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Analysis of Genetic Face Images with Respect to Reflexology for Prediction of Diseases

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ABSTRACT

A genetic disease or disorders is a hereditary issue caused by one or more abnormalities formed in the genome. Genetic disorders can be monogenic, multifactorial, or chromosomal. Like genetic disorders, facial features are also passed down genetically. This paper proposes to identify genetic disorders from facial features. However, it does not explain which facial features led to its prediction. In order to overcome the issues, face reflexology regions are analysed to predict the genetic diseases. Face reflexology regions are related to the internal organs and structure of the body. Genetic faces are analyzed with respect to face reflexology regions for the prediction of genetic diseases. Feature vectors are generated for the reflexology regions using Local binary pattern (LBP) with the combination of high frequency and low frequency textures. The Euclidean distance weight function is used for prediction of diseases using the feature vectors. The proposed method is not only using single face reflexology regions, but combined reflexology regions of n persons are used for finding multiple possibility of diseases. Based on the statistical measure analysis, the proposed algorithm works well in extracting the features for identifying the diseases linked to genetic disorders, potentially speeding up diagnosis of diseases.

1. INTRODUCTION

Identification of a blood relative is possible if two people have genetically similar looks. It is additionally known as kinship facial verification. The faces of the same family are genetic faces, whereas the faces of different families are non-genetic faces. In order to categorise genetic and non-genetic faces, an efficient genetically based face recognition programme is employed [1-3] which overcomes problems with position, lighting, age, and expression change. In this paper, a system for genetic illness identification is suggested in order to forecast genetic diseases with genetic faces. Like genetic disorders, facial features are also passed down genetically. Genetic disorders may be hereditary or non-hereditary, implying that they are passed down from the parents' genes. Most genetic disorders are very uncommon and influence one person in every several thousands or millions. Genetic diseases like diabetes, lung diseases, bald head, and cancer may come for the person having similar facial features or structure of the body. Genetic rare diseases may be predicted for the person having same facial features within the family [4, 5]. The study found that 8% of people had a hereditary condition, and the majority of them have comparable face traits. Diagnosing the Genetic rare disease takes many years and involves significant medical costs, because of the combination of poor understanding and delays in complex genomic data interpretation. In this paper, a new method has been introduced to analyse the familial face images with respect to reflexology regions for the prediction of rare genetic diseases.

Figure 1 shows the different reflexology regions with the corresponding internal organs of the body [6, 7]. If two persons are genetically very close, they may also have similar structure of the body or similar reflexology regions. If the son and father have similar reflexology regions, the son may have the genetic disease with respect to that region. Prediction of genetic rare diseases occur not only from the previous generation, it may occur from the current generation elder people such as brother, uncle. Genetic rare diseases influence almost 1:10 people globally, many of whom are children who go undiagnosed for significant lots of time. The proposed system could give hope to hundreds of millions of patients around the world and make cutting edge advancements in diagnostics and therapeutics for genetic diseases [8, 9]. It also has the potential to provide a more inexpensive diagnosis in far less time.

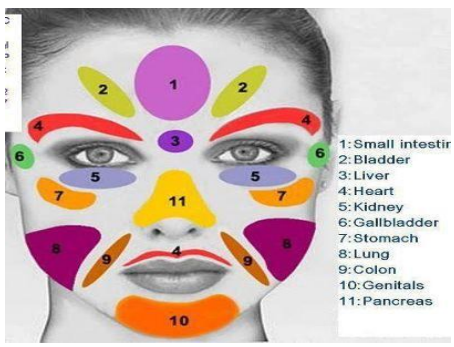

Figure 1. Face reflexology regions

Eight percent of the population, according to the research, has diseases with significant genetic components, and many of these individuals may have distinctive facial traits. It does not, however, specify whatever characteristics of the face made the prediction possible. In order to overcome the issues, in this paper, Face reflexology regions are analysed to predict the genetic diseases [10, 11]. Face reflexology regions are related to the internal organs and structure of the body. A new method has been introduced to analyze the familial face images with respect to reflexology regions for the prediction of rare genetic diseases. Initially, the current generation face is taken as an input and region of interest is extracted from the faces using bounding box coordinates. There are totally eleven basic reflexology regions in the face, however, in this study, only 6 areas are chosen for analysis. LBP is used to extract the characteristics of these areas, and the feature extraction is split into low- and high-frequency components that are treated independently. The noise can be reduced in the facial regions by this method [12, 13]. The features extracted from the current generation face regions are combined and compared with the face database of all the generation using Euclidean weight function. Based on the statistical measure analysis, the proposed algorithm works well in extracting the features for identifying the diseases linked to genetic disorders, potentially speeding up diagnosis of diseases [14, 15].

The paper is described as follows. In Section II, the work related to this paper are discussed. In Section III, proposed genetic face recognition algorithm is explained. In Section IV Genetic based face recognition application is described. In Section V, Results and implementation are performed out for several databases, highlighting the algorithm's successful operation. Conclusion and References are discussed in Section VI&VII.

