSV	**10 msec**				**30 msec**			
	EER (%)		**AUC**		**EER (%)**		**AUC**	
	$\boldsymbol{\lambda_{HI-UBM}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$	$\boldsymbol{\lambda_{HI-UB}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$	$\boldsymbol{\lambda_{HI-UBM}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$	$\boldsymbol{\lambda_{HI-UBM}}$	$\boldsymbol{\lambda_{\overline{Hyp}}}$
'method1'	13.043	26.08	0.933	0.872	25	25	0.75	0.81
'method2'	13.043	17.39	0.944	0.888	30	25	0.79	0.82
'method3'	13.043	21.73	0.941	0.887	35	25	0.77	0.85
'method4'	13.043	26.08	0.938	0.877	25	20	0.78	0.82

4.6.3.2 Sick infant detector with a specific disease

A lack of data, especially in the training data for a specific illness, causes difficulty in training and adapting well-defined models, such as the INSV model type for infants who have blood disorders. Even at the evaluation time, there are not a sufficient number of test samples in all of the diseases (see Table 4.5). Thus far, we have only used our detector for sick infants who suffer from neurological and respiratory disorders. In the interest of brevity, only the results for a shorter frame length and background speaker models $\lambda_{\overline{Hyp}}$ will be discussed.

Recording sick infants' cries that are available in the training CDB have been taken from a limited number of distinct infants, which are not the same as for the infants used in the test CDB. In total, 10 and 5 infants are used to train the respiratory and neurological disease models, respectively. In comparison to previous results in the healthy infant detector system, very low training errors plus test results for the unseen data depicted in Table 4.8 might be a sign of memorizing training data rather than learning.

This finding is due to an apparent lack of enough distinct infants in each corresponding class, especially for neurological disease. It is important to understand that the data collection process, training and adapting procedures are time-consuming, but that also, in spite of them, further corresponding full-term sick infants (as with healthy infants) result in better generalization by training well-defined models. Even using cross-validation, which is a method for preventing overfitting, is not a quick-fix solution. Therefore, collecting new data to increase the size of the training CDB to rebuild a pathology-independent background model and sickness models is a practical solution to improving the performance.

It has been shown in Table 4.8 that the methods that use BML adaptation, the 2nd, 3rd and 4th methods, have the highest AUC than our reference system with Bayesian adaptation.

Moreover, the respiratory sickness model has a better ability to verify sick infants due to having more distinct infants in its training phase. The ability of each cry type can be different based on the type of disease. Therefore, it is better to use both at the same time to make a final decision, to have more reliable detection.

Table 4.8 Results of the sick infant detector systems for Respiratory and Neurological disorders

Respiratory diseases				
	INSV-$\lambda_{\overline{Hyp}}$		**EXP-$\lambda_{\overline{Hyp}}$**	
10 msec	**EER (%)**	**AUC**	**EER (%)**	**AUC**
'method1'	28.94	0.80	34.61	0.75
'method2'	23.68	0.82	32.69	0.74
'method3'	26.31	0.81	36.53	0.73
'method4'	21.05	0.84	30.76	0.77
Neurological disorders				
10 msec	**EER (%)**	**AUC**	**EER (%)**	**AUC**
'method1'	40	0.607	33.80	0.727
'method2'	47.5	0.587	28.16	0.777
'method3'	47.5	0.572	29.57	0.770
'method4'	42.5	0.631	30.98	0.746

4.6.4 Fusion, calibration and decision

A more sophisticated system can be developed by integrating the evidence presented by multiple sources of information, similar to in multimodal biometric systems. Such a multimodal system is expected to be more reliable in contrast to a unimodal system, which relies on the evidence of a single source. Here, fusion of the proposed two subsystems (expiratory and inspiratory cry unit-based GMM) is performed to improve the overall performance. Generally speaking, the strategy of fusion can be categorized into three levels, which are called the data or feature level, matching score level, and decision level (Blum et Liu, 2005). Although the feature set is richer in discriminative information than the matching score or the output decision of a classifier, fusion at the match score level is usually preferred because it is relatively easy to obtain and there is no need to worry about the feature compatibility at the score level or rigid fusion at the decision level (Ross et Jain, 2004).

There are two different strategies for combining scores that are generated by multiple classifiers. In the first method, the final decision is made by a single scalar score that is a combination of individual scores (Ben-Yacoub, Abdeljaoued et Mayoraz, 1999; Dieckmann, Plankensteiner et Wagner, 1997). There are several techniques for addressing the combination problem; these techniques can be applied in different applications (Li, Han et Narayanan, 2013; Snelick et al., 2005). In the second approach, individual scores construct a feature vector to verify or classify two classes (Vatsa, Singh et Noore, 2007; Verlinde et Cholet, 1999). We took this approach to fuse the model scores that were obtained from the expiratory and inspiratory cry units of the test samples.

As in multi-modal identity verification systems, we want to combine the output match scores of two experts using the same features and arising from a specific measure, such as MFCCs (static and dynamic) but also driven from different cry types. The normalized log-likelihood ratio scores obtained from two EXP and INSV cry unit-based subsystems are concatenated to construct a two-dimensional feature space. Then, we used three classification models, namely the multilayer perceptron (MLP) using the back-propagation algorithm, probabilistic neural

networks (PNN) and a support vector machine (SVM) (see Table 4.9). These classifiers were evaluated using test datasets (see Table 4.4) that included cry signals that contained clean EXP and INSV labeled segments.

Table 4.9 Training parameters used in SVM, PNN and MLP

PNN	Number of neurons in layer 1 : 161
	First layer Transfer function : Radial basis transfer function
	Spread value: 0.1
	Number of neurons in layer 2 : 2
	Second layer Transfer function : Competitive transfer function
	Performance function : mse
	Learning algorithm : Scaled conjugate gradient
MLP	Number of hidden layers : 1
	Hidden layer neurons : 10
	Hidden activation function : Hyperbolic tangent sigmoid
	Output layer neurons : 2
	Output activation function : Softmax (normalized exponential)
	Max number of iteration : 1000
	Performance function : Crossentropy
	Learning algorithm : Scaled conjugate gradient
SVM	Number of iterations : 15000
	Kernel functions : 1- linear 2- Quadratic 3- Polynomial (order 3) 4- Gaussian RBF Kernel 5- Multilayer perceptron Kernel with SMO method to find the separating hyperplane

4.6.5 Results and discussion

To compare the generalizability of these three different algorithms and to find out the best algorithm for the available data, stratified K-fold cross-validation is used in which each fold has a roughly equal size and contains the same percentage of samples of each target class as in the whole dataset. Although 10-fold cross-validation is more common, in practice, usually the choice of the number of folds depends on the size of the dataset. Although there are different variants of cross-validated estimates (Refaeilzadeh, Tang et Liu, 2009), stratified 10-fold cross-validation is recommended by Kohavi (Kohavi, 1995) as the best model.

To obtain reliable performance estimation, multiple rounds of cross-validation are performed to test new and different random splits that result in smaller variance in the results and reduce the variability. Then, the validation results with three different values of K, depicted in Table 4.10, are averaged over the corresponding number of rounds.

Table 4.10 Number of folds and rounds

Value of K	3	5	10
Number of Iterations	400	200	100

The performances of the classifiers that use different adaptation methods are compared based on some widely used statistical measures, namely, the false positive rate, false negative rate, accuracy, sensitivity and specificity. These statistical measures can be calculated from the classifier's results, as described in (Fawcett, 2006). The error of the classifier follows a binomial distribution with the following mean and standard deviation:

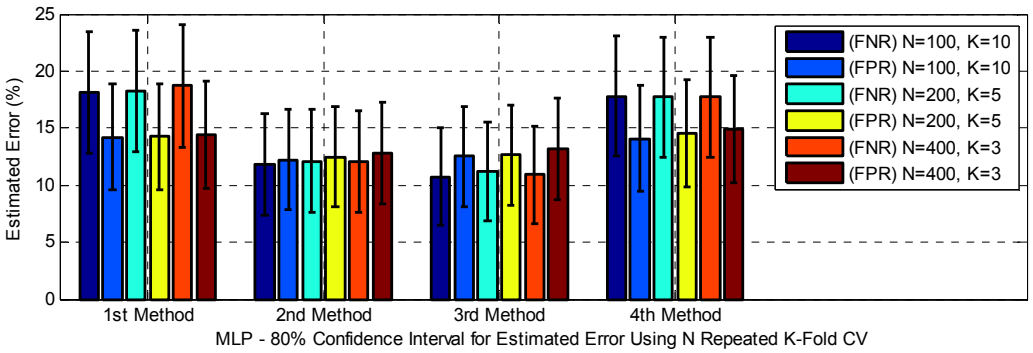
$$\mu_{error} = p_{cv}, \sigma_{error} = \sqrt{\frac{p_{cv}(1-p_{cv})}{n}} \tag{4.18}$$

where p_{cv} is the mean of K errors, and n is the number of samples. We can approximate the $100(1-\alpha)\%$ confidence interval for the error by the Wald confidence interval (Agresti et Coull, 1998), as follows:

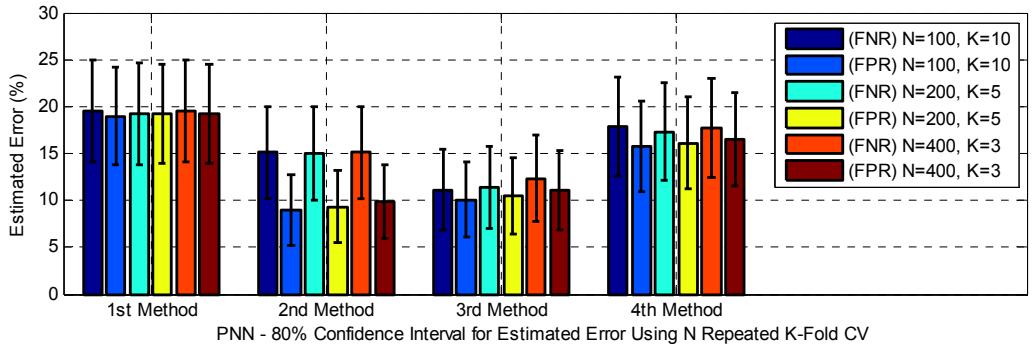
$$p_{cv} \mp z_{\alpha/2}\sigma_{error} \tag{4.19}$$

where z_β is the $1-\beta$ quantile of the standard normal distribution. In Table 4.5, the test dataset consists of 86 and 93 cry samples of healthy and sick infants whose recorded cry signals contain both EXP and INSV segments, which are used to detect healthy infants by fusing likelihood ratio scores obtained from expiratory and inspiratory cry units. In the first experiment, the dataset is tested by the aforementioned classifiers (listed in Table 4.9), which have different adaptation techniques that are used to train the subclass models, as described in previous sections. Figure 4.8 indicates both types of errors, the false positive rate (FPR or type I error) and the false negative rate (FNR or type II error), with an 80% confidence interval after applying stratified K-fold cross-validation for each classifier. Due to space limitations, we only plot the test errors over new observations (that were not used in the training phase of the K-fold cross-validation) and not training errors over the observations used in its training. For each method of adaptation (from methods 1-4), there is not much difference in the errors between the K-fold cross-validations with different values of folds. The Bayesian adaptation method (1st method), which is our reference method, has obviously higher errors than the other methods, especially the 2nd and 3rd methods. To obtain a better comparison between the performances of the adaptation methods, Table 4.11 depicts the average accuracy, sensitivity and specificity rates over all of the used classifiers for each adaptation method. Here, the accuracy rate indicates the proportion of true classified infants (both healthy and sick) among the total number of infants in the test dataset. The sensitivity measures the portion of healthy infants that are correctly identified, while the specificity measures the proportion of sick infants that are correctly verified. As is clear, the BML adaptation method for refining both the mean and variance vectors (2nd method) and the coupled BML adaptation estimations with old estimations (3rd method) are superior to the

