



Ministry of Higher Education and
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University of Diyala
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Department of Computer Science



Thalassemia Disease Classification Based On Machine Learning Techniques

A Research

Submitted to the Department of Computer Science\|
College of Sciences\| University of Diyala in a Partial
Fulfillment of the Requirements for the Degree of
Master in Computer Science

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بِسْمِ اللَّهِ الرَّحْمَنِ الرَّحِيمِ

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muna q. mohammed

DEDICATION

To the flower of life and its light and the most precious person in my life, my tender mother.

To whom I proudly carry your name, teach me how to make success and instill confidence in myself my dear father, may God extend your life.

To those who supported me in adversity and the source of my happiness, my companion to my path and my love, my dear husband.

To whom their love and blood flow in my veins, and I lived with them the most beautiful moments, my brothers and sisters.

To the honey of my love and my soul, my dear my daughter.

To the candles that illuminate the path of knowledge in my path, my distinguished teachers.

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ABSTRACT

Thalassemia is considered one of the most common genetic blood disorders that has received excessive attention in the medical research fields worldwide. It cannot be cured , but an early detection and classification using screening process is the best way to prevent the disease. If early classification is done, patients can get the right treatment. It helps them increase their life expectancy and reduce the risk of thalassemia to the next generation.

In this thesis, efficient thalassemia classification system have been design to increase the accuracy and decrease the error rate in the diagnosis process. This system based on two proposed approaches for classifying thalassemia disease. The first proposed approach is based on four machine learning technique which include artificial neural network (ANN), decision tree (DT), k-nearest neighbor (KNN) and logistic regression (LR). This approach consist of two main stages: pre-processing and classification of thalassemia disease .The second proposed approach based on two deep learning techniques , these are consist of convolutional neural network (CNN) and deep neural network (DNN).

The proposed system has been tested by using two thalassemia dataset .The first type of dataset contain 391 sample with nine features and split into 30% for testing and 70% for training and the second type of dataset contain 7108 image with nine type of erythrocytes and split into 20% for testing and 80% for training. The comparison results show that the proposed system has efficient diagnosis performance and can be used as a promising tool for thalassemia disease diagnosis compared to another existing method where the accuracy rate of first proposed approach for first dataset using ANN is 99%, DT is 99% ,LR is 99% and KNN is 98%. The result of second proposed approach for the second dataset using deep learning technique has an average accuracy of 99% for CNN and 83% for DNN.

List of Contents

<i>Subject</i>	<i>Page No.</i>
<i>List of Contents</i>	I
<i>List of Abbreviations</i>	VI
<i>List of Tables</i>	VIII
<i>List of Figures</i>	IX
<i>List of Algorithms</i>	IX
<i>Chapter One: General Introduction</i>	
1.1 Introduction	1
1.2 Related Works	3
1.3 Problem Definition	8
1.4 Aims of the Thesis	9
1.5 Thesis challenges	9
1.6 Thesis Outlines	10
<i>Chapter Two: Theoretical Background</i>	
2.1 Introduction	12
2.2 Thalassemia Disease	12
2.3 Preprocessing	13
2.3.1 dropping	14
2.3.2 Data Cleaning	14
2.3.3 Data normalization	14

<i>2.4 Classification</i>	15
<hr/>	
<i>2.5 Machine Learning techniques</i>	16
<hr/>	
<i>2.5.1 Artificial Neural Network (ANN)</i>	18
<hr/>	
<i>2.5.1.1 Activation Function</i>	19
<hr/>	
<i>2.5.1.2 Back Propagation Neural Networks</i>	20
<hr/>	
<i>2.5.2 Decision Tree</i>	22
<hr/>	
<i>2.5.3 Logistic Regression</i>	25
<hr/>	
<i>2.5.4 K- Nearest Neighbor (KNN)</i>	27
<hr/>	
<i>2.6 Medical Image Analysis</i>	28
<hr/>	
<i>2.7 Deep Learning</i>	29
<hr/>	
<i>2.8 Convolution Neural Network (CNN)</i>	30
<hr/>	
<i>2.8.1 Convolution operation</i>	31
<hr/>	
<i>A. The Size and Number of Filters</i>	33
<hr/>	
<i>B. Stride</i>	34
<hr/>	
<i>C. Padding</i>	35
<hr/>	
<i>D. The formula of the Convolutional</i>	36
<hr/>	
<i>2.8.2 Nonlinearity</i>	36
<hr/>	
<i>2.8.3 Pooling Layer</i>	36
<hr/>	
<i>2.8.4 Dropout Network</i>	37
<hr/>	
<i>2.8.5 Normalization Layer in Neural Networks</i>	38
<hr/>	
<i>2.8.6 SoftMax Layer</i>	39
<hr/>	
<i>2.9 Loss Function</i>	40
<hr/>	

