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Artificial Neural Networks and Gene Expression Programing based age estimation using facial features



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KEYWORDS

Neural networks; Neurons; Gene Expression Programing; Chromosomes; Age estimation

Abstract This work is about estimating human age automatically through analysis of facial images. It has got a lot of real-world applications. Due to prompt advances in the fields of machine vision, facial image processing, and computer graphics, automatic age estimation via faces in computer is one of the dominant topics these days. This is due to widespread real-world applications, in areas of biometrics, security, surveillance, control, forensic art, entertainment, online customer management and support, along with cosmetology. As it is difficult to estimate the exact age, this system is to estimate a certain range of ages. Four sets of classifications have been used to differentiate a person's data into one of the different age groups. The uniqueness about this study is the usage of two technologies i.e., Artificial Neural Networks (ANN) and Gene Expression Programing (GEP) to estimate the age and then compare the results. New methodologies like Gene Expression Programing (GEP) have been explored here and significant results were found. The dataset has been developed to provide more efficient results by superior preprocessing methods. This proposed approach has been developed, tested and trained using both the methods. A public data set was used to test the system, FG-NET. The quality of the proposed system for age estimation using facial features is shown by broad experiments on the available database of FG-NET. © 2015 The Authors. Production and hosting by Elsevier B.V. on behalf of King Saud University. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

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Contents

1.	. Introduction	459
	1.1. Age estimation	
	1.2. Previous related work	
	1.3. Overview of the work	460
2.	Data collection and preprocessing.	460
3.	Artificial Neural Network (ANN) model	460
4.	. Gene Expression Programing (GEP) model	461
5.	. Results and analysis	464
	5.1. ANN model	
	5.2. GEP model	
6.	Conclusion	467
	References	467

1. Introduction

An individual's face image carries an important amount of information comprising information about the identity, emotional state, ethnic origin, gender, age and head orientation of that person. Also the human face bears important noticeable evidence associated to individual traits. In this study, we try to prove that the computer can classify human age according to features extracted from human facial image. Here both Artificial Neural Network (ANN) web.iitd.ac.in/~sumeet/ Jain.pdf, http://www.learnartificialneuralnetworks.com as well as Gene Expression Programing (GEP) (Ferreira, 2001) based classification of human age using facial features has been studied and proposed. The problem of having a suitable approach for age estimation for getting more specific categories of age ranges is still a challenging problem.

1.1. Age estimation

The purpose of age estimation is to determine an individual's age based on biometric features. Estimation of the age of a person from a digital photo is an interesting task which includes the study of human aging procedure. Human being cannot resist the variations that take place with aging; it is extremely difficult to collect sufficient data for age estimation. Thus, most researchers working in this domain try to obtain the results in certain age groups. The experimented age ranges till date are still too wide as they normally are up to 15 or 20 years. The main difficulty that occurs while shrinking the size of the age ranges is the question of accurateness of the extracted features from the face. First we have classified the ages into two groups i.e., (0-34) and (35-69). And then both these groups have been subdivided into two groups each making the four categories i.e. (0-17), (18-34), (34-50) and (51-69). As our main goal is age estimation and not facial recognition, we use only front images, with face free of Glasses or beard. To make our system more efficient and accurate, we selected only those images which were clicked in good lighting conditions and were free from unnecessary blurring or wrong orientation.

The major hurdle of shrinking the size of the age ranges is the correctness of the extracted features. Accuracy of the results fluctuates depending on the extracted features and the way they are used for age estimation i.e., some researchers use 20, 22, 35, or 68 features. Some of the open databases like FG-NET http://www.fgnet.rsunit.com, 2015 and Morph have been used for testing age estimation systems. These datasets contain photos and ages of the people and there are usually ages from 0 to 70 years. We have used FG-NET database which contains 68 feature points.