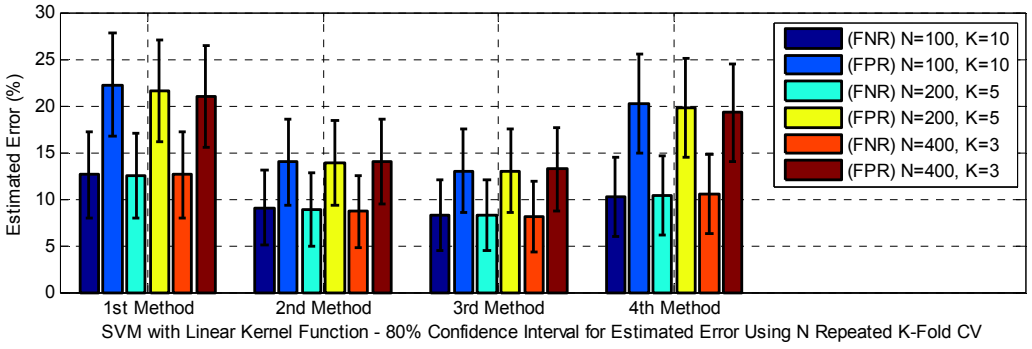
others, and even the BML adaptation for refining only the mean vectors (4th method) performs better than the Bayesian adaptation method (1st method).



(a) Multilayer Perceptron Neural Network

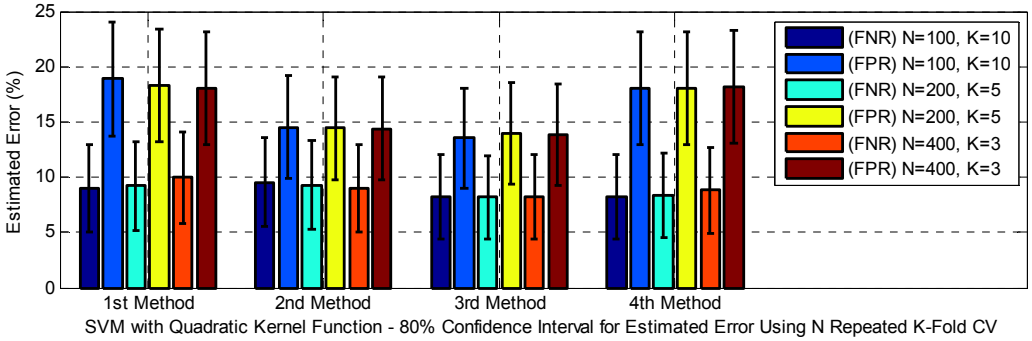


(b) Probabilistic Neural Network

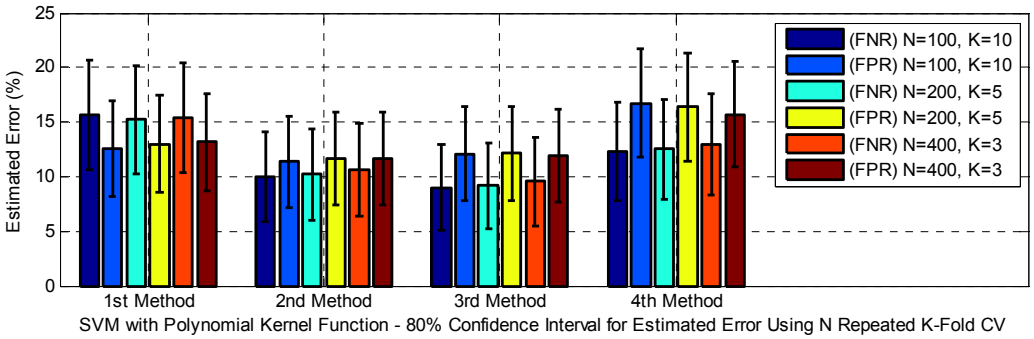


(c) SVM with Linear Kernel Fucntion

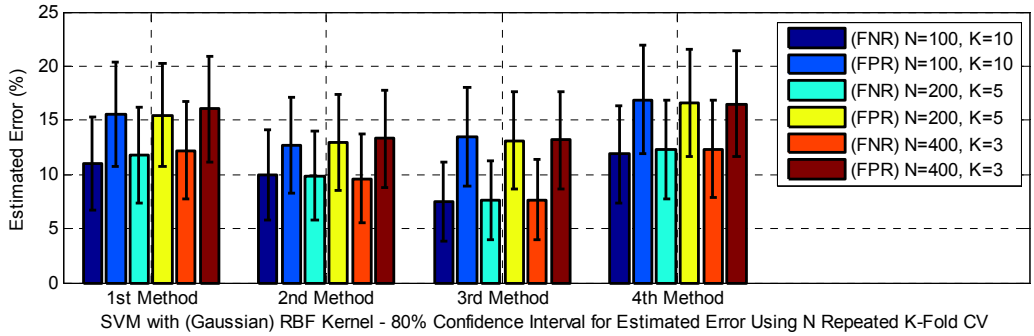
Figure continued on next page



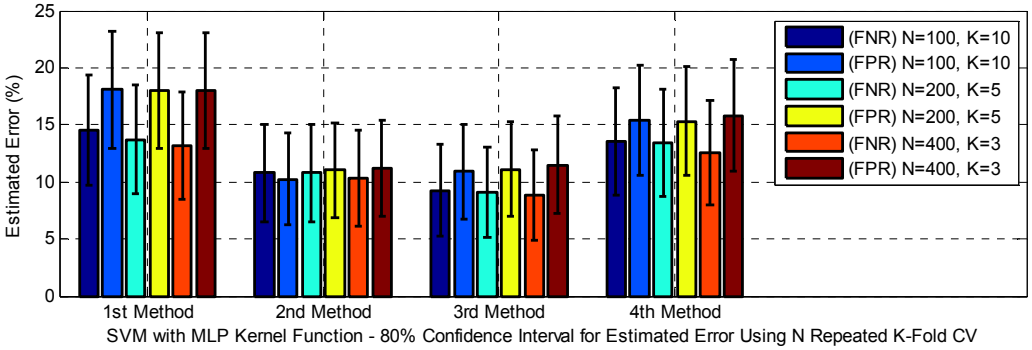
(d) SVM with Quadratic Kernel Fucntion



(e) SVM with Polynomial Kernel Function order 3



(f) SVM with Gaussian radial Basis Function Kernel



(g) SVM with Multilayer Perceptron Kernel Function

Figure 4.8 Type I and type II errors of the tested different healthy infant detector systems for each of the adaptation methods

Table 4.11 Average accuracy, sensitivity and specificity over the used classifiers in the healthy infant detection task

	Method 1	**Method 2**	**Method 3**	**Method 4**
Average Accuracy	85.21	89.13	89.76	85.98
Average Sensitivity	88.07	89.85	90.73	88.64
Average Specificity	82.53	88.37	88.41	82.74

Classifiers provide different false negative and false positive rates, but as we expected from the fusion approach, even in the worst case of each classifier using the 2nd and 3rd adaptation methods, we obtained a smaller error rate than the lowest equal error rate of the model using EXP and INSV units separately, which are 14.85% and 25.8%, respectively. The type I error and type II error were decreased by using fusion, which reached 8.84% for the false negative rate and 11.49% for the false positive rate using SVM-MLP with the 3rd adaptation method. The system with a smaller false positive leads to more false negatives, and vice versa. In biometric systems, the system with an approximately equal false rejection rate and false acceptance rate is called a tuned system (Tipton et Krause, 2007), and the goal is to tune this system to obtain an equal error rate that is as low as possible. Among all of the used classifiers, based on the error rates and accuracy rates depicted in Figure 4.9 to Figure 4.10, MLP and SVM with the MLP kernel function perform better than the others by providing almost the same type I and II errors (close to the EER point).

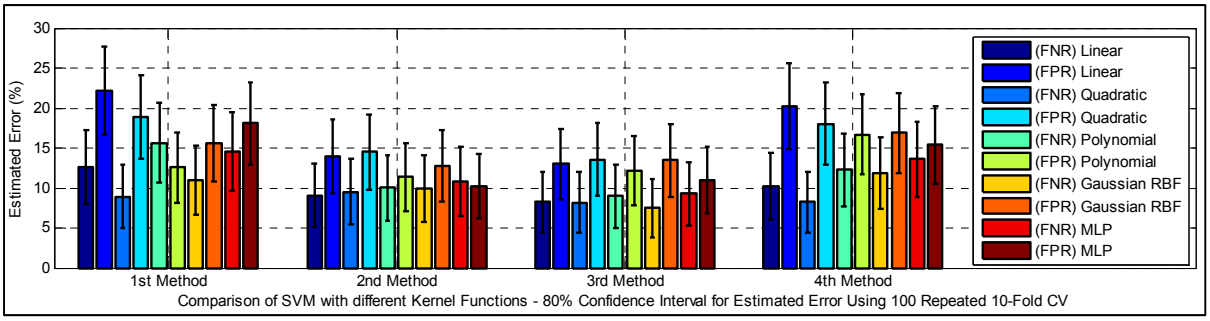


Figure 4.9 Type I and type II errors for the SVM with different kernel functions in the healthy infant detection task

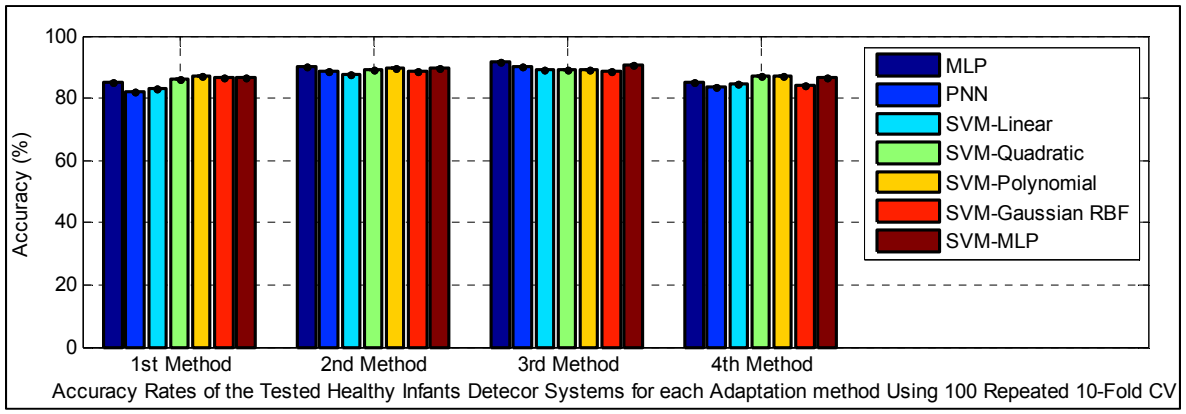


Figure 4.10 Comparison of the accuracy rates of all of the classifiers in the healthy infant detection task

Table 4.12 to Table 4.14 indicate in detail the accuracy rate, sensitivity and specificity of the classifiers respectively as statistical measures of the performance of the classification test.