2. RELATED WORKS

The region extraction algorithm for face expression identification has been done effectively [16]. Utilizing a typical neural network, the face's individual regions—including the left eye, right eye, and mouth regions—are extracted and trained. On the face pictures, histogram equalisation, rotation correction, and spatial normalising are performed in order to get computable features. By using a decision-level fusion technique, the output of recognition of facial expression is determined by majority voting among the results of the three CNNs. In all, 8% of the million people are affected by syndromic genetic diseases [17]. Numerous disorders have distinguishable face characteristics that are very useful to clinical geneticists. According to recent studies, face analysis systems may identify syndromes just as well as skilled physicians. These technologies only recognised a small number of illness phenotypes, which limited their application in clinical situations where multiple of diagnoses should be taken into account. Deep Gestalt is a framework for analysing face images that uses deep learning and computer vision algorithms to quantify similarity to several of syndromes. Reflexology is the methodical application of pressure to specific spots on the feet & faces to influence the health of associated body components [18, 19]. Semi-structured face-to-face interviews were used to get the data. Concurrent data analysis was done, and recruitment was halted once saturation was attained. All responders provided written authorization before participating. The results demonstrate that reflexology therapy is currently regarded as one of the best strategies to preserve overall health. Reflexologists contend that by detecting some bodily issues, people might become aware of health issues and seek more medical attention. According to [20, 21], non-rigid facial motions brought on by facial expressions on the human face result in observable changes to their typical forms and can occasionally obstruct certain facial feature regions, making face identification a challenge. This shows a method for automatically detecting regions of interest (ROI) in six types of expressive facial photos. The suggested method uses a hybrid approach based on face geometry. Faces within the family called Familial faces are analysed for the prediction of genetic diseases [22, 23].

3. METHODOLOGY

Figure 2 demonstrates the architecture diagram of the proposed system for analysis of genetic diseases. Initially, the current generation face is taken as an input and region of interest (ROI) is extracted from the faces using bounding box coordinates. There are totally 11 basic reflexology regions as shown in Figure 2, of which only 6 regions are used for analysis, in this work. The features of these regions are extracted using LBP and the texture feature is divided into low and high frequency components which are processed separately. This helps us in reducing the noise in the face regions. The features extracted from the current generation face regions are combined and compared with the face database of all the generation using Euclidean weight function. The comparison is also done with the combination of the regions of different familial faces to predict the genetic diseases accurately [24, 25]. The main aim of this work is to evaluate the efficiency of proposed method on different family databases.

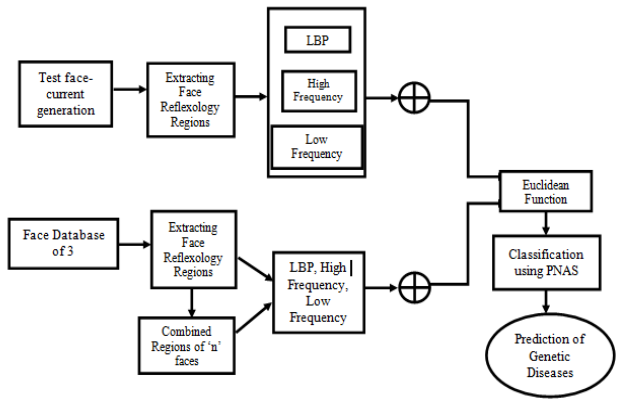

Figure 2. Architecture of proposed approach

Algorithm:

1. Face Images of current generation and about three generations are considered as Input images.
2. Current generation face image will be test image and three generations face images will be the training image.
3. Extraction of six reflexology regions from the face images is done using bounding box method.
4. In the training phase, reflexology regions are combined or added for 'n' generation faces to identify the disease from one or more persons.

5. After extracting the regions from the face image, features are extracted through LBP feature extractor.
6. High frequency and low frequency component are decomposed from the regions extracted from the face image using Total variation regularization (TVL1) method.
7. Concatenate LBP features and features from high frequency and low frequency component and this will be final features.
8. To classify two output photos and identify genetic diseases, Euclidean distance is calculated between them.

The suggested feature level fusion facial recognition system's steps are briefly described in the following subsections.

3.1 Extraction of face reflexology regions

In many situations, there are interested multiple targets or regions in an image. These targets or regions can be obtained by specific positions in the image. In computer vision, object detection or object recognition is used for extracting the regions from the images. Object detection is used in many fields such as in self-driving technology by identifying the location of vehicles, roads, pedestrians, and some obstacles. In object detection, bounding box is used to describe the target location in an image.

The bounding box is a rectangular box having two coordinates (x, y) in the upper-left corner and in the lower-right corner of the rectangle. Bounding boxes are used to represent a region in the image which is considered as a ROI. In general, every object detection algorithm returns the ROI in the form of pixel coordinates with its height and width. Using the starting pixel coordinates and its respective height and width, the bounding boxes are drawn for the regions in image [25].