1.2. Previous related work

Different researchers have used different approaches to estimate the human ages. Some have even tried to estimate the aging effect (Ramanathan et al., 2009) which is the counter process of age estimation. Fukai et al. (2008) proposed an age estimation system on the AIBO. AIBO is an autonomic entertainment robot produced by SONY, AIBO has many sensors to get information around itself and moves according to its instinct. AIBO takes the face images and then age feature is extracted from the Images by the fast Fourier transform (FFT), and it is selected by the GA. Then Age is estimated by the 1-dimensional Self organizing Map. An error of 7.46% in age estimation was attained. A three phase age estimation approach was used by Horng et al. (2001). The three phases of this method were Location, feature extraction and age classification. They constructed two back propagation models. The verification percentage for first model was 99.1% and for second model, it was 78.49%. A subspace method known as AGES (Aging pattern Subspace) was used by Geng et al. (2007). The basic idea of AGES is to model the aging pattern, which is demarcated as an order of a specific individual's face images organized in time order, by building a typical linear subspace. The Main Absolute Error of this approach is 6.77% which is enhanced than method of the AIBO and the ages in AIBO scheme are between 15 and 64, while in AGES they are between 0 and 69. This work was further improved by Geng et al. (2008). In order to match the nonlinear nature of the human aging progress, a new algorithm named KAGES is proposed based on a nonlinear subspace trained on the aging patterns, which are defined as sequences of individual face images sorted in time order. The Main Absolute Error for this approach is 6.18% which is better than other approaches. Hewahi et al. (2010) used BPANN (Back Propagation ANN) based EasyNN Tool for their training and testing to compare their results with human observations. Our proposed methods are totally unique in nature, the way we classify the age ranges here, are not similar to any of these. The main difference between all the previous work and our approach is that we employ a totally different age range in our study, which was not explored earlier. In this work two approaches i.e., ANN and GEP have been followed and their results are compared. In the case of the ANN model we have used Matlab for creating, testing and validating our network based on ANN (Sivanandam et al., 2015; Haykin, 1999). In the case of the GEP model we developed the algorithm using GEP and combined the developed models in Matlab to obtain results. The numbers of neurons have been varied in the case of ANN and chromosomes in the case of GEP for the systems to obtain better results. The results shown by these technologies have been really good.

A proper ANN model as well as GEP model has to be constructed for that. Getting specific categories of age ranges is a common problem as the approach for age estimation depends on it inherently. Many people make errors in estimating human ages, making it a human problem too. To achieve this goal, a good database of all age groups is required to be used for training and testing the proposed system. Then after applying both the methods they have to be compared to each other.

1.3. Overview of the work

The age estimation using facial features based on ANN and GEP has been proposed here. The ages were classified into four categories i.e., 0–17, 18–34, 35–50 and 51–69. The FGNET database has been used to develop and test the proposed systems. In the ANN model we got the highest accuracy with 29 neurons in the hidden layer and in GEP model the maximum accuracy is obtained by combining different models with different numbers of chromosomes, for the first model it is 22, for the second model 26 and for the third model it is 20. Then we compared the results of these two individual methods. The results are sensitive to parameter choice however, and future research challenges are identified.

2. Data collection and preprocessing

Before beginning, either ANN or GEP design process, sample/ test data has to be collected and prepared. The database used here is from the FG-NET. The FG-NET database contains 68 pairs of points as features http://personalpages.manchester.ac. uk/staff/timothy.f.cootes/data/xm2vts/xm2vts_markup.html. The features are taken from the mouth, nose, eye, lips and the face surroundings. The used points' landmarks on the image are shown in Fig. 1. Each point's location on the face is illustrated in Table 1. A total of 260 best images have been chosen for ANN and GEP from the FG-NET database.

After the data have been collected, a step that needs to be performed is preprocessing of the available features. We have employed a new technique in this section where we have represented each pair by a single value. For example each point in a pair is represented by x and y co-ordinates. We find out the modulus of these two points by the following formula in Eq. (1)

$$r = \sqrt{x^2 + y^2} \tag{1}$$

We represented each (x, y) co-ordinate of 260 images by the above formula for training and testing purposes for both the technologies. For evolving the algorithm using GEP, we

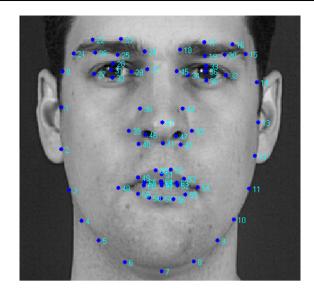


Figure 1 FG-NET points as landmarks.