Table 4.12 Accuracy rates for the used classifiers in the healthy infant detection task

Classifier	**Method 1**	**Method 2**	**Method 3**	**Method 4**
MLP	85.03	89.95	91.68	84.99
PNN	82.11	88.79	89.93	83.82
SVM-Linear	83.12	87.67	89.33	84.82
SVM-Quadratic	86.11	88.98	88.98	87.25
SVM-Polynomial	86.99	89.82	89.27	87.08
SVM-Gaussian RBF	86.59	88.78	88.75	84.33
SVM-MLP	86.57	89.85	90.41	86.60
Average Accuracy	85.21	89.13	89.76	85.98

Table 4.13 Sensitivity rates for the used classifiers in the healthy infant detection task

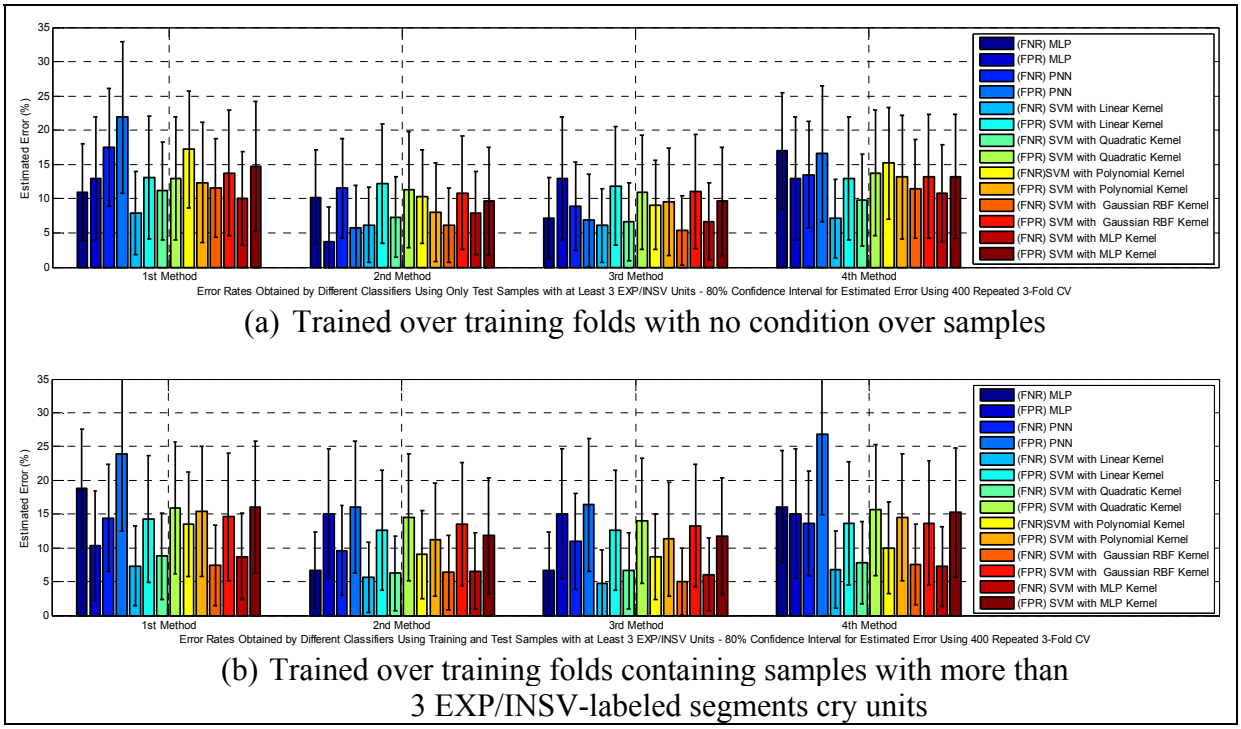
Classifier	Method 1	Method 2	Method 3	Method 4
MLP	84.86	90.83	93.05	91.11
PNN	82.77	87.08	89.44	83.88
SVM-Linear	89.58	89.44	91.80	90.55
SVM-Quadratic	93.19	90.97	92.08	93.19
SVM-Polynomial	85.69	90.27	90.27	88.19
SVM-Gaussian RBF	88.47	89.72	90.83	86.25
SVM-MLP	91.94	90.69	90.69	87.36
Average Sensitivity	88.07	89.85	90.73	88.64

Table 4.14 Specificity rates for the used classifiers in the healthy infant detection task

Classifier	Method 1	Method 2	Method 3	Method 4
MLP	85	89	90.22	79.77
PNN	81.66	90.22	90.22	83.77
SVM-Linear	77.11	85.88	87	79.33
SVM-Quadratic	79.55	87.11	86.11	81.66
SVM-Polynomial	88	89.22	88.11	85.88
SVM-Gaussian RBF	84.88	88.11	87	82.77
SVM-MLP	81.55	89.11	90.22	86
Average Specificity	82.53	88.37	88.41	82.74

Earlier, we showed that using test samples with more INSV cry units can reduce the equal error rate down to 13% (see Table 4.6). Likewise, in the next experiment, we used only the cry samples that had more than 3 cry units of clean EXP and INSV-labeled segments (32 healthy and 23 sick samples). Due to having a small resulting test dataset, 3-fold cross-

validation is applied to evaluate the performance of the classifiers. We imposed this condition on existing samples in the test folds once and then on existing samples in both the training and test folds separately. The error reduction is clear by comparing the obtained results depicted in Figure 4.11a with individual results for each classifier on the entire set of test data depicted in Figure 4.8. For example, in the PNN classifier using the 3rd adaptation method, the type I error and type II error are decreased to 6.8% and 8.8%, respectively. In the second experiment by applying the aforementioned condition on the existing samples, we have a training problem due to a lack of data that resulted in a high type I error (see Figure 4.11b).



(a) Trained over training folds with no condition over samples

(b) Trained over training folds containing samples with more than 3 EXP/INSV-labeled segments cry units

Figure 4.11 Type I and type II errors of the classifiers used in the healthy infant detection task using 400 repeated 3-fold CVs for the test samples that contain more than 3 EXP and INSV-labeled cry units

After the first step of our cry-based diagnostic system, if the test infant is identified as a sick infant who suffers from one of our available diseases in the CDB, we should test it again with a predefined sick infant detector system to identify the most probable sickness. It is worthwhile mentioning that because of having a small number of infants and cry samples in

our CDB at this time, the GMMs were adapted from the corresponding pathology-independent UBM for only infants who suffer from neurological problems and respiratory disorders. Likewise, the classifiers listed in Table 4.9 were used to fuse the likelihood ratio scores that were obtained from the expiratory and inspiratory cry units. For this purpose, all of the cry samples that were recorded from sick infants that have both expiratory and inspiratory segments, as depicted in Table 4.5, were used to test these two sick infant detector systems. The stratified K-fold cross-validation estimates the prediction error in each task to make an assessment of different adaptation methods.

In the test dataset, we have 29 and 45 cry samples recorded from sick infants who suffer from neurological and respiratory disorders, respectively. For the first task, we had an imbalanced dataset (29 target and 64 non-target cry samples), and there are a few ways to address this problem; these approaches can be divided into data and algorithmic levels (Han, Wang et Mao, 2005). Because the dataset was small, the idea of under-sampling or data reduction techniques that remove only a majority of class samples is not an ideal solution. Another approach is to apply a higher misclassification cost to the minority class. This approach can balance out our imbalanced dataset, but here we assumed equal costs for the two types of error. Consequently, we simply increased the size of our minority class (target class) by duplicating the data. Although it was reported in (Kolcz, Chowdhury et Alspector, 2003) that usually duplicating samples in a dataset has a detrimental effect on the model and accuracy rate, many re-sampling methods (Han, Wang et Mao, 2005) have been proposed in data mining algorithms as a solution to imbalanced data sets. Here, simple random over-sampling has been performed to balance the data set through duplicating some random samples of the minority class. It was observed that smaller error rates resulted for the created balanced data set. Figure 4.12 indicates the type I and type II errors of the classifiers in the sick infant (those affected by neurological problems) detection task for the balanced data set. For the sake of brevity, we have illustrated only the error rates of the classifier using 100 repeated 10-fold cross-validation in these two sick infant detection tasks. As depicted in Figure 4.13, almost all of the classifiers in this task that were adapted by either the 2^{nd} or 3^{rd} methods have higher accuracy rates, except for PNN, which has low false negative and false positive error

rates (specifically, 26.4% and 24.6%, respectively) by the 4th adaptation method, in contrast to other adaptation methods.

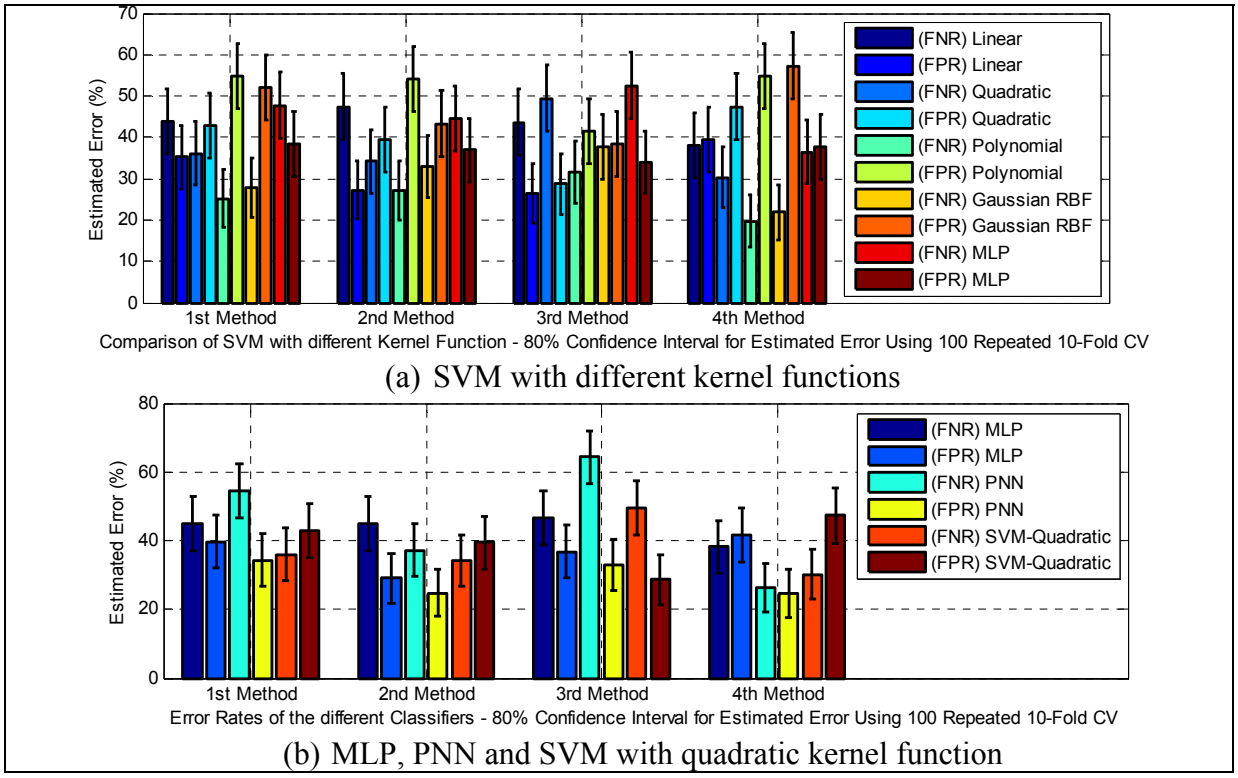


Figure 4.12 Type I and type II errors for the different classifiers in the sick infant (affected by neurological problems) detection task