<i>2.10 Stochastic Gradient Descent with Adamax (SGDA)</i>	41
<i>2.11 Multilayer Neural Network (MLNN)</i>	42
<i>2.12 Evaluation Measures</i>	43
<i>A. Accuracy</i>	44
<i>B. Precision</i>	44
<i>C. Recall</i>	44
<i>D. F1-Score</i>	45
<i>E. Calculating the number of Parameters</i>	45
Chapter Three: The Proposed System Implementation	
<i>3.1 Introduction</i>	48
<i>3.2 The proposed Models</i>	48
<i>Case1: The First Proposed Approach Is Classification with Machine Learning Technique</i>	48
<i>3.3 Pre-processing Stage</i>	49
<i>3.3.1 Dropping</i>	50
<i>3.3.2 Data cleaning</i>	50
<i>3.3.3 Data Normalization</i>	50
<i>3.4 The Proposed Technique Of The First Approach</i>	51
<i>3.4.1 Artificial Neural Networks</i>	51
<i>A. Training Phase</i>	52
<i>B. Testing Phase</i>	52
<i>3.4.2 Decision Tree</i>	54

<i>A. Training Phase</i>	55
<i>B. Testing Phase</i>	55
3.4.3 <i>Logistic regression</i>	56
<i>A. Training Phase</i>	56
<i>B. Testing Phase</i>	56
3.4.4 <i>K-Nearest-Neighbor</i>	57
<i>A. Training Phase</i>	58
<i>B. Testing Phase</i>	58
<i>Case2: The Second Proposed Approach: Classification with Deep Learning</i>	59
3.5 <i>Image Pre-processing Stage</i>	60
3.6 <i>Data visualization</i>	61
3.7 <i>Convolutional Neural Network</i>	62
3.8 <i>Data Preparation for CNN Training</i>	63
3.9 <i>The proposed Network Architecture</i>	64
3.9.1 <i>Input layer</i>	66
3.9.2 <i>Convolution Layer</i>	66
3.9.3 <i>Non-linear Layer (Activation Function)</i>	66
3.9.4 <i>Pooling Layer</i>	66
3.9.5 <i>Normalization Layer</i>	67
3.9.6 <i>Fully Connected Layer</i>	68
3.9.7 <i>Softmax Activation Function</i>	68

<i>3.10 CNN Training</i>	69
<i>3.5.5 Training Option (Training Algorithm)</i>	70
<i>A. Stochastic Gradient Descent with AdaMax Optimizer</i>	70
<i>B. Max Epoch</i>	70
<i>C. Shuffle</i>	71
<i>D. Loss Function</i>	71
<i>3.6 CNN Testing</i>	71
<i>3.7 Deep Neural Network</i>	72
<i>A. Training Phase</i>	73
<i>B. Testing Phase</i>	73
Chapter Four: Experiments Rustles and Evaluation	
<i>4.1. Introduction</i>	78
<i>4.2. Implementation Environment</i>	78
<i>4.3. Dataset</i>	79
<i>4.4 Data Sets Acquisition</i>	79
<i>Case One :The System Results for the First proposed approach</i>	82
<i>4.5 Pre-Processing Results</i>	82
<i>4.5.1 Dropping</i>	82
<i>4.5.2 data cleaning</i>	83
<i>4.5.3 Normalization</i>	83
<i>4.5.4 Splitting the Dataset</i>	84
<i>4.6 The Results Of The Techniques For First Approach</i>	85

<i>4.6.1 Artificial Neural Network Result</i>	85
<i>4.6.2 Decision Tree Result</i>	86
<i>4.6.3 Logistic Regression Result</i>	88
<i>4.6.4 K-nearest Neighbors Result</i>	89
<i>4.7 Comparison, Between the Proposed Systems (Using the ANN,DT, LR and Using KNN Algorithm)</i>	91
<i>Case2: The System Results for the Second proposed model</i>	92
<i>4.8. The result of Convolution Neural Network</i>	92
<i>4.9 The result of the Deep Neural Network</i>	98
<i>4.10 Proposed Algorithm vs. Related Works</i>	103
<i>Chapter Five: Conclusions and Future Work</i>	
<i>5.1 Conclusions</i>	104
<i>5.2 Future Work</i>	105
<i>References</i>	
<i>References</i>	106