Т	able	1	Facial	landmarks
1	able	T	гастат	landmarks

Face regions	Points Id	Number of points
Face edges	0–14	15
Bottom lip	55-59	5
Top lip	49–53	5
Lip outline	48, 54, 60-66	9
Nose	37-45, 67	10
Left eye	27-30	4
Right eye	32-35	4
Left eyebrow	21-26	6
Right eyebrow	15-20	6
Left iris	31	1
Right iris	36	1
Nostrils	46, 47	2

created a 260×69 excel sheet for first model and two more excel sheets for the two sub-groups. For testing the network in MATLAB, we created a MAT (Microsoft access table) file in MATLAB of size 260×68 which represents the inputs. We also created a MAT file of size 260×4 , which represents the outputs that are to be obtained. For ANN, we created a MAT (Microsoft access table) file in matlab of size 260×68 which represents the inputs. Now we need to have the targets which are required for training, validating and testing. Since we are classifying the whole age group into 4 categories, we need to have 4 targets. We created a MAT file of size 260×4 , which represents the outputs that are to be obtained. Then we combine these two files in a single MAT file so that the program can access the database whenever it requires. This completes our collection and preprocessing of the data.

3. Artificial Neural Network (ANN) model

The proposed system uses a supervised neural network with Back propagation algorithm. First the image is entered into the system and then the features are extracted; after that the image is classified in one of the four age classes predefined as

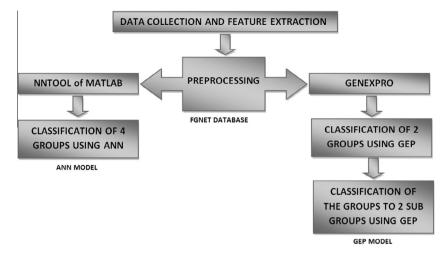


Figure 2 ANN and GEP model combined flow diagram.

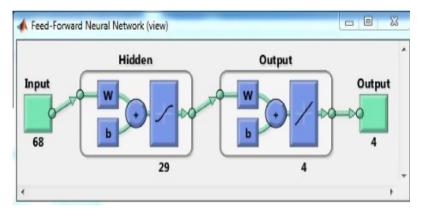


Figure 3 Neural Network Architecture.

shown in Fig. 2. In the first step the features of the images are extracted, which is already done by FG-NET. After preprocessing, the data are entered. Then network is created, trained, validated and tested using BPANN (Back Propagation ANN). BPANN is a generalization of the delta rule and is a supervised learning method. Some recent applications of ANN in performance analysis by Barma et al. (2011), in integration of shape by Kumar and Kumar (2012) and in MEWMA-ANN by Masood and Hassan (2012).

Before training any network, the general practice is to first divide the data into three subsets training, validating and testing. We have used the "dividerand" function of Matlab. It divides the data randomly. Out of the whole database 60% has been used for training, 20% for validation and rest 20% for testing. The number of data in each group has been kept balanced with utmost care. Moreover for validation the data should cover the whole range of the age group.

Next using the function feedforward net, a multilayer feedforward network is created. We have used a single hidden layer for our network. Networks are sensitive to the number of neurons in their hidden layers. Too few neurons can lead to underfitting. Too many neurons can contribute to overfitting. The number of neurons in a given layer has been vary from 29 to 43. The number of output neurons is determined by the number of elements in the target vector. The network has been manually configured for better performance. Then the multilayer feed forward network is trained for classifying the data into different groups. We have used Scaled Conjugate Gradient (trainscg) (Meiller, 1993) algorithm for our purpose. When training large networks, and when training pattern recognition networks, trainscg is a good choice. Its memory requirements are relatively small, and yet it is much faster than standard gradient descent algorithms. When the training is complete, the network performance is checked and changes required to be made to the training process, the network architecture or the data sets are addressed. The network formed for 29 neurons in the hidden layer is shown in Fig. 3.