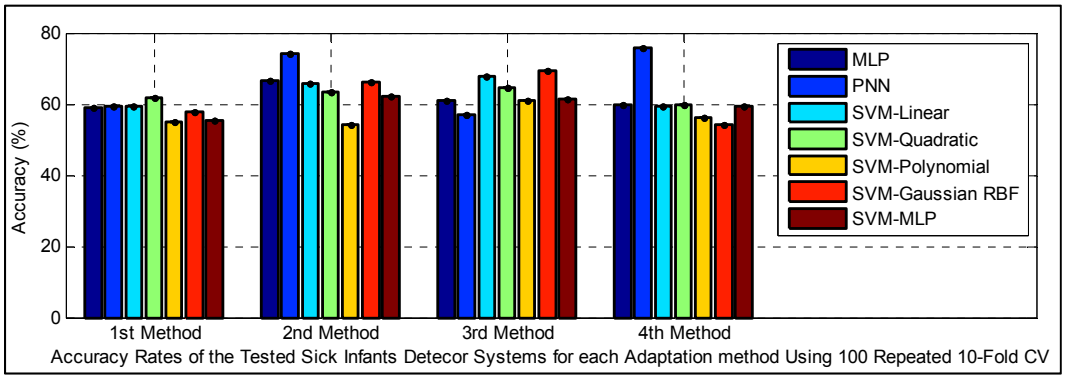


Figure 4.13 Comparison of the accuracy rates of all of the classifiers in the sick infant (affected by neurological problems) detection task

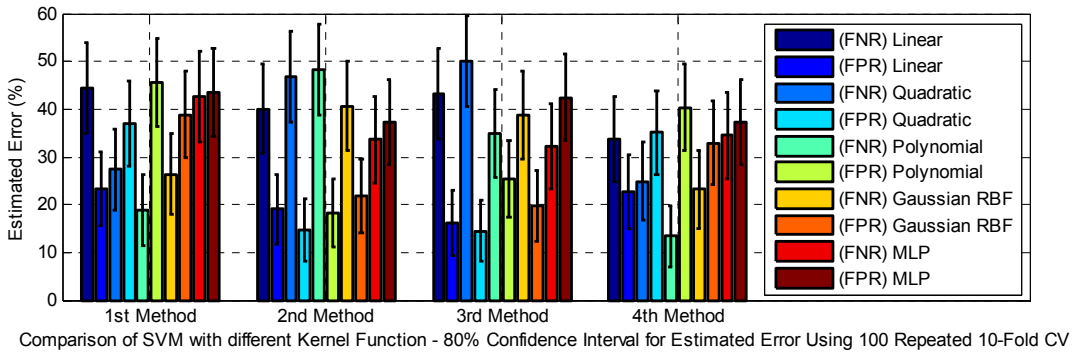
According to Table 4.15, it appears that the 3rd method is more focused on specificity, while the 4th method is more focused on sensitivity. In this case, the sensitivity and specificity contribute to the overall accuracy by having different weights, which is not ideal due to the equal cost assumption. Moreover, Table 4.15 indicates that the 2nd method has almost equal and the highest proportions of either actual healthy or sick infants that are correctly identified, among the adaptation methods.

Table 4.15 Average accuracy, sensitivity and specificity over the used classifiers in the sick infant (affected by neurological problems) detection task

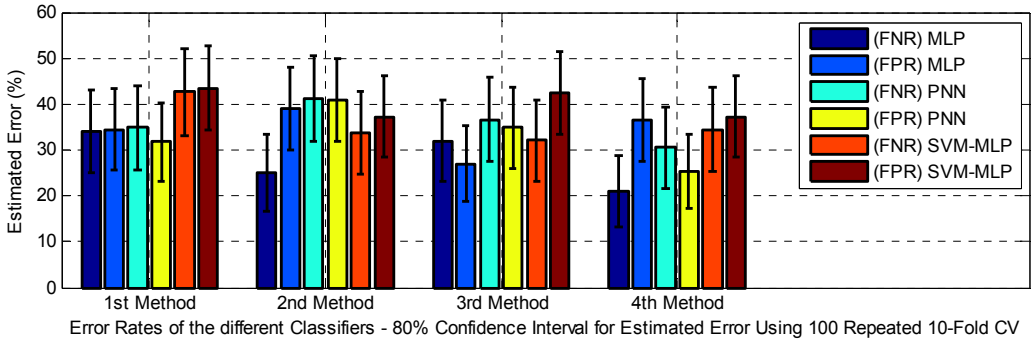
Neurological	Method 1	Method 2	Method 3	Method 4
Average Accuracy	58.26	64.57	63.15	60.67
Average Sensitivity	57.85	63.3	54.76	67.85
Average Specificity	58.29	65.06	66.25	57.03

Because the respiratory disorders class has more infants and also more cry samples than the neurological problems class, on average, the sick infant (affected by respiratory disorders) detection task performed slightly better, with a smaller generalization error than that for neurological disorders. The type I and type II errors of the classifiers are depicted in Figure 4.14. It appears that adapting only the mean vectors by the BML method (the 4th method) has smaller error rates for all of the classifiers and the PNN classifier has more balanced error rates than the others (30.5% false negative, 25.4% false positive error rates).

The statistical measures of the performance of the test are summarized in Table 4.16, which indicates that the 4th adaptation method is more accurate than the others (see Figure 4.15), while it is more focused on specificity (the same as the first method), in contrast to the other two methods, which are more focused on sensitivity.



(a) SVM with different kernel functions



(b) MLP, PNN and SVM with MLP kernel function

Figure 4.14 Type I and type II errors for the different classifiers in the sick infant (affected by respiratory disorders) detection task

Table 4.16 Average accuracy, sensitivity and specificity over the used classifiers in the sick infant (affected by respiratory disorders) detection task

RDS	**Method 1**	**Method 2**	**Method 3**	**Method 4**
Average Accuracy	65.22	67.68	68.18	69.59
Average Sensitivity	68	61.85	61.71	74
Average Specificity	62.85	73.50	74.50	65.71

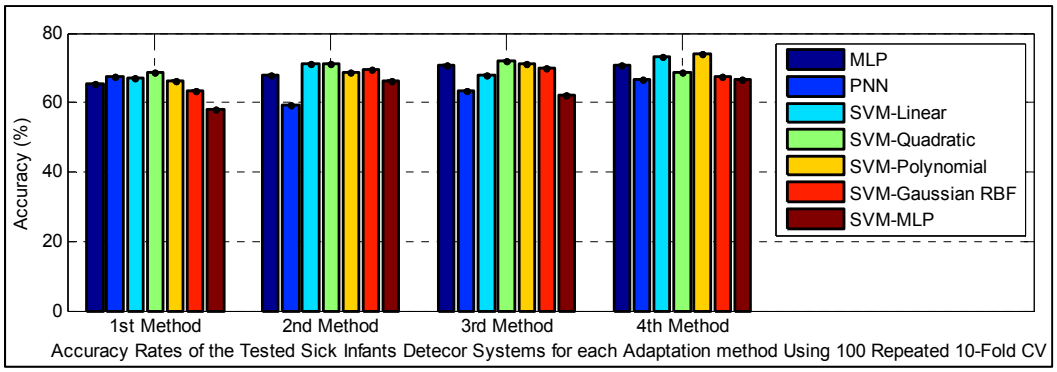


Figure 4.15 Comparison of the accuracy rates of all of the classifiers in the sick infant (affected by respiratory disorders) detection task

4.7 Conclusion and further discussion

In this paper, we used the potential of newborn infant cry signals, which indicate the integrity of the central nervous system, to introduce a cry-based diagnostic system. The principal aim of the proposed system is to broaden the diagnostic system to address the most life-threatening illnesses and defects that occur in newborn infants. We believe that by developing this system we will create new possibilities for infants who suffer from birth defects or undetectable diseases, to obtain the treatment faster and protect them from health threats. In contrast to previous studies on infant cry signals, which usually address binary classification tasks, a hierarchical scheme that consists of subsystems is proposed to narrow down the health condition of an infant to one of the possibilities that is considered in our experiments; most of these possibilities have not been previously studied. It is worthwhile mentioning that due to the motivation for developing such a system in low-income countries without complex and advanced technology, there is no constraint placed on the recording steps of the cry signals. The fact that our cry data set is not clean and noise-free could harm the analysis process and reduce the NCDS system performance. After the analysis of infant cry vocalizations and the segmentation of sounds in baby cry audio recordings, the dynamic MFCC features along with static MFCC features are selected and extracted for both the expiratory and inspiratory cry unit types to make a discriminative feature vector.

Here, in our infant health-condition verification/detection system, the UBM is an infant-independent GMM that is trained with cry samples from our cry dataset based on the HTK (Hidden Markov Model Toolkit) software tool to represent the general acoustic characteristics of crying. Then, for healthy or sick infants with an enrolled disease, a unique cry-pattern has been trained by the adaptation procedure. In our previous papers (Farsaie Alaie et Tadj, 2012; 2013), we showed that the BML method, compared to other learning mixture models, has the great advantage of adding new mixture components in such a way that the greatest improvement is obtained in the predefined objective function. We used this idea to present a novel adapted BML process to derive subclass models from the GMM-UBM. The Bayesian adaptation method is assumed here to be our reference system for the adaptation procedure. The paper compares the obtained results for Bayesian and three different variants of adapted BML methods on each classification task.

Both expiratory and inspiratory cry unit types have their own ability to classify test infants for each task, and therefore, a score level fusion of the proposed two subsystems is performed to make a more reliable decision. In brief, the system for each model has two main sequential steps, which are called encoding and making a decision. In the encoding stage, we show how a cry signal represents itself in both the expiration and inspiration cry units within the GMM models by a set of extracted MFCC feature vectors and how to create log-likelihood ratio scores. At the score level, the detection decision on each test infant's cry is based on whether the set of feature vectors observed on the presented cry signal is more likely to have been produced by the hypothesized health-condition class or by the other available alternative classes. In the next step, the fusion of the obtained individual scores is performed to construct a new feature vector. The efficiency of the various classifiers, such as SVM, MLP, and PNN, has been evaluated to compare the adaptation methods in each task.

Two health-independent and pathology-independent GMMs were trained by pooling the corresponding training data in a balanced version of CDB together (39 healthy, 22 sick), and we used the remainder of the unseen infant recordings in CDB for adapting the subclass

models. Then, testing was performed on all of the unseen 42 healthy and 40 sick infants, to evaluate the accuracy of each model. The results indicated that independent of the type of the cry units (EXP/INSV), adaptation method and task of the detector, the experiments on a shorter frame length (10 msec) have lower equal error rates (EER) than the 30 msec frame length in most of the cases. Moreover, based on the obtained results, the Bayesian or MAP adaptation method (1^{st} method) not only has a higher EER but also has a lower AUC than the other three variants of the adapted BML method. In the first task, which was designed to detect healthy infants from sick infants who suffer from specific diseases according to the optimal likelihood ratio test, 14.85% and 25.8% equal error rates were achieved for the EXP and INSV cry units, respectively. This finding indicates that there is a higher ability for expiratory sounds to distinguish healthy and sick full-term infants in contrast to a sick infant detector for respiratory disorders, while the trained model based on inspiratory sounds has a lower error rate than those based on expiratory sounds.