List of Abbreviations

<i>Abbreviations</i>	<i>Description</i>
<i>AI</i>	<i>Artificial Intelligent</i>
<i>ANN</i>	<i>Artificial Neural Networks</i>
<i>BN</i>	<i>Bayesian Networks</i>
<i>CAD</i>	<i>Computer Aided Diagnosis</i>
<i>CBC</i>	<i>Complete Blood Count</i>
<i>CNN</i>	<i>Convolutional Neural Network</i>
<i>CT</i>	<i>Computed Tomography</i>
<i>DL</i>	<i>Deep Learning</i>
<i>DNN</i>	<i>Deep Neural Network</i>
<i>DT</i>	<i>Decision Tree</i>
<i>FC</i>	<i>Fully Connected</i>
<i>FCM</i>	<i>Fuzzy C-Means</i>
<i>FKRCM</i>	<i>Fuzzy Kernel C-Means</i>
<i>FRCM</i>	<i>Fuzzy Robust C-Means</i>
<i>HB</i>	<i>Hemoglobin Electrophoresis</i>
<i>HCDP</i>	<i>hierarchical clustering based on density peaks</i>
<i>HCT</i>	<i>Hematocrit Test</i>
<i>HCTM</i>	<i>Hospital Canselori Tuanku Muhriz</i>
<i>K-NN</i>	<i>K-Nearest Neighbor</i>
<i>LR</i>	<i>Logistic Regression</i>
<i>MCV</i>	<i>Mean Corpuscular Volume</i>
<i>ML</i>	<i>Machine Learning</i>
<i>MLNN</i>	<i>Multilayer Neural Network</i>
<i>MLP</i>	<i>Multi-Layer Perceptron</i>

<i>MRI</i>	<i>Magnetic Resonance Imaging</i>
<i>NB</i>	<i>Naive Bayes</i>
<i>PCA</i>	<i>Principal Components Analysis</i>
<i>PET</i>	<i>Positron Emission Tomography</i>
<i>PTPP</i>	<i>Punjab Thalassaemia Prevention Programme</i>
<i>RBC</i>	<i>Red Blood Cell</i>
<i>RBFN</i>	<i>Radial Basis Function Network</i>
<i>ReLU</i>	<i>Rectified Linear Unit</i>
<i>ResNet</i>	<i>Residual Neural Network</i>
<i>RGB</i>	<i>Red, Green, Blue</i>
<i>SEM</i>	<i>Scanning Electron Microscope</i>
<i>SGR-VC</i>	<i>SVM, GBM , RF-voting classifier</i>
<i>SMOTE</i>	<i>Synthetic Minority Oversampling Technique</i>
<i>SVM</i>	<i>Support Vector Machine</i>

List of Tables

Table No.	Description	Page
Table (2.1)	<i>Confusion Matrix of Two Classes</i>	43
Table (4.1)	<i>the result of splitting for two dataset</i>	84
Table (4.2)	<i>the evaluation criteria of the ANN algorithm for thalassemia dataset</i>	85
Table (4.3)	<i>the evaluation criteria of the DT algorithm for thalassemia dataset</i>	87
Table (4.4)	<i>the evaluation criteria of the LR algorithm for thalassemia dataset</i>	88
Table (4.5)	<i>the evaluation criteria of the KNN algorithm for thalassemia dataset</i>	90
Table (4.6)	<i>Comparison of accuracy between the proposed systems</i>	91
Table (4.7)	<i>The parameter of the CNN with a fully connected layer for the Thalassemia Disease dataset</i>	93
Table (4.8)	<i>Comparison of the different ratio of the size of data in training and testing for the overall accuracy rate for Thalassemia dataset by using CNN</i>	96
Table (4.9)	<i>The parameter of the DNN with a fully connected layer Thalassemia Disease dataset</i>	99
Table (4.10)	<i>Comparison of the different ratio of the size of data in training and testing for the overall accuracy rate for Thalassemia dataset by using DNN</i>	100
Table (4.11)	<i>Comparison between other Existing works and the proposed work.</i>	103