4. Gene Expression Programing (GEP) model

Genetic Algorithm (GA) (Holland, 1975) is one of the best and popular algorithms among the class of the Evolutionary Algorithm (EA). In the conventional version, chromosomes were represented as a fixed length binary string. Another version of GA is Genetic Programing (GP) (Koza, 1992), where chromosomes are represented as a LISP expression translated graphically into a tree. LISP (LISt Processing) is a old programing language. Linked lists are one of Lisp language's major data structures, and Lisp source code is itself made up of lists. A newly introduced version of the Evolutionary Algorithms, called Gene Expression Programing (GEP) was proposed by Candida Ferreira in 2001 who got motivation from biological evolution. It overcomes certain limitations of GA and GP by working with two elements, the chromosome and the expression tree. The chromosome is the encoder of the candidate solution which is then translated into an expression tree. GEP is an example of a full-fledged replicator/phenotype system where the chromosome/expression trees form a truly functional, indivisible whole (Ferreira, 2006). That's why GEP is a big breakthrough in evolutionary computation, and it is continuously attracting more and more researcher attentions recently, especially in the areas of data mining. It should be noted that GEP chromosomes are multigenic. It encodes multiple expression trees or sub-programs, later on which can be structured into a much more complex program. Because of this, as like the DNA/protein system of life on Earth, the gene/tree system of GEP not only explores all the crannies and paths of the solution space but it also has the scope to explore sophisticated levels of organization. Some recent applications of GEP are image watermarking by Majumder et al. (2014), fingerprint watermarking by Shaw et al. (2013). Recent applications of GA in prediction of stock indices by Majhi et al. (2013).

The proposed system is using GEP in three stages. First of all the individual's image is loaded into the system, then in the next step features are extracted from the image, and then image is classified in two age classes and further both age groups are divided in two subgroups each. This process is shown in Fig. 2. In this system we will classify the whole age step by step, i.e., first we will divide it into two groups, and then further classify it into four groups, i.e., each group will give two subgroups. Three different models are created for the study. Then we will combine these three models using

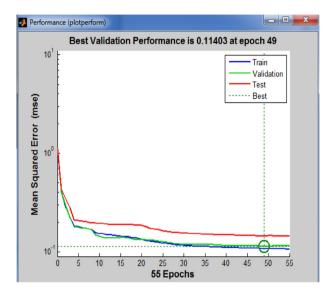


Figure 5 Performance plot of ANN method.

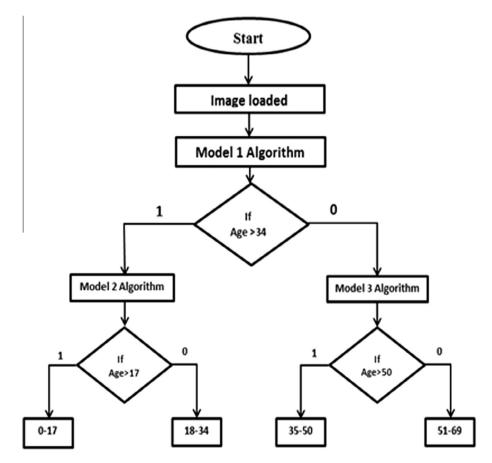


Figure 4 Flowchart for GEP technology.

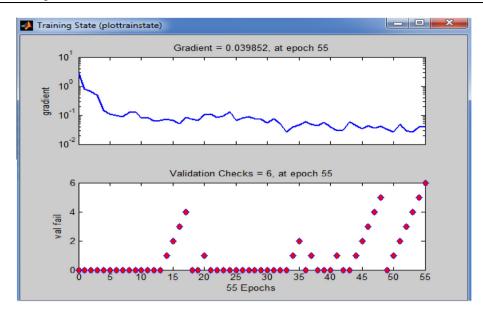


Figure 6 The training state plot.

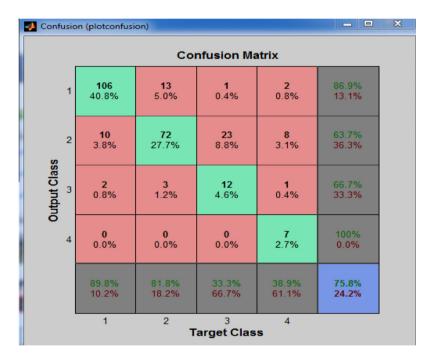


Figure 7 The confusion matrix for ANN based system.

MATLAB. Our first approach is to develop the algorithm for the first model. For developing algorithm and finding out functions we have used GEP.

The aim of very first model is to divide the whole age 0–69 into age groups, 0–34 and 35–69. We assign 1's to 0–34 group and 0's to 35–69. Then the database is saved in Microsoft Excel format and loaded in the software based on GEP. Since our main aim is to make a complete structure of classification in MATLAB, so we are generating the algorithm in terms of MATLAB code. Similarly two more sub models for classification of groups of 0–34 and 35–69 are created and algorithms are generated to classify the data into 0–17, 18–34, 35–50

and 51–69. Each individual model is brought in MATLAB for developing the complete structure. Then we combine the models so that it performs according to the following flow-chart, as shown in Fig. 4.