Although the presence of noise in the database has caused a loss of some portion of the INSV and EXP sounds in the baby cry audio recordings, the fact that the duration of the expiratory sounds is usually larger than the inspiratory sounds in newborn infant cries makes the average LLR score computed over expiratory cry units a more reliable estimate of the true value than the inspiratory cry units. We have shown that the length of the expiratory or inspiratory sounds that are available in a test file has a direct effect on the classification performance. In other words, the more information that is available (the EXP/INSV length inside each file), the more likely it is to have a more reliable decision and less uncertainty about the detected pathological condition. Those infants whose sample cries do not contain sufficient evidence should be asked to provide more samples. We concluded from the results on the healthy infant and sick infant (with neurological and respiratory disorders) that the ability of each cry type can vary by the type of disease or the general health condition.

Afterward, the obtained scores for each cry sample were used to construct a feature vector to combine expiratory and inspiratory cry-based individual scores. Several classifiers have been

employed to evaluate the performance of the methods of adapting healthy and pathological subclasses after the score level fusion. The error rates dropped from $\mathrm{EER_{EXP}} = 14.85\%$ and $\mathrm{EER_{INSV}} = 25.8\%$ in the healthy infant detector systems to an 8.84% false negative rate and 11.49% false positive rate using SVM-MLP with a variant of the BML adaptation method. Likewise, the error rates in sick infant (with neurological and respiratory disorders) detector systems were decreased by using score level fusion, and they even reached a 26.4% false negative and 24.6% false positive error rate and a 30.5% false negative and 25.4% false positive error rate using the PNN classifier with a variant of the BML adaptation method (4th method) on each task, respectively. Overall, the 2nd and 3rd adaptation methods, which use both the mean and variance vectors of the BML adaptation estimates, have almost the highest accuracy, sensitivity and specificity among the adaptation methods. The poor performance of the disease models (especially for infants with neurological disorders) in comparison to healthy or sick infant models is largely due to having a limited number of infants and also a lack of corresponding cry recordings. Consequently, the trained GMMs with corresponding cry samples were not defined as well as the healthy or sick models were when representing the general cry characteristics of the enrolled diseases.

4.8 Acknowledgment

The authors would like to thank Dr. Barrington and members of the neonatology group of Mother and Child University Hospital Center in Montreal (QC) for their dedication to the collection of the Infant cry data base. This research has been funded by a grant from the Bill & Melinda Gates Foundation through the Grand Challenges Explorations Initiative.

CONCLUSION

This thesis is conceived as a research work of MMS laboratory of Université du Québec, École de technologie supérieure under the direct supervision of Dr. Chakib Tadj.

The ambitious goal – the non-invasive newborn cry-based diagnostic system – is design of an additional tool or health care system that can be trained to work as an indispensable assistant to help the pediatricians who have misgivings arrive at a decision. The system would be able to classify healthy and sick infants who suffer from different enrolled diseases or pathological conditions. If you break down this goal into smaller steps, in this thesis we reached a significant milestone one the way to the newborn cry-based diagnostic system.

Most of the previous works on assessment of infant cry provide a binary classification of healthy infants from sick infants who suffer from a known (specific) disease such as deaf babies. Nonetheless, in this work the focus of attention in the domain is shifted into the open-set multi-pathology recognition scenario. In other words, there is a class called “others” or “none-of-the-above” in the target set dedicated solely to the test sick infants who suffer from unseen out-of-set sicknesses that are not enrolled in the system yet. Therefore, an informed choice of pathological states and collecting of the infant cry data base were necessary and unavoidable which have been done in the neonatology departments of several hospitals in Canada and Lebanon. It is worth mentioning that due to the inspiration behind this research work, there was no constraint placed on the recording procedure of infant cry signals.

Our work employed Gaussian Mixture Models (GMMs) as a flexible and powerful probabilistic tool for modeling multivariate stochastic feature vectors extracted from infant cry signals. Our basic goal in learning GMM is to estimate the unknown parameters of Gaussian mixture distributions that the extracted cry features are hypothetically come from. Adapted BML method was introduced in this work to learn growing GMM in an incremental and recursive manner. We have shown that not only the value of the log-likelihood for GMM trained with adapted BML method bears a close resemblance to that of GMM trained with

the traditional EM algorithm, but using this method has some benefits such as adding a new component to the direction that increase the predefined objective function the most, reducing sensitivity to initial parameters and estimating the optimum number of components based on incremental manner.

In data preprocessing, including selection and extraction of pathologically-informed features, different frame lengths (10-30 mec) with the same overlap percentage between two consecutive windows were considered for short-term processing of infant cry signals. The well-known acoustic features of speech, the dynamic MFCC features along with static MFCC features, have been extracted from both manually segmented expiratory and inspiratory infant cry vocalizations separately in this study. The results indicated that independent of the type of the cry units, adaptation method and classification task, the experiments on a shorter frame length have lower error rates in most of the cases.

We also brought the Gaussian Mixture Model - Universal Background Model (UBM) framework which is widely used in speaker recognition and verification domains, into newborn cry-based pathology recognition. Two health-independent and pathology-independent GMM-UBMs with a large number of mixture components were trained from a large amount of cry uttered by lots of full-term healthy and sick infants to represent the general cry feature characteristics for each population. Due to limitation of training infant cry data from an enrolled pathological condition, a target pathology model is derived from adapting the parameters of UBM using the infants' enrollment cries. A variant of boosted mixture learning (BML) method is employed in order to derive a unique cry-pattern for each enrolled disease from the GMM-UBM by adaptation of GMM parameters. We have shown how this boosting-based approach can also enhance maximum a-posterior (MAP) or Bayesian adaptation of the parameters of GMM-UBM. Note that the traditional EM algorithm and MAP adaptation method are assumed to be our reference systems in the GMM training process and adaptation of GMM in this work.

In our investigation into short-time power spectrum of cry signals, we found that more than 94% of the energy in typical healthy and sick infant cry signals is stored within less than 4 kHz of bandwidth. However, the results indicates that the energies of the inspiration cry vocalizations for sick infants tend to accumulate at a slower rate than the energies of the expiration segments, especially in cases of RDS disorders. Moreover, since in typical infant cry signals inspiration is much shorter than expiration and therefore the average likelihood ratio over expiration cry units is more reliable than inspiration cry units. As a result of above-mentioned differences in the types of cry sounds, expiration–based models have more distinctive abilities than inspiration-based models in classifying healthy and sick infants independent of the frame length.

The detection decision on each test infant's cry is based on whether the set of feature vectors observed on the presented cry signal is more likely to have been produced by the hypothesized health-condition class or by the other available alternative classes. In the next step, individual scores for both types of cry sounds construct a new feature vector in order to make a score level fusion. The results of experiments confirm that this approach is able to provide valuable information that comes from the fusion of the proposed two independent subsystems to a more reliable decision making process.

In fact, we have achieved what we have aimed for in our objective and accordingly have contributed in advancement of the algorithm for learning statistical Gaussian mixture models. Moreover, Maximum a-Posterior (MAP) adaptation of the parameters of the GMM-UBM is enhanced with the implementation of ideas used for boosted mixture learning method. In brief, the proposed diagnostic system depicted in Figure 4.16 is built around the likelihood ratio test by using GMMs for likelihood functions and GMM-UBM models to derive subclass models from the related UBM via the adapted-BML method instead of common Bayesian adaptation.

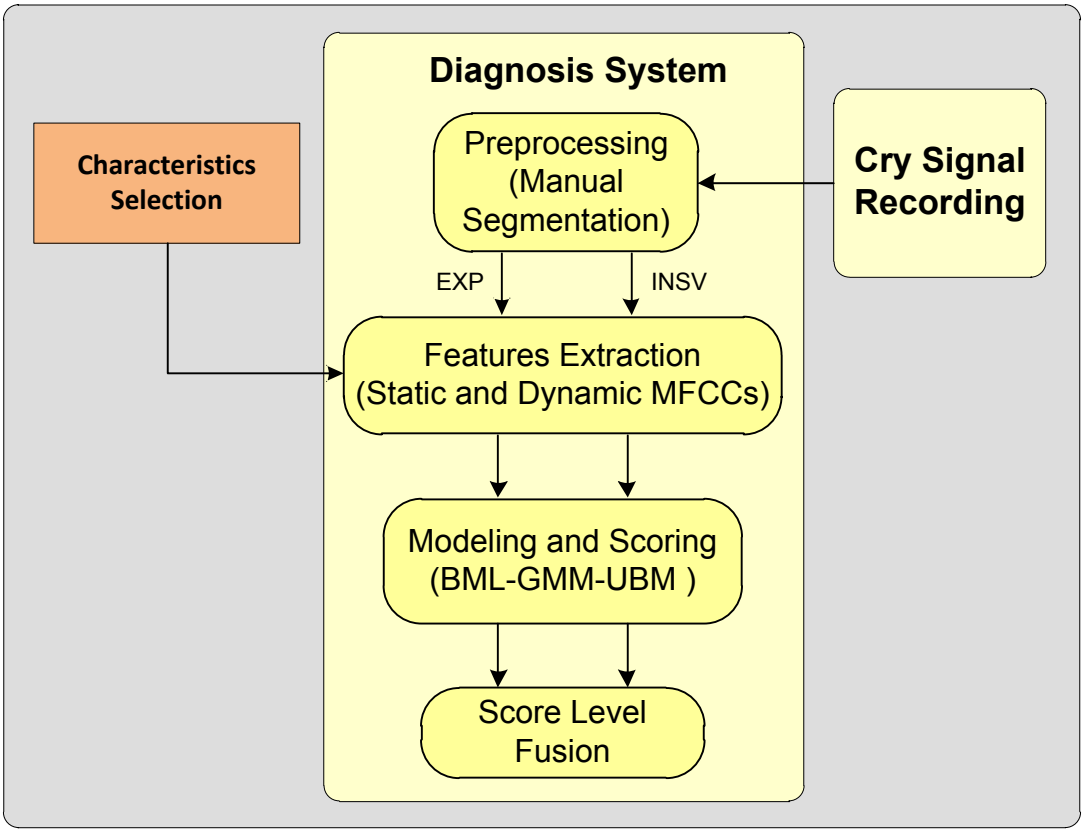


Figure 4.16 Introduced system overview

Our work differ from previous works in the domain in the sense that while others usually deal with binary classification tasks between healthy and sick infant with only one specific disorder. In effect, the cry-based diagnostic system that we have designed along with all of its techniques has a hierarchical scheme that focus into multi-pathology classification problem via combination of individual classifiers. In addition, as it is clear this approach totally is compatible to be extended for more diseases and syndromes, providing enough corresponding infant cry data. Moreover, it is worthwhile mentioning that the chosen diseases have not been previously studied.