List of Figures

Figure No.	Description	Page
Figure (2.1)	<i>Erythrocyte Cell Seen in Thalassemia Patient. a: individuals healthy Peripheral blood smear sample image b: thalassemia peripheral blood smear</i>	13
Figure (2.2)	<i>Learning phase of machine learning (ML) process</i>	17
Figure (2.3)	<i>The Most Famous Used Activation Functions</i>	19
Figure (2.4)	<i>Decision Tree Classification[</i>	23
Figure (2.5)	<i>The two-class LR model is a generalized linear model with a logistic link function P</i>	26
Figure (2.6)	<i>An example KNN classification task with k=5</i>	28
Figure (2.7)	<i>Learned features from a CNN</i>	31
Figure (2.8)	<i>Convolution layer operation, sliding filter over the given image data of input</i>	32
Figure (2.9)	<i>5x5 filter convolving around an input volume and producing activation man. a:Sliding the filter over the input image. b: the result in the output feature map</i>	33
Figure (2.10)	<i>The stride effect on the output size</i>	34
Figure (2.11)	<i>Zero-padding operation</i>	35
Figure(2.12)	<i>(a) Network before Dropout, (b) Network after Dropout network</i>	38
Figure (2.13)	<i>The location of the Softmax layer in the network</i>	40
Figure (2.14)	<i>Architectures of Multilayer Neural Network</i>	42
Figure (3.1)	<i>The block diagram for the first proposed Approach</i>	49
Figure (3.2)	<i>The block diagram for the second proposed Approach.</i>	60
Figure (3.3)	<i>Resizing Thalassemia Disease image</i>	61
Figure (3.4)	<i>the type and number of Dataset</i>	61
Figure (3.5)	<i>The structure of CNN for Thalassemia Disease</i>	65
Figure (3.6)	<i>The structure of DNN for Thalassemia Disease</i>	75
Figure (4.1)	<i>Samples of Original Thalassemia Data.</i>	80
Figure (4.2)	<i>Samples of Original Thalassemia Data.</i>	81
Figure (4.3)	<i>sample of data after dropping</i>	82
Figure (4.4)	<i>sample of data after data cleaning</i>	83

Figure (4.5)	<i>dataset after applying Normalization</i>	84
Figure (4.6)	<i>The values Confusion Matrix of ANN algorithm for Thalassemia patient dataset</i>	86
Figure (4.7)	<i>The values Confusion Matrix of DT algorithm for Thalassemia Patient Dataset</i>	88
Figure (4.8)	<i>The values Confusion Matrix of LR algorithm for Thalassemia patient dataset</i>	89
Figure (4.9)	<i>The values Confusion Matrix of KNN algorithm for Thalassemia patient dataset</i>	90
Figure (4.10)	<i>A model for accuracy comparison</i>	91
Figure (4.11)	<i>The effect of layers number on recognition accuracy for thalassemia dataset</i>	96
Figure (4.12)	<i>The Epochs numbers for best accuracy and loss for Thalassemia Disease</i>	97
Figure (4.13)	<i>The Values Confusion Matrix using CNN for Thalassemia Disease</i>	97
Figure (4.14)	<i>The result of CNN algorithm for classification thalassemia disease</i>	98
Figure (4.15)	<i>The effect of layers number on recognition accuracy for thalassemia data</i>	100
Figure (4.16)	<i>The best training performance for Thalassemia</i>	101
Figure (4.17)	<i>The Values Confusion Matrix using MLNN for thalassemia</i>	101
Figure (4.18)	<i>the result of DNN algorithm</i>	102
Figure (4.19)	<i>The result of CNN and DNN algorithm for classification thalassemia disease</i>	102

List of Algorithms

<i>ALgo. No.</i>	<i>Description</i>	<i>Page</i>
□ ḡri□□□ (3.1)	<i>Data Cleaning Algorithm</i>	50
□ ḡri□□□ (3.2)	<i>Z- Score Normalization</i>	51
□ ḡri□□□ (3.3)	<i>Artificial neural network for Thalassemia Disease classification</i>	53
□ ḡri□□□ (3.4)	<i>Decision tree for Thalassemia Disease classification</i>	55
□ ḡri□□□ (3.5)	<i>logistic regression for Thalassemia Disease classification</i>	57
□ ḡri□□□ (3.6)	<i>K-nearest neighbors for Thalassemia Disease classification</i>	57
□ ḡri□□□ (3.7)	<i>CNN training algorithm to classify Thalassemia Diseases</i>	62
□ ḡri□□□ (3.8)	<i>Batch Normalization</i>	67
□ ḡri□□□ (3.9)	<i>Softmax layer function</i>	68
□ ḡri□□□ (3.10)	<i>DNN training algorithm to classify Thalassemia Disease</i>	74