The first step is the image database loading. Here we loaded the database into MATLAB workspace. The database first passes through the model 1. Depending upon the value obtained through the algorithm it will decide whether the individual belongs to age group 0–34 or 35–69. If the age is between 0–34 then it will call the model 2 otherwise it will call the model 3. As before here also depending upon the value obtained through the algorithm it will decide whether the indi

Sl. No.	No. of neurons	Iterations	Best validation performance (MSE)	Correct classification (%)				Overall correct
				(0-17)	(18–34)	(35–50)	(51–69)	classification (%)
1	29	55	0.12	86.9	63.7	66.7	100	75.8
2	30	54	0.10	77.6	65.5	69.4	72.7	72.6
3	31	47	0.11	77.9	71.8	58.5	80.0	74.2
4	32	47	0.13	76.9	72.2	64.6	81.8	71.8
5	33	37	0.10	79.2	67.3	57.1	66.7	69.1
6	34	34	0.14	75.9	67.8	63.5	100	70.2
7	35	49	0.13	82.4	69.6	53.4	100	70.2
8	36	59	0.12	80.0	65.5	66.0	75.0	71.7
9	37	42	0.13	76.9	70.8	56.7	100	69.4
10	38	52	0.12	87.7	63.2	55.7	87.5	70.2
11	39	43	0.11	80.6	66.7	60.4	83.3	71.7
12	40	55	0.12	84.5	65.6	61.4	75.0	72.3
13	41	51	0.13	76.8	72.1	63.6	81.8	73.3
14	42	41	0.14	75.9	73.3	58.3	71.4	69.6
15	43	67	0.11	82.9	66.0	59.3	77.8	70.7

vidual whose age group was in 0-34 comes under the 0-17 or 18–34 group. Similarly if it runs the model 3, the individual's age group which was in 35–69 will further diverge either to 35–50 or 51–69. This way we will arrive at the final classification of an individual's age into four groups i.e., 0-17, 18–34, 35–50 and 51–69.

For evaluating the performance of the algorithm developed the mean square error value and confusion matrix http:// www.mathworks.in/help/stats/confusionmat.html, en.wikipedia.org/wiki/Confusion_matrix plot may be checked. The numbers of chromosomes are varied to obtain different results at different numbers of chromosomes for each of the three models. This helped us in obtaining the best result for combining the three models. The best functions from each of the three models are selected and combined. The results have been shown in the next section.

5. Results and analysis

5.1. ANN model

This system uses a supervised neural network with BPANN (back propagation ANN) algorithm. The image information once entered to the system, image is classified into four age classes via the extracted features. The four classes are 0-17, 18-34, 35-50 and 51-69.

After the network has been created and tested, we have obtained various results showing the accuracy of our system using different parameters like mean squared error (mse). It is obtained through the performance plot. The performance plot shows the value of the performance function versus the iteration number. It plots training, validation and test performances. A plot of the training errors, validation errors, and test errors appears, as shown in the Fig. 5. The best validation performance occurred at iteration 49, and the network at this iteration is returned.

But before the training stopped it had continued for 6 more iterations even on reaching 49. This figure actually doesn't indicate any major problems with the training, as the test and validation curves are very much similar. But there could have been chances of over fitting if the test curve had increased significantly before the increase of validation curve. Reinitialization and re-training was carried out for the sake of achieving more accuracy.

The progress of other training variables, such as the number of validation checks, the gradient magnitude, etc. are shown in Fig. 6, the training state plot.

To analyze the network response, we can plot the Confusion matrix between the response of the network and required output. A confusion matrix plot is shown in Fig. 7 which shows different types of errors occurred for the final trained network.

Number of correctly classified cases was indicated by the diagonal cells (in green) and the off-diagonal cells show the misclassified cases. In the bottom right the blue cell indicates the total percent of correctly classified cases (in green) and the total percent of misclassified cases (in red).Bottom right

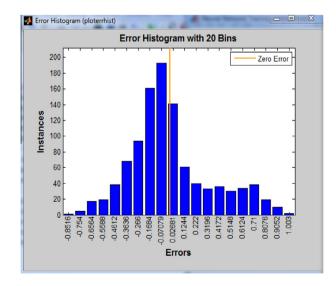


Figure 8 The Error histogram obtained.

cell indicates the total number correctly classified cases (green) and misclassification in (red). For example in the figure shown, the target class is divided into 4 categories. In the 1st target class 106 cases were correctly classified, while 13 cases are misclassified and being taken as target 2, also 1 other case was misclassified and being taken as target 3 by the network. There are 2 misclassifications for target class 4. Similarly from the confusion matrix we can see that 72, 12 and 7 cases were correctly classified in the target class 2, 3 and 4 respectively. Bottom right cell indicates the total number of correctly classified cases (green) and misclassification (in red) during the whole process of training, testing and validation which is 75.8% and 24.2% respectively.