Today, we are in the early stage of understanding how the cry features can distinguish between newborn infants with different pathologies. Although we have delivered the first major milestone in our final goal, but there are still a lot of work to do. However, this work was also the juncture at which the extracted (static and dynamic) MFCCs and adapted

boosted mixture learning method gathered around the Gaussian mixture models to help us to gradually get closer to our goal. Despite the main limitation of the current work stated in content which is small cry database corpus, in the 2nd and 3rd chapters we showed the ability of GMMs to create cry patterns for healthy and sick infants by using static MFCCs. Afterward, in the 4th chapter, some experiments that investigate the ability of both expiratory and inspiratory cry vocalizations separately were described. Moreover, due to lack of cry corpus for sick infants especially with some specific diseases, we tried to categorize diseases based on the grouping of symptoms and organs affected. Consequently, in each of five new categories we had more data to train Gaussian models. Procedure of collecting infant cry data base is still in progress but so far it is not enough to create a universal background model for infant cry signals due to small number of infants in each category. Consequently, we still have a long way to go and more research must be done to ensure that the system is practical and reliable.

RECOMENDATIONS

Some directions for future research related to current study are proposed in the following: Humans use several levels of information to recognize the reason behind the babies' cry, but automatic systems are still dependent on the low-level acoustic information. The challenges in this area are to find, reliably extract, and effectively use these higher levels of information from the cry signal. It is likely that these higher levels of information will not provide good performance on their own and may need to be fused with more acoustic-based systems. Techniques to fuse and apply high-level information with low-level acoustic features need to be developed in a way that makes the feature classes work synergistically.

Same as multi-modal identity verification systems, combination of the output score of different experts using different and independent cry feature characteristics such as MFCCs, MFDWC, fundamental frequency and formants can represent a remarkable achievement in the domain. We recommend testing the performance of the diagnostic system using a fuzzy classifier to classify and identify different pathological cries. This classifier uses fuzzy logic to model and classify the different cries. Fuzzy logic rule can be defined for each kind of pathology to describe the relationship between the features and pathological condition. The time-domain and frequency-domain pathological cries characterization presented in this work such as (hyper-phonic and dysphonic segments, the irregularity of fundamental frequency) might enhance the performance of the diagnostic system. We also recommend the merger of the two classifiers (GMM classifier and fuzzy).

In human speech signals there is not much information above 6.8 kHz. It has been shown in this work that cry signals of full-term healthy and sick infants have more than 94% of their energies below 4 kHz. So far, information up to 4 kHz bandwidth of recorded infant cry signals has been used and therefore, the idea of band splitting and sub-band features on the upper frequency band might be worthwhile to try in order to make sure that there is no loss of information.

As we discussed it earlier, classification systems that integrate information at an early stage of processing are believed to be more effective than those systems which perform integration at a later stage. Considering this fact that the feature set contains richer information about the input data than matching score or the output decision of a matcher, any effort toward fusion at this level will be beneficial. However, fusion at this level is difficult to achieve in practice because different feature sets might not be compatible. In case of using different compatible characteristic features, multiple data streams could be used with tied-mixture systems as an alternative approach.

There are other related research works in the domain where advancement is being sought. Among them would be: (a) Cross-entropy (CE) method - Inspired by the intuitive idea behind BML method that new component should focus more on difficult-to-classify samples in which they are prone to make mistakes by current model, the cross-entropy objective function seems to have great potential especially by adding a weighting term to the cross-entropy objective function to boost the difficult samples. (b) Cost function - In order to make minimum-expected cost decision we need meaningful cost values for either false acceptance (FA) or false rejection (FR or miss) errors. In fact, costs result from combining several factors measured in different units: money, time or quality of life. However, a new definition of cost function is being sought in order to keep the efficiency of the classifier and at the same time reduce the risk of medical mistakes by individualized training program based on maternal issues such as birth weight and gestational age. (c) Wavelet Transform-based Cepstral Coefficients (WTCC) and Gammatone Frequency Cepstral Coefficients (GFCC) – It would be worthwhile to substitute WTCC for DFT analysis with poor joint time-frequency resolution which doesn’t match perceptual hearing attributes. Moreover, the novel multi-resolution time frequency feature called, GFCC, which are introduced based on an auditory periphery model by a Cepstral analysis are definitely worth investigating.

LIST OF REFERENCES

Agresti, Alan, et Brent A. Coull. 1998. « Approximate is Better than "Exact" for Interval Estimation of Binomial Proportions ». *The American Statistician,* vol. 52, n° 2, p. 119-126.

Akaike, H. 1974. « A new look at the statistical model identification ». *Automatic Control, IEEE Transactions on,* vol. 19, n° 6, p. 716-723.

Akande, Olatunji O., et Peter J. Murphy. 2005. « Estimation of the vocal tract transfer function with application to glottal wave analysis ». *Speech Communication,* vol. 46, n° 1, p. 15-36.

Amaro-Camargo, Erika, et Carlos Reyes-García. 2007. « Applying Statistical Vectors of Acoustic Characteristics for the Automatic Classification of Infant Cry ». In *Advanced Intelligent Computing Theories and Applications. With Aspects of Theoretical and Methodological Issues*, sous la dir. de Huang, De-Shuang, Laurent Heutte et Marco Loog. Vol. 4681, p. 1078-1085. Coll. « Lecture Notes in Computer Science »: Springer Berlin / Heidelberg.

Bauer, Eric, et Ron Kohavi. 1999a. « An Empirical Comparison of Voting Classification Algorithms: Bagging, Boosting, and Variants ». *Machine Learning,* vol. 36, n° 1, p. 105-139.

Bauer, Eric, et Ron Kohavi. 1999b. « An Empirical Comparison of Voting Classification Algorithms: Bagging, Boosting, and Variants ». *Machine Learning,* vol. 36, n° 1-2, p. 105-139.

Ben-Yacoub, S., Y. Abdeljaoued et E. Mayoraz. 1999. « Fusion of face and speech data for person identity verification ». *Neural Networks, IEEE Transactions on,* vol. 10, n° 5, p. 1065-1074.

Bengtsson, Thomas, et Joseph E. Cavanaugh. 2006. « An improved Akaike information criterion for state-space model selection ». *Computational Statistics & Data Analysis,* vol. 50, n° 10, p. 2635-2654.

Benson, J.B., et M.M. Haith. 2009. *Social and Emotional Development in Infancy and Early Childhood*. Elsevier Science.

Benson, Janette. 2009. *Social and emotional development in infancy and early childhood*. Elsevier [u.a.].

Benzeghiba, M., R. De Mori, O. Deroo, S. Dupont, T. Erbes, D. Jouvet, L. Fissore, P. Laface, A. Mertins, C. Ris, R. Rose, V. Tyagi et C. Wellekens. 2007. « Automatic speech

recognition and speech variability: A review ». *Speech Communication,* vol. 49, n° 10–11, p. 763-786.

Berlinet, A., et Ch Roland. 2007. « Acceleration schemes with application to the EM algorithm ». *Computational Statistics & Data Analysis,* vol. 51, n° 8, p. 3689-3702.

Bishop, Christopher. 2006. *Pattern recognition and machine learning*. Springer.

Blum, R.S., et Z. Liu. 2005. *Multi-Sensor Image Fusion and Its Applications*. CRC Press.

Boyu, Wang, Wong Chi Man, Wan Feng, Mak Peng Un, Mak Pui In et I. Vai Mang. 2010. « Gaussian mixture model based on genetic algorithm for brain-computer interface ». In *Image and Signal Processing (CISP), 2010 3rd International Congress on*. (16-18 Oct. 2010) Vol. 9, p. 4079-4083.

Brummer, Niko. 2010. « Measuring, refining and calibrating speaker and language information extracted from speech ». Stellenbosch: University of Stellenbosch.

Cacace, Anthony T., Michael P. Robb, John H. Saxman, Herman Risemberg et Peter Koltai. 1995. « Acoustic features of normal-hearing pre-term infant cry ». *International Journal of Pediatric Otorhinolaryngology,* vol. 33, n° 3, p. 213-224.

Cano Ortiz, Sergio, Daniel Escobedo Beceiro et Taco Ekkel. 2004a. « A Radial Basis Function Network Oriented for Infant Cry Classification ». In *Progress in Pattern Recognition, Image Analysis and Applications*, sous la dir. de Sanfeliu, Alberto, José Martínez Trinidad et Jesús Carrasco Ochoa. Vol. 3287, p. 15-36. Coll. « Lecture Notes in Computer Science »: Springer Berlin / Heidelberg.

Cano Ortiz, SergioD, DanielI Escobedo Beceiro et Taco Ekkel. 2004b. « A Radial Basis Function Network Oriented for Infant Cry Classification ». In *Progress in Pattern Recognition, Image Analysis and Applications*, sous la dir. de Sanfeliu, Alberto, JoséFrancisco Martínez Trinidad et JesúsAriel Carrasco Ochoa. Vol. 3287, p. 374-380. Coll. « Lecture Notes in Computer Science »: Springer Berlin Heidelberg. < http://dx.doi.org/10.1007/978-3-540-30463-0_46 >.

Cano, Sergio, Israel Suaste, Daniel Escobedo, Carlos Reyes-García et Taco Ekkel. 2006. « A Combined Classifier of Cry Units with New Acoustic Attributes ». In *Progress in Pattern Recognition, Image Analysis and Applications*, sous la dir. de Martínez-Trinidad, José, Jesús Carrasco Ochoa et Josef Kittler. Vol. 4225, p. 416-425. Coll. « Lecture Notes in Computer Science »: Springer Berlin / Heidelberg.

« Congenital anomalies ». 2014. World Health Organization (WHO), Fact sheet N°370. < http://www.who.int/mediacentre/factsheets/fs370/en/ >.

Corwin, M. J., B. M. Lester et H. L. Golub. 1996. « The infant cry: what can it tell us? ». *Current Problem Pediatrics,* vol. 26, n° 9, p. 325-34.

Cunningham FG, Leveno KJ, Bloom SL, F. Gary Cunningham, Kenneth J. Leveno, Steven L. Bloom, John C. Hauth, Dwight J. Rouse et Catherine Y. Spong. 2010. « Fetal growth and development ». In *Williams Obstetrics*. New York, NY: McGraw-Hill.

Davis, S., et P. Mermelstein. 1980. « Comparison of parametric representations for monosyllabic word recognition in continuously spoken sentences ». *Acoustics, Speech and Signal Processing, IEEE Transactions on,* vol. 28, n° 4, p. 357-366.

Deller, J.R., J.G. Proakis et J.H.L. Hansen. 1993. *Discrete-time processing of speech signals*. Macmillan Pub. Co.

Dempster, A. P., N. M. Laird et D. B. Rubin. 1977. « Maximum Likelihood from Incomplete Data via the EM Algorithm ». *Journal of the Royal Statistical Society. Series B (Methodological),* vol. 39, n° 1, p. 1-38.

Dieckmann, U., P. Plankensteiner et T. Wagner. 1997. « SESAM: A biometric person identification system using sensor fusion ». *Pattern Recognition Letters,* vol. 18, n° 9, p. 827-833.

Divakaran, Ajay. 2009. *Multimedia Content Analysis: Theory and Applications (Signals and Communication Technology)*. Springer-Verlag.

Dobrovic, M. M., V. D. Delic, N. M. Jakovljevic et I. D. Jokic. 2012. « Comparison of the automatic speaker recognition performance over standard features ». In *Intelligent Systems and Informatics (SISY), 2012 IEEE 10th Jubilee International Symposium on*. (20-22 Sept. 2012), p. 341-344.

Donald F, Specht. 1990. « Probabilistic neural networks ». *Neural Networks,* vol. 3, n° 1, p. 109-118.

Duda, Richard, et Peter Hart. 1973. *Pattern Classification and Scene Analysis*. New York: John Wiley & Sons Inc.