Chapter One

General

Introduction

Chapter One

General Introduction

1.1 Introduction

人體內的紅血球會運送氧氣到身體各處，並將二氧化碳帶回肺部。當紅血球運送氧氣時，它會結合一種叫做血紅蛋白的蛋白質。血紅蛋白是由四個亞基組成的複合物，每個亞基都含有鐵原子。當鐵原子與氧氣結合時，就會形成氧合血紅蛋白，這種蛋白質比未結合氧氣的血紅蛋白更能有效地運送氧氣。當紅血球運送二氧化碳時，它會解離出鐵原子，並將二氧化碳釋放到血液中。這就是為什麼在高濃度的二氧化碳環境下，紅血球會釋放更多的二氧化碳。

人類的紅血球含有約 300 萬個血紅蛋白分子。每個血紅蛋白分子由四個亞基組成：α₁、α₂、β₁ 和 β₂。α₁ 和 α₂ 亞基由常染色體上的基因編碼，而 β₁ 和 β₂ 亞基則由 X 染色體上的基因編碼。α₁ 和 α₂ 亞基的氨基酸序列與 β₁ 和 β₂ 亞基不同，因此它们的功能也不同。α₁ 和 α₂ 亞基的主要功能是運送氧氣，而 β₁ 和 β₂ 亞基的主要功能是運送二氧化碳。