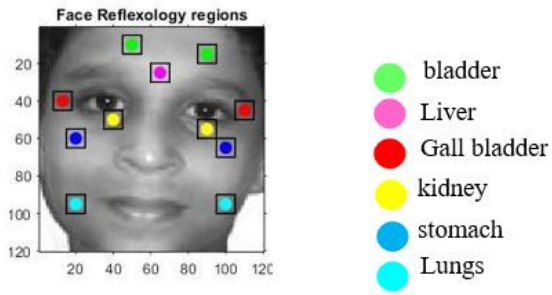

Figure 3. Identification of reflexology regions

In this research work, the face reflexology regions are extracted using bounding box coordinates. The basic face reflexology regions are connected to the 11 internal organs of the body specified in Figure 1. In the family database, all the previous generation people are having the disease like diabetes, wheezing, gall bladder stone, kidney stone and hormonal problems. So, only six regions are concentrated to find the genetic diseases, in this work. The regions are kidney, lungs, bladder, Gall bladder, stomach and liver. Figure 3 shows the six reflexology regions in the face. These regions are extracted by bounding box coordinates that acts as a ROI for analysis and detection of diseases from face image. Figure 4 shows the extraction of reflexology regions from the face image. Bladder 1 and 2 refers to the left and right forehead of the face, Liver points to centre head, Kidney1 and 2 refers to the left and right most corner of the eye, Gall bladder1 and 2 refers to the regions below the left and right eye, Stomach1 and 2 refers to the left upper and right upper cheeks, Lungs1 and 2 refers to the left lower and right lower cheeks.

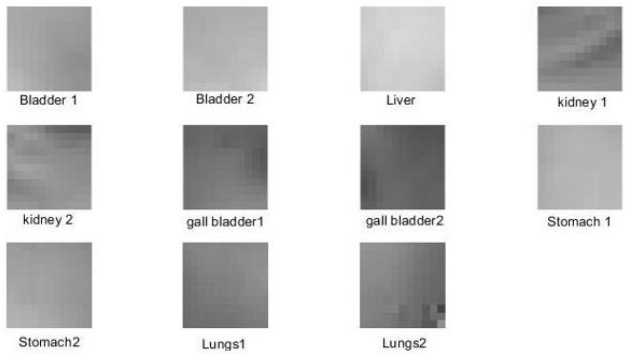

Figure 4. Extraction of reflexology regions

3.2 Feature extraction of the regions

Reflexology areas are removed from the faces, and features are then retrieved from the regions using a feature extractor. To extract the features in this study, LBP with high frequency and low frequency components is employed.

3.2.1 Local binary pattern (LBP)

LBP is a straightforward yet very effective texture operator that identifies each pixel in the image by thresholding its immediate surroundings and treating its result as a binary integer. The LBP texture operator has gained popularity as a strategy in many applications due to its detection accuracy and computational simplicity [26-35]. It is a unified method for the statistics and structural models of texture classification.

Several applications, such as facial recognition software, facial expression recognition, textural classification, CBIR, and others, utilise the LBP operator. The primary characteristic of the LBP operator is invariance to monotonic changes in grey level brought on by changes in light. It recognises regional trends in the immediate area. It helps with the local pattern identification of borders, spots, curves, flat regions, and so forth.

LBP Code Calculation

The 3×3 neighbourhoods are used to calculate the LBP code, with the centre pixel serving as a threshold. The grey scale difference is first calculated, and the difference is then multiplied by the weights of the relevant pixels.

An LBP code is generated for each pixel of a given picture using,

$$LBP_{P,Q} = \sum_{i=0}^{P-1} 2^i . f(g_i - g_c) \quad (1)$$

$$f(x) = \begin{cases} 1, \text{and} x \geq 0 \\ 0, \text{andelse} \end{cases} \quad (2)$$

where, $f(g_i - g_c)$gc is the intensity value of the centre pixel, g_i is the intensity value of its neighbours, P is the total number of neighbours involved, and Q is the radius of the neighbourhood. This function is applied on the grey level difference. Figure 5 displays the LBP value for the 3 x 3 image's central pixel, g c.

3.2.2 High frequency and low frequency components

Facial appearance changes like furrows and wrinkles, due to age variation and expression are reflected through texture in faces. Structure-texture based segmentation of pictures is carried out and suggested in this study to eliminate violations in the restrictions caused by variations in lighting and expression in the face images [36]. To overcome and eliminate the changes in illumination, different skin tones algorithm is implemented in this work. The Total Variation (TV) regularisation term and the L1 data fidelity component make up the TV-L1 model. Given that it better maintains geometric characteristics, the L1 norm is especially suitable for the low frequency + high frequency components decomposition. The texture of a picture is divided into two parts using the TVL1 method: the lower frequencies component (u) and the frequency component. The breakdown of pictures is shown in Figure 6. Colors and edges of objects make up the geometric, smoothly shifting low frequency component known as the cartoon component. An oscillating high frequency band or texture can capture the finer characteristics of noise. The high frequency component mainly represents expression and wrinkles by textures present in the image and less dependent on illumination. The lighting and skin tone of the facial picture continue to affect the low frequency component. To produce u and v (u-low frequency and v-high frequency component) picture deconstruction, where low frequency element and high frequency element are compelled into various functional spaces, variation models provide a generic framework.