Duda, Richard O, Peter E Hart et David G Stork. 2001. *Pattern classification*. John Wiley & Sons, 654 p.

Farsaie Alaie, Hesam, et Chakib Tadj. 2012. « Cry-Based Classification of Healthy and Sick Infants Using Adapted Boosting Mixture Learning Method for Gaussian Mixture Models ». *Modelling and Simulation in Engineering,* vol. 2012, p. 10.

Farsaie Alaie, Hesam, et Chakib Tadj. 2013. « Splitting of Gaussian Models via Adapted BML Method Pertaining to Cry-Based Diagnostic System ». *Engineering,* vol. 5, p. 277-283.

Fawcett, Tom. 2006. « An introduction to ROC analysis ». *Pattern Recognition Letters,* vol. 27, n° 8, p. 861-874.

Flynn, Ronan, et Edward Jones. 2008. « Combined speech enhancement and auditory modelling for robust distributed speech recognition ». *Speech Communication,* vol. 50, n° 10, p. 797-809.

Freund, Yoav, et Robert E. Schapire. 1997. « A Decision-Theoretic Generalization of On-Line Learning and an Application to Boosting ». *Journal of Computer and System Sciences,* vol. 55, n° 1, p. 119-139.

Friedman, Jerome. 2001. « Greedy function approximation: A gradient boosting machine ». *Annals of Statistics,* vol. 29, p. 1189-1232.

Galaviz, Orion, et Carlos García. 2005. « Infant Cry Classification to Identify Hypo Acoustics and Asphyxia Comparing an Evolutionary-Neural System with a Neural Network System ». In *MICAI 2005: Advances in Artificial Intelligence*, sous la dir. de Gelbukh, Alexander, Álvaro de Albornoz et Hugo Terashima-Marín. Vol. 3789, p. 949-958. Coll. « Lecture Notes in Computer Science »: Springer Berlin / Heidelberg.

Gauvain, J., et Lee Chin-Hui. 1994. « Maximum a posteriori estimation for multivariate Gaussian mixture observations of Markov chains ». *Speech and Audio Processing, IEEE Transactions on,* vol. 2, n° 2, p. 291-298.

Gilbert, H. R., et M. P. Robb. 1996. « Vocal fundamental frequency characteristics of infant hunger cries: birth to 12 months ». In *Int J Pediatr Otorhinolaryngol*. Vol. 34, p. 237-43. 3. Ireland. NLM.

Gray, A., Jr., et J. Markel. 1974. « A spectral-flatness measure for studying the autocorrelation method of linear prediction of speech analysis ». *Acoustics, Speech and Signal Processing, IEEE Transactions on,* vol. 22, n° 3, p. 207-217.

Han, Hui, Wen-Yuan Wang et Bing-Huan Mao. 2005. « Borderline-SMOTE: A New Over-Sampling Method in Imbalanced Data Sets Learning ». In *Advances in Intelligent Computing*, sous la dir. de Huang, De-Shuang, Xiao-Ping Zhang et Guang-Bin Huang. Vol. 3644, p. 878-887. Coll. « Lecture Notes in Computer Science »: Springer Berlin Heidelberg. < http://dx.doi.org/10.1007/11538059_91 >.

Hariharan, M., R. Sindhu et Sazali Yaacob. 2012. « Normal and hypoacoustic infant cry signal classification using time-frequency analysis and general regression neural network ». *Comput. Methods Prog. Biomed.,* vol. 108, n° 2, p. 559-569.

Hariharan, M., Sazali Yaacob et Saidatul Ardeenaawatie Awang. 2011. « Pathological infant cry analysis using wavelet packet transform and probabilistic neural network ». *Expert Systems with Applications,* vol. 38, n° 12, p. 15377-15382.

He, Haibo. 2011. *Self-Adaptive Systems for Machine Intelligence*.

Heck, L. P., et K. C. Chou. 1994. « Gaussian mixture model classifiers for machine monitoring ». In *Acoustics, Speech, and Signal Processing, 1994. ICASSP-94., 1994 IEEE International Conference on*. (19-22 Apr 1994) Vol. vi, p. VI/133-VI/136 vol.6.

Heigold, G., H. Ney, P. Lehnen, T. Gass et R. Schluter. 2011. « Equivalence of Generative and Log-Linear Models ». *Audio, Speech, and Language Processing, IEEE Transactions on,* vol. 19, n° 5, p. 1138-1148.

Heigold, Georg, Patrick Lehnen, Ralf Schlüter et Hermann Ney. 2008. « On the equivalence of {Gaussian} and log-linear {HMMs} ». In *INTERSPEECH*. p. 273-276.

Heron, Melonie 2013. « Deaths: Leading Causes for 2010 ». *National Vital Statistics Reports (NVSR),* vol. 62(6), n° National Center for Health Statistics

Higgins, A., L. Bahler et J. Porter. 1991. « Speaker verification using randomized phrase prompting ». *Digital Signal Processing,* vol. 1, n° 2, p. 89-106.

Holmes, J and Holmes, W. 2001. *Speech Synthesis and Recognition*, second. Taylor & Francis, 298 p.

Hong, L., et A. Jain. 1998. « Integrating faces and fingerprints for personal identification ». *Pattern Analysis and Machine Intelligence, IEEE Transactions on,* vol. 20, n° 12, p. 1295-1307.

Huang, Xuedong , Alejandro Acero et Hsiao-Wuen Hon. 2001a. *Spoken language processing : A guide to theory, algorithm, and system development*. Upper Saddle River, N.J. : Prentice Hall PTR, 980 p.

Huang, Xuedong, Alex Acero et Hsiao-Wuen Hon. 2001b. *Spoken Language Processing: A Guide to Theory, Algorithm and System Development*. Prentice Hall PTR.

John R. Deller, Jr., John G. Proakis et John H. Hansen. 1993. *Discrete Time Processing of Speech Signals*. Prentice Hall PTR, 800 p.

Jun, Du, Hu Yu et Jiang Hui. 2011. « Boosted Mixture Learning of Gaussian Mixture Hidden Markov Models Based on Maximum Likelihood for Speech Recognition ». *Audio, Speech, and Language Processing, IEEE Transactions on,* vol. 19, n° 7, p. 2091-2100.

Kheddache, Yasmina. 2014. *Caractérisation des cris des nourrissons en vue du diagnostic précoce de différentes pathologies* (2014). Montréal: École de technologie supérieure, 1 ressource en ligne (xx, 184 pages) p.

Kim, Minyoung, et Vladimir Pavlovic. 2007. « A recursive method for discriminative mixture learning ». In *Proceedings of the 24th international conference on Machine learning*. (Corvalis, Oregon), p. 409-416. 1273548: ACM.

Kohavi, Ron. 1995. « A study of cross-validation and bootstrap for accuracy estimation and model selection ». In *Proceedings of the 14th international joint conference on Artificial intelligence - Volume 2*. (Montreal, Quebec, Canada), p. 1137-1143. 1643047: Morgan Kaufmann Publishers Inc.

Kohavi, Ron, et Foster Provost. 1998. « Glossary of Terms ». *Editorial for the Special Issue on Applications of Machine Learning and the Knowledge Discovery Process,* vol. 30, n° 2-3, p. 271-274.

Kolcz, Aleksander, Abdur Chowdhury et Joshua Alspector. 2003. « Data duplication: an imbalance problem ? ». In *The Twentieth International Conference on Machine Learning (ICML-2003) Workshop on Learning from Imbalanced Data Sets II*.

LaGasse, Linda L., A. Rebecca Neal et Barry M. Lester. 2005. « Assessment of infant cry: Acoustic cry analysis and parental perception ». *Mental Retardation and Developmental Disabilities Research Reviews,* vol. 11, n° 1, p. 83-93.

Lederman, Dror. 2002. « Automatic Classification of Infants' Cry ». Master of Science Thesis. BEN-GURION University of the NEGEV 121 p.

Li, Ming, Kyu J. Han et Shrikanth Narayanan. 2013. « Automatic speaker age and gender recognition using acoustic and prosodic level information fusion ». *Computer Speech & Language,* vol. 27, n° 1, p. 151-167.

Lind, K., et K. Wermke. 2002. « Development of the vocal fundamental frequency of spontaneous cries during the first 3 months ». In *Int J Pediatr Otorhinolaryngol*. Vol. 64, p. 97-104. 2. Ireland. NLM.

Lobo, Ingrid , et Kira Zhaurova. 2008. « Birth defects: causes and statistics ». *Nature Education* vol. 1, p. 1:18.

Longbiao, Wang, K. Minami, K. Yamamoto et S. Nakagawa. 2010. « Speaker identification by combining MFCC and phase information in noisy environments ». In *Acoustics Speech and Signal Processing (ICASSP), 2010 IEEE International Conference on*. (14-19 March 2010), p. 4502-4505.

Ma, Jiyong, et Wen Gao. 1998. « The supervised learning Gaussian mixture model ». *Journal of Computer Science and Technology,* vol. 13, n° 5, p. 471-474.

Makhoul, John, et R Viswanathan. 1974. « Adaptive Preprocessing for Linear Predictive Speech Compression Systems ». *Journal of the Acoustical Society of America*. p. 475-476.

Martin, Alvin, George Doddington, Terri Kamm, Mark Ordowski et Mark Przybocki. 1997. « The DET Curve in Assessment of Detection Task Performance ». In *Proc. Eurospeech '97*. p. 1895-1898.

Matsui, Tomoko, et Sadaoki Furui. 1994. « Similarity normalization method for speaker verification based on a posteriori probability ». In *ESCA Workshop on Automatic Speaker Recognition, Identification and Verification*. p. 59-62.

Matsui, Tomoko, et Sadaoki Furui. 1995. « Likelihood normalization for speaker verification using a phoneme- and speaker-independent model ». *Speech Communication,* vol. 17, n° 1–2, p. 109-116.

McLachlan, Geoffrey., et David . Peel. 2004. *Finite Mixture Models*. Coll. « Wiley Series in Probability and Statistics ». John Wiley & Sons, 456 p.

Metz, C. E. 1978. « Basic principles of ROC analysis ». *Seminars in nuclear medicine,* vol. 8, n° 4, p. 283-298.

Michelsson, K. 1971. « Cry analyses of symptomless low birth weight neonates and of asphyxiated newborn infants ». *Acta Paediatr Scand Suppl,* vol. 216, p. 1-45.

Michelsson, K., K. Eklund, P. Leppanen et H. Lyytinen. 2002. « Cry characteristics of 172 healthy 1-to 7-day-old infants ». In *Folia Phoniatr Logop*. Vol. 54, p. 190-200. 4. Switzerland: 2002 S. Karger AG, Basel. NLM.

Michelsson, K., et O. Michelsson. 1999. « Phonation in the newborn, infant cry ». *Int J Pediatr Otorhinolaryngol,* vol. 49 Suppl 1, p. S297-301.

Miller, B.F., et M.T. O'Toole. 2003. *Encyclopedia and dictionary of medicine, nursing, and allied health*. v. 1. Saunders.

Mporas, Iosif, Todor Ganchev, Otilia Kocsis et Nikos Fakotakis. 2011. « Context-adaptive pre-processing scheme for robust speech recognition in fast-varying noise environment ». *Signal Processing,* vol. 91, n° 8, p. 2101-2111.