The results shown above are for 29 numbers of neurons in the hidden layer. We have varied the number of neurons in a range (29–43) and the various results obtained can be shown in the Table 2.

The results for the training, validation, and testing, i.e. the three data sets show very good recognition. The error histogram plot of Fig. 8 shows the distribution of the network errors obtained. As shown in Fig. 8 most of the large errors are occurring near the Zero error (at the center) mainly. This is a very good sign and instances of higher values of errors are gradually decreasing at both the ends of zero error.

For better accuracy, the steps that might be taken are:

- Initially reset the network to new values of weights and biases before each training.
- Iteratively hidden neurons are to be increased.
- Iteratively training vectors are to be increased.
- Iteratively numbers of input values are to be increased.
- Change the training algorithm time to time.

With the increase of the number of neurons in the hidden layer, the network attains more flexibility due to increase of

Table 3 Gep results obtained from the the	ree models
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No. of chromosomes	Function 1		Function 2		Function 3		Overall	
	Best fitness (out of 1000)	Accuracy (%)	Best fitness (out of 1000)	Accuracy (%)	Best fitness (out of 1000)	Accuracy (%)	Accuracy (%)	
20	685.86	83.85	675	86.41	1000	100	72.69	
22	811.33	93.46	656.01	84.95	1000	100	73.46	
24	614.43	84.62	732.47	89.81	918.20	96.30	73.08	
26	745.62	88.46	786.25	93.21	972.22	98.15	80.00	
28	705.92	89.23	672.68	85.92	944.44	98.15	75.00	
30	652.32	86.15	613.40	83.50	833.33	94.44	70.38	
32	622.80	84.23	618.55	83.01	888.88	96.30	78.85	
34	607.61	83.85	695.87	87.38	1000	100	71.54	
36	690.90	85.38	690.37	87.38	1000	100	73.46	
38	738.00	88.85	636.59	83.98	944.44	98.15	74.23	
40	632.01	79.62	673.53	86.41	972.22	98.15	66.54	
42	655.91	86.54	671.13	85.92	918.20	96.30	73.46	

📣 Confusio	on (plotconfusi	on)				23
		Со	n <mark>fusion M</mark> a	atrix		
1	101 38.8%	8 3.1%	1 0.4%	1 0.4%	91.0% 9.0%	
2 02	14 5.4%	71 27.3%	3 1.2%	0 0.0%	80.7% 19.3%	
Output Class	0 0.0%	<mark>6</mark> 2.3%	32 12.3%	0 0.0%	84.2% 15.8%	
4	3 1.2%	3 1.2%	0 0.0%	17 6.5%	73.9% 26.1%	
	85.6% 14.4%	<mark>80.7%</mark> 19.3%	88.9% 11.1%	94.4% 5.6%	85.0% 15.0%	
	1	2 T	3 arget Clas	4 S		

Figure 9 Confusion matrix in GEP.

Curve fitting method	Algorithm	Coefficients	Goodness of fit			
			SSE	R-square	Adjusted R-square	RMSE
Smoothing splines	ANN	p = 0.99414847	75.92	0.7289	0.389	3.496
f(x) = piecewise polynomial from p	GEP	p = 0.92534399	288.1	0.4964	-0.1488	7.729
Quadratic polynomial fitting $f(x) = P_1 x^2 + P_2 x + P_3$	ANN	$P_1 = -0.3486$ $P_2 = 49.35$ $P_3 = -1709$	205.6	0.2657	0.1433	4.139
	GEP	$P_1 = 0.07778$ $P_2 = -12.05$ $P_3 = 495.6$	503.5	0.1197	-0.07589	7.48

optimize able parameters. This would lead to the gradual increase in number and size of the layers. But if the hidden layer is too large under-characterizing problem may occur as the network would constrain these parameters, as it would have to optimize more number of parameters as compared to the number of data vectors.