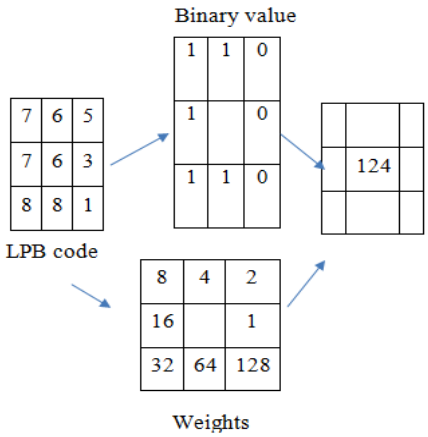

Figure 5. LBP code generation

Figure 6. TVL1 decomposition o (a) original image (b) low frequency component(c) high frequency component

3.2.3 Feature level fusion

This work proposes a method that combines features from LBP and TVL1 to realize a higher identification of genetic diseases [37]. Face recognition, video extraction, and multi-biometrics performance may all be improved by image fusion, which combines characteristics from many sources. Fusion is typically carried out at three levels: the feature level, the decision level, and the score level. The technique of integrating two feature vectors into one that is more discriminatory than any of input feature vectors is known as feature level fusion. By using the proper feature normalisation, transformation, and reduction strategies, feature-level fusion unifies the feature sets originating from several sources into a single feature set. The two modalities X and Y's training and test data matrices are obtained, and they are grouped into a single feature set Z. The main advantage of feature-level fusion is the discovery of connected feature values produced by several feature extraction algorithms, which leads to the identification of a small collection of salient features that can increase recognition accuracy [38].

3.2.4 Euclidian distance measure

The test image from the database is processed with the algorithm and similarly the training images with different combinations also processed with the same proposed algorithm [39]. The distance here between pictures is determined using the Euclidian metric € to determine how similar the training examples and test images are to one another.

$$€=\|f_l - f1\|2 \quad (3)$$

According to the distance, the genetic diseases are identified for the persons of current generations with the previous generation people. A smaller distance indicates a higher contribution [40].

4. EXPERIMENTAL RESULTS

The suggested approach for genetic illness analysis portrayed in Figure 2 was assessed with regard to both the current and earlier generations of people using Face picture databases. For this method, a total of 50 face photos from various generations are employed. The suggested algorithm has been utilised to identify genetic disorders with regard to various ages of various generations of individuals, taking into account that various ages and generations would be in various lighting, backgrounds, and positions. Therefore, this approach has demonstrated success in identifying genetic disorders.

Database 1

The face images in this database are gathered according to current generation (sons) and previous generation (father). Three images—two of fathers and one of sons—with various backdrops and lighting are included in database 1.

Figure 7 shows the Database 1 in which Image 1 belongs to father and Images 2 and 3 belongs to sons. The face image of the 1st person is given as the input to the proposed system. The features extracted from the reflexology regions for the test image are compared with training images to identify the genetic diseases. If the input image is having the diseases in the internal organs related to reflexology regions, then the corresponding reflexology regions of the face images having the minimum distance value is identified such that that person will have the same disease.

The face image used as an input image is having diseases such as bladder stone, wheezing, ulcer and gall bladder stone. These diseases are related to the reflexology regions bladder, lungs, stomach and gall bladder. Table 1 and Figure 8 shows the distance values for identification of genetic diseases for database 1.

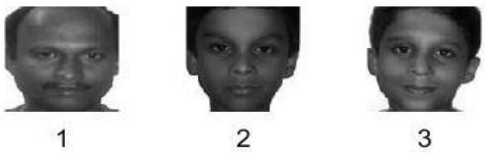

Figure 7. Database 1

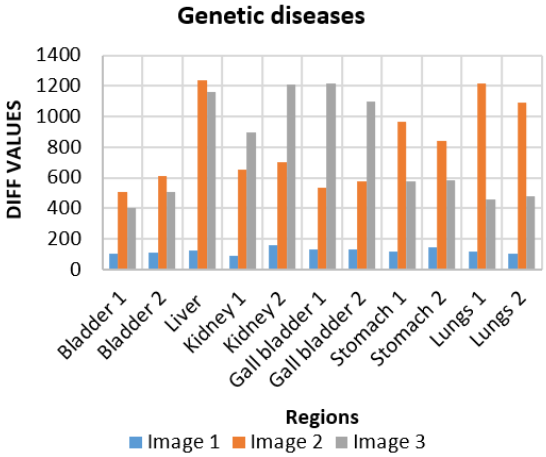

Figure 8. Distance values for identification of genetic diseases for database 1

Table 1. Distance values for identification of genetic diseases for database 1

Regions	Image 1	Image 2	Image 3
Bladder 1	105	506	402
Bladder 2	107	609	507
Liver	123	1239	1162
Kidney 1	91	656	896
Kidney 2	156	704	1211
Gall bladder 1	132	532	1217
Gall bladder 2	129	579	1097
Stomach 1	115	965	575
Stomach 2	142	843	580
Lungs 1	119	1219	460
Lungs 2	103	1093	478