Murty, K. S. R., et B. Yegnanarayana. 2006. « Combining evidence from residual phase and MFCC features for speaker recognition ». *Signal Processing Letters, IEEE,* vol. 13, n° 1, p. 52-55.

Nengheng, Zheng, Lee Tan et P. C. Ching. 2007. « Integration of Complementary Acoustic Features for Speaker Recognition ». *Signal Processing Letters, IEEE,* vol. 14, n° 3, p. 181-184.

Newman, J.D. 1985. *The infant cry of primates: an evolutionary perspective*. New York: Plenum Press.

Ng, Shu-Kay, et Geoffrey J. McLachlan. 2004. « Speeding up the EM algorithm for mixture model-based segmentation of magnetic resonance images ». *Pattern Recognition,* vol. 37, n° 8, p. 1573-1589.

Nwe, Tin Lay, Say Wei Foo et Liyanage C. De Silva. 2003. « Speech emotion recognition using hidden Markov models ». *Speech Communication,* vol. 41, n° 4, p. 603-623.

O'Shaughnessy, Douglas. 2000a. *Speech Communications: Human and Machine*. Wiley-IEEE Press.

O'Shaughnessy, Douglas. 2000b. *Speech Communications: Human and Machine*. Coll. « Speech Communications: Human and Machine ». Montréal, Québec, Canada: Wiley-IEEE Press, 547 p.

O'Shaughnessy, Douglas. 2008. « Invited paper: Automatic speech recognition: History, methods and challenges ». *Pattern Recognition,* vol. 41, n° 10, p. 2965-2979.

Orozco, J. , et C.A.R. Garcia. 2003. « Detecting pathologies from infant cry applying scaled conjugate gradient neural networks ». In *European Symposium on Artificial Neural Networks*. (Bruges-Belgium), p. 349-354.

Ortiz, S.D.C., D.I.E. Beceiro et T. Ekkel. 2004. *A radial basis function network oriented for infant cry classification*. Coll. « Lecture notes in computer science 3287 », p. 374-380.

Partanen, T. J., O. Wasz-Hockert, V. Vuorenkoski, K. Theorell, E. H. Valanne et J. Lind. 1967. « Auditory identification of pain cry signals of young infants in pathological conditions and its sound spectrographic basis ». *Ann Paediatr Fenn,* vol. 13, n° 2, p. 56-63.

Pavlovic, V. 2004. « Model-based motion clustering using boosted mixture modeling ». In *Computer Vision and Pattern Recognition, 2004. CVPR 2004. Proceedings of the 2004 IEEE Computer Society Conference on*. (27 June-2 July 2004) Vol. 1, p. I-811-I-818 Vol.1.

Plumpe, M. D., T. F. Quatieri et D. A. Reynolds. 1999. « Modeling of the glottal flow derivative waveform with application to speaker identification ». *Speech and Audio Processing, IEEE Transactions on,* vol. 7, n° 5, p. 569-586.

Prescott, R. 1975. « Infant cry sound; developmental features ». *J Acoust Soc Am,* vol. 57, n° 5, p. 1186-91.

Quatieri, T. F. 2002. *Discrete-time speech signal processing : principles and practice*. Upper Saddle River, NJ: Prentice Hall.

Rabiner, L. R., et R. W. Schafer. 1978. *Digital Processing of Speech Signals*. Prentice-Hall.

Redner, Richard, et Homer Walker. 1984. « Mixture Densities, Maximum Likelihood and the Em Algorithm ». *SIAM Review,* vol. 26, n° 2, p. 195-239.

Refaeilzadeh, Payam, Lei Tang et Huan Liu. 2009. « Cross Validation ». In *Encyclopedia of Database Systems*, sous la dir. de Özsu, Tamer, et Ling Liu. Springer.

Reynolds, D. A. 1997. « Comparison of background normalization methods for text-independent speaker verification ». In *Proc. of 5th European Conf. on Speech Communication and Technology (Eurospeech)*. Vol. 2, p. 963-966.

Reynolds, D. A., et R. C. Rose. 1995. « Robust text-independent speaker identification using Gaussian mixture speaker models ». *Speech and Audio Processing, IEEE Transactions on,* vol. 3, n° 1, p. 72-83.

Reynolds, Douglas. 2009. « Universal Background Models ». In *Encyclopedia of Biometrics*, sous la dir. de Li, StanZ, et Anil Jain. p. 1349-1352. Springer US. < http://dx.doi.org/10.1007/978-0-387-73003-5_197 >.

Reynolds, Douglas A. 1995a. « Automatic speaker recognition using gaussian mixture speaker models ». *Lincoln Laboratory Journal,* vol. 8, n° 2, p. 173-191.

Reynolds, Douglas A. 1995b. « Speaker identification and verification using Gaussian mixture speaker models ». *Speech Communication,* vol. 17, n° 1–2, p. 91-108.

Reynolds, Douglas A., Thomas F. Quatieri et Robert B. Dunn. 2000. « Speaker Verification Using Adapted Gaussian Mixture Models ». *Digital Signal Processing,* vol. 10, n° 1–3, p. 19-41.

Rosales-Pérez, Alejandro, CarlosA Reyes-García, JesusA Gonzalez et Emilio Arch-Tirado. 2012. « Infant Cry Classification Using Genetic Selection of a Fuzzy Model ». In *Progress in Pattern Recognition, Image Analysis, Computer Vision, and Applications*, sous la dir. de Alvarez, Luis, Marta Mejail, Luis Gomez et Julio Jacobo. Vol. 7441, p. 212-219. Coll. « Lecture Notes in Computer Science »: Springer Berlin Heidelberg. < http://dx.doi.org/10.1007/978-3-642-33275-3_26 >.

Rosenberg, Aaron E, Joel DeLong, Chin-Hui Lee, Biing-Hwang Juang et Frank K Soong. 1992. « The use of cohort normalized scores for speaker verification ». *ICSLP,* vol. 92, p. 599-602.

Ross, A., et A. K. Jain. 2004. « Multimodal Biometrics: an overview ». In *12th European Signal Processing Conference (EUSIPCO)*. (Vienna, Austria), p. 1221-1224.

Rosset, Saharon. 2005. « Robust boosting and its relation to bagging ». In *Proceedings of the eleventh ACM SIGKDD international conference on Knowledge discovery in data mining*. (Chicago, Illinois, USA), p. 249-255. 1081900: ACM.

Rynn, L.Cragan, J.Correa, A. 2008. « UPdate on overall prevalence of major birth defects-Atlanta, Georgia, 1978-2005 ». *JAMA,* vol. 299, n° 7, p. 756-758.

Sagi, Abraham. 1981. « Mothers' and non-mothers' identification of infant cries ». *Infant Behavior and Development,* vol. 4, p. 37-40.

SaveTheChildren. 2013. *State of the World's Mothers 2013: Surviving the First Day*. Save the Children.

Schwarz, Gideon. 1978. « Estimating the Dimension of a Model ». *The Annals of Statistics,* vol. 6, n° 2, p. 461-464.

Silverthorne, Andrea 2014. *New reports reveal higher birth-defect rates in Canadian babies than American*. The New Brunswick Beacon.
< http://www.newbrunswickbeacon.ca/39849/reports-reveal-higher-birthdefect-rates-canadian-babies-american/ >.

Snelick, Robert, U. Uludag, Alan Mink, M. Indovina et A. Jain. 2005. « Large-scale evaluation of multimodal biometric authentication using state-of-the-art systems ». *Pattern Analysis and Machine Intelligence, IEEE Transactions on,* vol. 27, n° 3, p. 450-455.

T.J., Mathews, et Marian F. MacDorman. 2013. « Infant Mortality Statistics from the 2010 Period Linked Birth/Infant Death Data Set ». *National Vital Statistics Reports (NVSR),* vol. 62(8), n° National Center for Health Statistics.

Thomas, James P. 1985. « Detection and identification: how are they related? ». *Journal of the Optical Society of America A,* vol. 2, n° 9, p. 1457-1467.

Tipton, H.F., et M. Krause. 2007. *Information Security Management Handbook, Sixth Edition*. Taylor & Francis.

Update on overall prevalence of major birth defects—atlanta, georgia, 1978-2005. 2008. *JAMA,* vol. 299, n° 7, p. 756-758.

Vatsa, Mayank, Richa Singh et Afzel Noore. 2007. « Integrating Image Quality in 2ν-SVM Biometric Match Score Fusion ». *International Journal of Neural Systems,* vol. 17, n° 05, p. 343-351.

Verduzco-Mendoza, Antonio, Emilio Arch-Tirado, CarlosA Reyes García, Jaime Leybón Ibarra et Juan Licona Bonilla. 2009. « Qualitative and Quantitative Crying Analysis of New Born Babies Delivered Under High Risk Gestation ». In *Multimodal Signals: Cognitive and Algorithmic Issues*, sous la dir. de Esposito, Anna, Amir Hussain, Maria Marinaro et Raffaele Martone. Vol. 5398, p. 320-327. Coll. « Lecture Notes in Computer Science »: Springer Berlin Heidelberg. < http://dx.doi.org/10.1007/978-3-642-00525-1_32 >.

Verlinde, P., et G. Cholet. 1999. « Comparing decision fusion paradigms using k-NN based classifiers, decision trees and logistic regression in a multi-modal identity verification application ». In *Proc. AVBPA*. p. 188-193.

Wasz-Hockert, O., J. Lind, V. Vuorenkoski, T Partanen et E. Valanne. 1968. *The infant cry : A spectrographic and auditory analysis*. Coll. « Clinics in developmental Medicine ». Philadelphia: Lippincott.

Wasz-Hockert, O., K. Michelsson et J. Lind. 1985. *Twenty-five years of Scandinavian cry research*. Coll. « Infant crying: Theoretical and research perspectives ». New York, 83-104 p.

Wasz-Hockert, O., E. Valanne, V. Vuorenkoski, K. Michelsson et A. Sovijarvi. 1963. « Analysis of some types of vocalization in the newborn and in early infancy ». *Ann Paediatr Fenn,* vol. 9, p. 1-10.

« The World factbook ». 2013-14. Washington, DC: Central Intelligence Agency: The World factbook.
< https://www.cia.gov/library/publications/the-world-factbook/index.html >.

Xu, Lei, et Michael I. Jordan. 1996. « On Convergence Properties of the EM Algorithm for Gaussian Mixtures ». *Neural Computation,* vol. 8, n° 1, p. 129-151.

Young, S. J., G. Evermann, M. J. F. Gales, T. Hain, D. Kershaw, G. Moore, J. Odell, D. Ollason, D. Povey, V. Valtchev et P. C. Woodland. 2006a. *The HTK Book (for HTK version 3.4)*. Cambridge University Engineering Department.

Young, S. J., G. Evermann, M. J. F. Gales, T. Hain, D. Kershaw, G. Moore, J. Odell, D. Ollason, D. Povey, V. Valtchev et P. C. Woodland. 2006b. *The HTK Book, version 3.4*. Cambridge University Engineering Department.

Young, Steve, Gunnar Evermann, Mark Gales, Thomas Hain, Dan Kershaw, Xunying Liu, Gareth Moore, Julian Odell, Dave Ollason, Dan Povey, Valtcho Valtchev et Phil Woodland. 2006c. *The HTK Book (for HTK Version 3.4)*. Cambridge University Engineering Department.

Zill, Dennis, Warren wright et Michael Cullen. 2011. *Advanced engineering mathematics*, Fourth. 884 p.