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31i³¹ 32i³² 33i³³ 34u³⁴ 35e³⁵. 36e³⁶ 37r³⁷ 38j³⁸ 39e³⁹ 40e⁴⁰ 41i⁴¹ 42e⁴²
43e⁴³ 44i⁴⁴ 45re⁴⁵ 46r⁴⁶ 47e⁴⁷ 48e⁴⁸ 49e⁴⁹ 50e⁵⁰ 51i⁵¹ 52e⁵² 53e⁵³
54e⁵⁴ 55u⁵⁵ 56i⁵⁶ 57u⁵⁷ 58i⁵⁸ 59e⁵⁹ 60e⁶⁰ 61i⁶¹ 62e⁶² 63e⁶³
64e⁶⁴ 65u⁶⁵ 66i⁶⁶ 67e⁶⁷ 68i⁶⁸ 69e⁶⁹ 70e⁷⁰ 71i⁷¹ 72e⁷² 73e⁷³
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84e⁸⁴ 85u⁸⁵ 86i⁸⁶ 87e⁸⁷ 88i⁸⁸ 89e⁸⁹ 90e⁹⁰ 91i⁹¹ 92e⁹² 93e⁹³
94e⁹⁴ 95u⁹⁵ 96i⁹⁶ 97e⁹⁷ 98i⁹⁸ 99e⁹⁹ 100e¹⁰⁰ 101i¹⁰¹ 102e¹⁰² 103e¹⁰³
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124e¹²⁴ 125u¹²⁵ 126i¹²⁶ 127e¹²⁷ 128i¹²⁸ 129e¹²⁹ 130e¹³⁰ 131i¹³¹ 132e¹³² 133e¹³³
134e¹³⁴ 135u¹³⁵ 136i¹³⁶ 137e¹³⁷ 138i¹³⁸ 139e¹³⁹ 140e¹⁴⁰ 141i¹⁴¹ 142e¹⁴² 143e¹⁴³
144e¹⁴⁴ 145u¹⁴⁵ 146i¹⁴⁶ 147e¹⁴⁷ 148i¹⁴⁸ 149e¹⁴⁹ 150e¹⁵⁰ 151i¹⁵¹ 152e¹⁵² 153e¹⁵³
154e¹⁵⁴ 155u¹⁵⁵ 156i¹⁵⁶ 157e¹⁵⁷ 158i¹⁵⁸ 159e¹⁵⁹ 160e¹⁶⁰ 161i¹⁶¹ 162e¹⁶² 163e¹⁶³
164e¹⁶⁴ 165u¹⁶⁵ 166i¹⁶⁶ 167e¹⁶⁷ 168i¹⁶⁸ 169e¹⁶⁹ 170e¹⁷⁰ 171i¹⁷¹ 172e¹⁷² 173e¹⁷³
174e¹⁷⁴ 175u¹⁷⁵ 176i¹⁷⁶ 177e¹⁷⁷ 178i¹⁷⁸ 179e¹⁷⁹ 180e¹⁸⁰ 181i¹⁸¹ 182e¹⁸² 183e¹⁸³
184e¹⁸⁴ 185u¹⁸⁵ 186i¹⁸⁶ 187e¹⁸⁷ 188i¹⁸⁸ 189e¹⁸⁹ 190e¹⁹⁰ 191i¹⁹¹ 192e¹⁹² 193e¹⁹³
194e¹⁹⁴ 195u¹⁹⁵ 196i¹⁹⁶ 197e¹⁹⁷ 198i¹⁹⁸ 199e¹⁹⁹ 200e²⁰⁰ 201i²⁰¹ 202e²⁰² 203e²⁰³
204e²⁰⁴ 205u²⁰⁵ 206i²⁰⁶ 207e²⁰⁷ 208i²⁰⁸ 209e²⁰⁹ 210e²¹⁰ 211i²¹¹ 212e²¹² 213e²¹³
214e²¹⁴ 215u²¹⁵ 216i²¹⁶ 217e²¹⁷ 218i²¹⁸ 219e²¹⁹ 220e²²⁰ 221i²²¹ 222e²²² 223e²²³
224e²²⁴ 225u²²⁵ 226i²²⁶ 227e²²⁷ 228i²²⁸ 229e²²⁹ 230e²³⁰ 231i²³¹ 232e²³² 233e²³³
234e²³⁴ 235u²³⁵ 236i²³⁶ 237e²³⁷ 238i²³⁸ 239e²³⁹ 240e²⁴⁰ 241i²⁴¹ 242e²⁴² 243e²⁴³
244e²⁴⁴ 245u²⁴⁵ 246i²⁴⁶ 247e²⁴⁷ 248i²⁴⁸ 249e²⁴⁹ 250e²⁵⁰ 251i²⁵¹ 252e²⁵² 253e²⁵³
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324e³²⁴ 325u³²⁵ 326i³²⁶ 327e³²⁷ 328i³²⁸ 329e³²⁹ 330e³³⁰ 331i³³¹ 332e³³² 333e³³³
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614e⁶¹⁴ 615u⁶¹⁵ 616i⁶¹⁶ 617e⁶¹⁷ 618i⁶¹⁸ 619e⁶¹⁹ 620e⁶²⁰ 621i⁶²¹ 622e⁶²² 623e⁶²³
624e⁶²⁴ 625u⁶²⁵ 626i⁶²⁶ 627e⁶²⁷ 628i⁶²⁸ 629e⁶²⁹ 630e⁶³⁰ 631i⁶³¹ 632e⁶³² 633e⁶³³
634e⁶³⁴ 635u⁶³⁵ 636i⁶³⁶ 637e⁶³⁷ 638i⁶³⁸ 639e⁶³⁹ 640e⁶⁴⁰ 641i⁶⁴¹ 642e⁶⁴² 643e⁶⁴³
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1.2 Related Work

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I.Ahmed et al .(2018) □1□□ □i□re□e□r□□□ □i□e □e□i□g □□□r□□□e□ □□
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range 50–85% and rising to 98.99% for 100 carriers and 98.20% for non-carriers.

S. SADIQ et al.(2021) In 17 databases from carrier detection studies using either quantitative or qualitative methods, the frequency of carriers was 3051 (50.66%) and non-carriers were 2015 (39.34%). The frequency of carriers was higher than non-carriers in all studies. The frequency of carriers ranged from 93% to 98.99%. The frequency of non-carriers ranged from 98.20% to 100%. In this database out of 5066 records 3051 patients are β -thalassemia carriers and 2015 records are β -thalassemia carriers. The frequency of carriers and non-carriers were 50.66% and 39.34% respectively. The frequency of carriers was higher than non-carriers in all studies. The frequency of carriers ranged from 93% to 98.99%. The frequency of non-carriers ranged from 98.20% to 100%.

1.3 Problem Statement

The main problem in our study is to identify the carriers of hemoglobinopathies. The frequency of carriers is higher than non-carriers. The frequency of carriers is higher than non-carriers in all studies. The frequency of carriers ranged from 93% to 98.99%. The frequency of non-carriers ranged from 98.20% to 100%. The frequency of carriers was higher than non-carriers in all studies. The frequency of carriers ranged from 93% to 98.99%. The frequency of non-carriers ranged from 98.20% to 100%.

1.6 Thesis Outlines

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