Database 2

The face images in this database are gathered according to current generation (grandsons), previous generation (daughters and son) and old generation (grandfather and grandmother). In the database 2, there are 9 images (4 grandsons, 2 daughters, 1 son, and 2 grandparents) with a different backdrop arrangement and lighting. Figure 9 shows the Database 2 in which Image 1 belongs to Grandfather Image 2 belongs to grandmother, Image 3 belongs to son, Image 4 and 5 belongs to daughters and Image 6-9 belongs to grandsons. The face image of the 1st person is given as a input image to the proposed system and compared with all other images in the database. This person is having the genetic diseases diabetes and bladder stone. These diseases are related to the reflexology regions bladder and kidney.

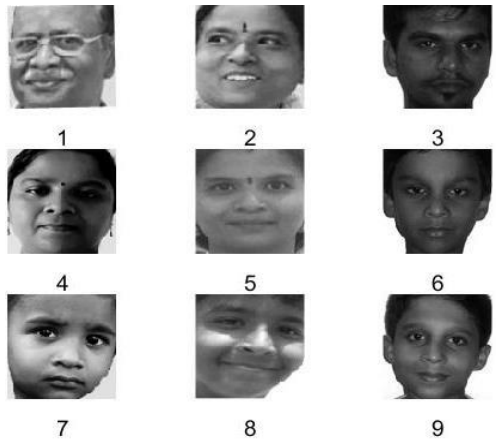

Figure 9. Database 2

Table 2 shows the distance values for identification of genetic diseases for database 2.

The person of image 1 is same as the input image with age variations, so the distance values are more or less below 150. The distance values of the reflexology regions for the Image 2 is less in some regions and is having more value in some regions. Specifically, the regions Gall bladder 1 and 2 and Bladder 1 and 2 are having less value compared to the other regions. This person (son1) will have the genetic disease gall bladder stone and bladder stone. For Image 3, the regions Lungs1 and 2, Bladder 1 and 2 and stomach 1 and 2 are having less value compared to the other regions. Already the person (son 2) of Image 3 is having wheezing from early days. So, from this analysis it is proved that the proposed system works well in identifying the genetic diseases. Additionally, this person will have genetic diseases Bladder stone and ulcer in future days.

Figure 8 shows the graph for Distance values for Identification of genetic diseases for database 1. From this graph, it clearly shows that the Image 2 will be having the genetic disease related to Bladder 1 and 2 and Gall bladder 1 and 2. Image 3 is having the genetic disease related to bladder 1 and 2, stomach 1 and 2 and Lungs 1 and 2.

Table 2. Distance values for Identification of genetic diseases for database 2

Regions	Image 1	Image 2	Image 3	Image 4	Image 5	Image 6	Image 7	Image 8	Image 9
Bladder 1	0	992.1	485.5	1064.2	960.5	959.1	432.4	373.2	1075.4
Bladder 2	0	1059.6	446.9	1152.6	1109.3	1168.0	519.4	469.1	998.7
Liver	0	1102.8	1147.9	957.7	1094.6	988.7	988.7	940.1	1016.1
Kidney 1	0	921.5	478.8	532.3	733.2	1051.5	513.8	827.4	992.7
Kidney 2	0	1036.3	581.9	526.6	1155.1	912.8	599.6	1272.8	842.5
Gall bladder 1	0	1010.5	1177.0	884.1	1022.6	1253.5	1237.6	883.3	844.3
Gall bladder 2	0	1042.5	1245.0	1060.1	1041.9	937.6	740.0	1070.6	846.6
Stomach 1	0	1179.4	1300.9	1231.1	1086.7	1218.3	1356.6	1116.0	805.1
Stomach 2	0	1350.9	1350.3	1064.1	1353.1	865.0	999.7	1023.1	923.1
Lungs 1	0	1058.0	1030.8	1157.8	1154.4	1169.2	1245.5	1192.1	1103.6
Lungs 2	0	1176.2	1196.8	1021.0	1011.6	1139.3	981.5	1213.9	1221.1

The distance values of the reflexology regions for some images are less in Bladder 1 and 2 and Kidney 1 and 2 and is having more value in remaining all regions. Specifically, the images 3, 4, 7 and 8 are having less values in the regions Bladder 1 and 2 and Kidney 1 and 2. The person (son) of image 3 will have the chance of getting genetic disease bladder stone and diabetes, as the distance value of both the regions related to this disease are having less value compared to other regions. Kidney 1 and 2 have a lower value for Image 4 (the daughter) than the other locations. So, this person may get diabetes in future. For Image 7 and 8 (grandsons), one person is having less value in two regions Bladder 1and2 and Kidney 1and2 and another person is having less value in only one region Bladder 1 and 2. Two persons have the chance of getting the diseases in future. So, from this analysis it is proved that the proposed system works well in identifying the genetic diseases. Figure 10 shows the graph for the Distance values for Identification of genetic diseases for database 2. From this graph, it clearly shows that the Image 3, 4, 7 and 8 will be having the genetic disease related to Bladder 1 and 2 and Kidney 1 and 2. Another analysis has been done in Database 2, only Image 2, 4 and 5 is taken for comparison. Image 2 (Mother) is given as an input to compare with Image 4 and 5 (Daughters). Image 2 is having the disease with stomach (uterus) and gall bladder stone. So, it is only compared to the daughters.