The highest number of iterations i.e., 67 was obtained for 43 neurons while for 30 neurons the best validation performance to be 0.10760 was obtained. But the highest correct classification was obtained while using 29 neurons and it was 75.8%.

5.2. GEP model

Here the ages were classified into two groups, i.e., (0-34) and (35-69). Each of these groups had been later subdivided further into two groups, thereby generating four categories. The four categories are (0-17), (18-34), (34-50) and (51-69). For our study, we have varied the number of chromosomes and obtained different results at different numbers of chromosomes for each of the three models. The tabulated result which

we obtained after varying the number of chromosomes is shown below. Here the table shows the best fitness and accuracy for each of the three functions at different number of chromosomes. The best fitness is out of 1000 and the result is better if the fitness is near to 1000. Accuracy shows the percentage of correct classification for each function (see Table 3).

We have varied number of chromosomes from 20 to 42. At 26 chromosomes we have got best accuracy i.e., 80%. But for a better accuracy we selected the best functions from each of the three and combine them in MATLAB. For function 1, the best result is obtained at 22 chromosomes, for function 2, the best result is obtained at 26 chromosomes, while for the third function the best result has been obtained at 20, 22, 34 and 36 chromosomes. We can select any one of these four. We have selected the function generated at 20 chromosomes since the program size depends upon the number of chromosomes used. The result obtained by combining the above mentioned best three functions in MATLAB can be shown through confusion matrix which we have plotted using MATLAB. On combining the three best models, the overall accuracy for our system comes to be 85%. To analyze the program response, we plot

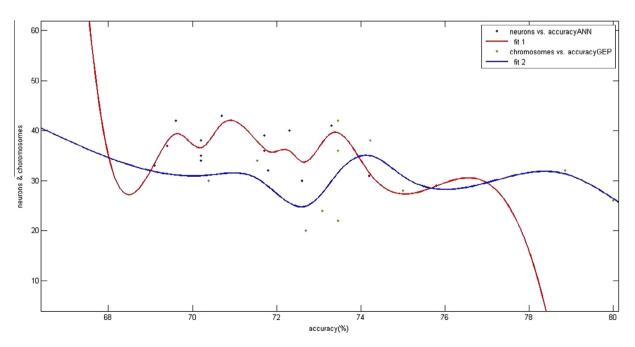


Figure 10 Curve fitting on GEP and ANN algorithm outputs using smoothing spline.

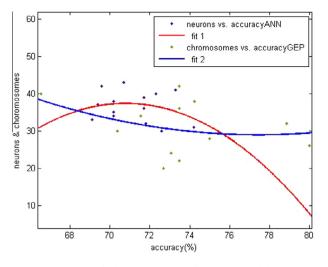


Figure 11 Curve fitting on GEP and ANN algorithm outputs using second order polynomial.

the Confusion matrix between the response of the program and required output as in Fig. 9.

The curve fitting also had been employed to see the fitting of the data obtained by the ANN and GEP based algorithms. The details are given in Table 4 below. The goodness of fit was not that good, but as both are totally different methods it is normally accepted to be so. Here two methods of curve fitting have been employed for both the algorithms. The first is using the Smoothing Splines with f(x) = Piecewise Polynomial from 'p'. Here 'p' lies between 0 and 1. A least-squares straight-line fit to the data is generated by 'p' = 0 produces, while for cubic spline interpolant the 'p' = 1. The second curve fitting algorithm is using a simple quadratic equation or second order polynomial. The figures of both have been shown in Figs. 10 and 11.

6. Conclusion

The age estimation using facial features based on ANN and GEP has been proposed here. The ages were classified into four categories so far. The FGNET database has been used to test the proposed system. Theoretically, while the learning models are based on only the training sets, the proposed method can be utilized in any other modalities. Our approach of using different number of neurons and chromosomes for obtaining a better result proved beneficial. Due to the usage of different number of chromosomes the combining of the best three models was possible with better accuracy. Moreover both the soft computing methodologies were compared for the same application. This work can be expanded to estimate ages on the basis of the ethnic group one belongs to. But that will require a huge database containing images of the individuals from different ethnic groups. Age estimation based on 3-D images could also be explored. This work can also be improved to a real-time system with inclusion of a camera for capturing the face of the individuals. The camera data used to determine the 68 point coordinates of that face by usage of any hardware or software after preprocessing can be later tested using our program for obtaining the age group.

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