Table 3. Distance values for identification of genetic diseases of image 2, 4, 5

Regions	Image 2	Image 4	Image 5
Bladder 1	0	998.0	867.6
Bladder 2	0	989.0	1084.9
Liver	0	1118.0	1204.0
Kidney 1	0	1099.4	1000.9
Kidney 2	0	1055.9	1058.4
Gall bladder 1	0	552.3	933.0
Gall bladder 2	0	638.3	1101.6
Stomach 1	0	462.2	626.7
Stomach 2	0	525.4	550.8
Lungs 1	0	1040.6	888.2
Lungs 2	0	1063.8	1035.6

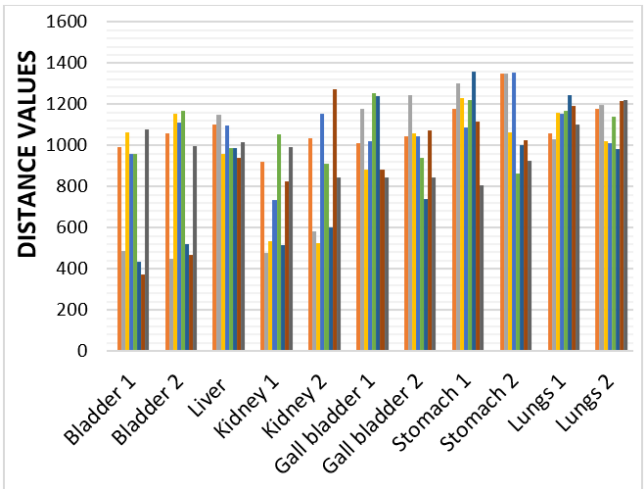

Figure 10. Graph for distance values for identification of genetic diseases for database 2

Table 3 shows the distance values for identification of genetic diseases for Image 2, 4, and 5. The distance values of the reflexology regions for images 4 and 5 are less in Gall Bladder 1 and 2 and Stomach 1 and 2 and is having more values in remaining all regions. Image 4 is having less value in both the regions Gall Bladder 1 and 2 and Stomach 1 and2, so this person has the chance of getting the genetic disease related to stomach (uterus) and Gall bladder stone. Image 4 is having less value only in one region Stomach 1and 2, so this person has the chance of getting stomach (uterus) problem. Figure 10 shows the graph for the Distance values for Identification of genetic diseases of Image 2,4,5.

Database 3

The face images in this database are gathered according to current generation (sons), previous generation (father) and old generation (grandfather). In the database 3, there are 4 images (2 sons, 1 father, and 1 grandfather) with different background setup and different illumination.

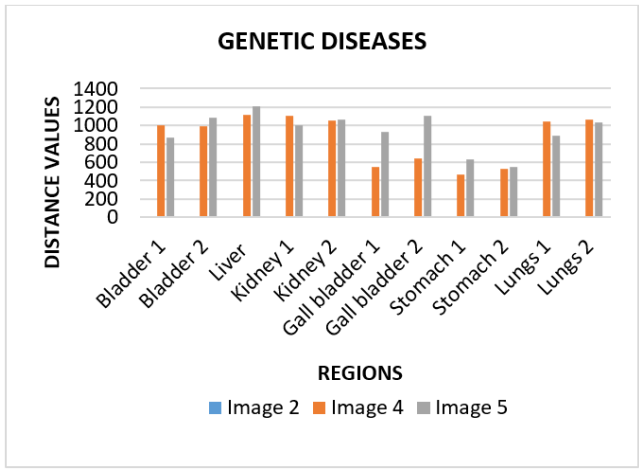

Figure 11. Distance values for identification of genetic diseases of Image 2, 4, 5

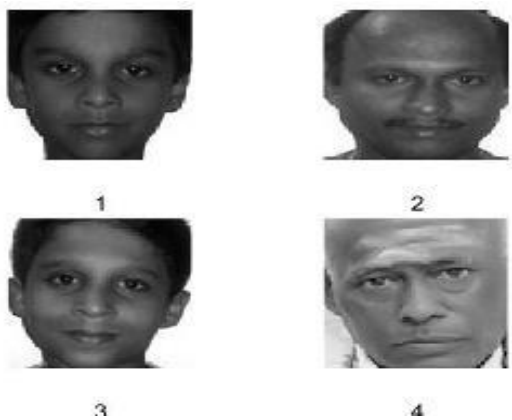

Figure 12. Database 3

Figure 11 shows the Database 3 in which Image 1 and3 belongs to sons, Image 2 belongs to father and Image 4 belongs to grandfather. In this analysis, as mentioned in Figure 12 the regions are combined from 2 images, Image 2 and4 (son and father). The purpose of the combined regions to identify the disease for both the sons from father and grandfather. The image 1 and 3 (sons) are compared with the combined regions of image (2 and 4) to identify the genetic diseases from father and grandfather. Image 2 (father) is having the diseases such as such as bladder stone, wheezing, ulcer and gall bladder stone. Image 4 (Grandfather) is having the diseases such as diabetes, liver infection and stomach problem.

Table 4. Distance values for identification of genetic diseases of image 2

Regions	Image 1
Bladder 1	532
Bladder 2	617
Liver	1162
Kidney 1	896
Kidney 2	1211
Gall bladder 1	1217
Gall bladder 2	1097
Stomach 1	485
Stomach 2	523
Lungs 1	432
Lungs 2	469

The Image 1 (son) is used as an input image and compared with the combined regions. Table 4 shows the distance values of Image 1. The distance values of the regions Bladder 1 and 2, Gall bladder 1 and 2 and Liver are having less value compared to the other regions. Already from Database 1, it proved the Image 1 will have the chance of getting Bladder stone and Gall bladder stone, additionally through this analysis this person may get the disease related to liver problem from his grandfather. Figure 13 shows the graph for distance values of Image 1and clearly shows the Genetic disease identification.

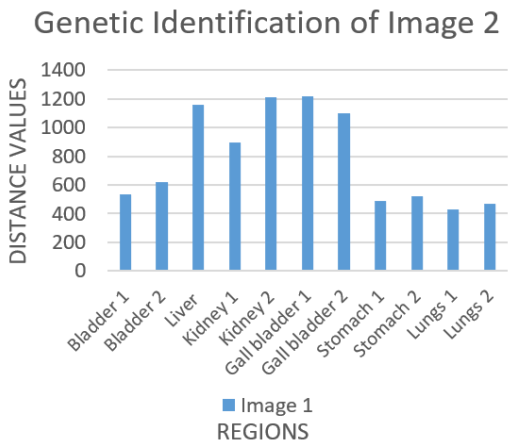

Figure 13. Graph for distance values of image 2

5. COMPARATIVE ANALYSIS

The datasets, implementation information, and experimental methods utilised to assess the efficacy of the suggested representation learning employing integrated features using LBP and TVL1 to achieve a greater identification of genetic illnesses are described in this part.

5.1 Datasets

The following four freely accessible databases are used to gauge the efficacy of the suggested genetic face verification technique.

_ UBKinFace Dataset,
_ Cornell Kinship Dataset [28],
_ KinFace-I [32], and
_ KinFace-II [32].

Table 5 describes the traits of each of the five databases used in our proposed model.

Table 5. Describes the traits of each of the five databases

Database	Subjects	Total Images	Genetic Relations	Outside images
Cornell Kin [28]	286	286	4	No
UB KinFace	400	600	4	No
KinFaceW-I [32]	1066	1066	4	No
KinFaceW-II [32]	2000	2000	4	No
Genetic Database	164	1000	6	Yes

In addition to these 4, we have also created a new genetic repository with several pictures of the same family's members. A total of 1000 facial pictures from the same family's several generations have been used [38]. There are six types of kinship relationships: brother-brother (BB), sister-sister (SS), mother-daughter (MD), mother-son (MS), father-son (FS), and father-daughter (FD) (FD). Every pair in the database comprises six photos, including 15 couples of BB, 13 couples of SS, 14 couples of FD, 24 couples of FS, 11 couples of MD, and 5 pairs of MS. Variations in position, lighting, and occlusion are also present in the many photos for each kin-pair [40].

5.2 Implementation details

A huge number of face images are needed to train the proposed methodology to understand the feature representation for genetic connection. About 500,000 facial photos are utilised for this. These pictures were gathered from a variety of places, including the Youtube faces database and the CMU Multi PIE. Be aware that while suggested technique needs big data to develop useful face representation for genetic verification, existing approaches do not utilise external data.

All of the photos are aligned for face detection using the Viola-Jones face detection technique and affine transformation. LBP is used to extract the characteristics of these areas, and the feature extraction is split into low- and high-frequency components that are treated independently. Each image's facial parts are taken out and scaled to 32 32. The resized areas are transformed into a vector of 1024 bytes, which is then used as input for each PNAS deep learning algorithm (Progressive Neural Architecture Search) [39, 41, 42].

5.3 Training

The training, validating, and test picture sets from the original and enhanced datasets utilised in this study have percentages of 90%, 7%, and 3%, correspondingly. The tests are used to evaluate the recognition performance of proposed strategy, whereas the first sets are being used to train and fit the model suggested in this article.

5.4 Performance assessment

The performance indicators sensitivity (SN), specificity (SP), accuracy (A), and precision (P) are used to examine the performance (P). We have used various cutting-edge studies from the literature survey section, including Deep Convolutional Generative Adversarial Network (DCGAN), Global Pooling Deep CNN (GPDCNN), and Support Vector

Machine (SVM), to compare the performance metrics of our suggested technique.

The comparative studies of the suggested work's correctness using various datasets are shown in Table 6.

Figure 14 shows the losses and accuracy curve for the suggested PNAS model. The train and test accuracy curves are depicted by the dark blue and red colours. The train and test curves overlap after a few epochs, which causes them to train.

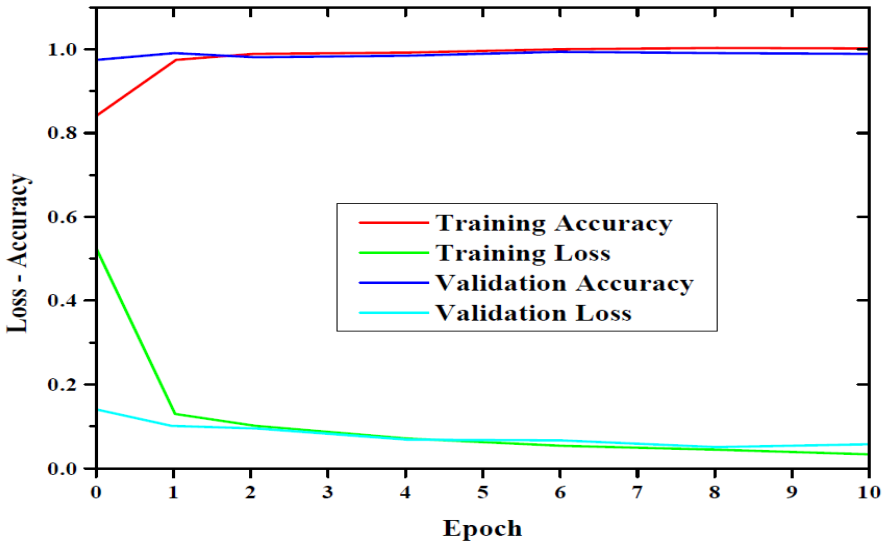

Figure 14. Convergence curves for training and validation datasets

Table 6. Comparative analysis in terms of Accuracy with other datasets

Year	Authors	Algorithm	Database	Accuracy (%)	Outside Training
2010	Fang et al. [27]	Pictorial structure model	Cornell KinFace	70.67	No
2011	Xia et al. [28]	Transfer learning	Kin Database	60.00	No
	Shao et al. [29]	Transfer subspace learning UB	Kin Database	69.67	
	Zhou et al. [30]	Spatial pyramid learning based	kinship Private Database	67.75	
2014	Lu et al. [31]	Multiview neighborhood repulsed metric learning	KinFace-I	69.90	No
			KinFace-II	76.50	
	Yan et al. [32]	Discriminative multimetric learning	Cornell KinFace	73.50*	No
			KinFace-I	72.00*	
	Dehghan et al. [33]	Discrimination via gated autoencoders	KinFace-I	74.5	No
			KinFace-II	82.2	
2015	Liu et al. [34]	Inheritable Fisher Vector Feature based kinship	KinFace-I	73.45	No
			KinFace-II	81.60	
	Alirezazadeh et al. [35]	Genetic Algorithm for feature selection for kinship	KinFace-I	81.30	No
			KinFace-II	86.15	
2019	Zhang et al. [40]	Resnet for Appearance+Shape	KinFaceW-I	78.3	No
2020	Zhang et al. [41]	Adversarial Convolutional Network for Kinship Verification	KinFaceW-I	79.6	No
			KinFaceW-II	89.9	
2021	Li et al. [42]	Reasoning Graph Networks for Kinship Verification	KinFaceW-I	82.6	No
			KinFaceW-II	91.6	
2022	Proposed	Kinship verification and disease prediction via proposed approach	Cornell KinFace	89.50	Yes
			UB Kin Database	91.80	
			KinFace-I	96.10	
			KinFace-II	96.20	
			WVU Kinship Database	98.00	

6. CONCLUSIONS

This paper proposed an analysis of genetic face images with respect to reflexology for prediction of diseases. Feature vectors are generated for the reflexology regions using LBP with the combination of high frequency and low frequency textures. The Euclidean distance weight function is used for prediction of diseases among the feature vectors. The proposed method is used not only by using single face reflexology regions, but some combined reflexology regions of n persons are used for finding multiple possibility of diseases. Based on the statistical measure analysis, the proposed algorithm works well in extracting the features for identifying the diseases linked to genetic disorders, potentially speeding up diagnosis of diseases. The experimental results for this work is shown in Tables 1 to 4 and its graphical representation is shown in Figures 8 to 11. The distance values are calculated and compared with all the reflexology regions of all the images in

the databases. The values shows that there is similarity in regions and prediction of genetic diseases. Using statistical analysis, distance values have been calculated and it is proved that similarity measure between the specific reflexology regions related to genetic disease has less value compared to the other regions.

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