Title: Family Verification based on Similarity of Individual Family Member's Facial Segments

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Abstract:

Humans process faces to recognize family resemblance and act accordingly. Undoubtedly, they are capable of recognizing their kin and family members. In this paper, we study the facts and valid assumptions of facial resemblance in family members' facial segments. Our analysis and psychological studies show that the facial resemblance differs from member to member and depends on image segments. Firstly, we estimate the degree of resemblance of each member's image segment. Then, we propose a novel method to fuse similarity of each member's facial image segments to perform family verification. Employing the proposed approach on the collected 5400-sample family database achieves considerable improvement compared to the state-of-the-art fusion rule in 3 designated test scenarios. Experimental results also show that the proposed approach could estimate the similarity slightly more accurate than human perception. We believe the public availableness of the database may advance the development in this domain.

Keywords: Family members, facial patches, score fusion

1. Introduction

Humans compare facial information to recognize their relatives and regulate their behavior accordingly [1,2]. Various research works imply that humans use facial resemblance as a cue to identify their relatives such as making decisions of paternal investment to people with self-resembling faces [3]. The ability of processing facial resemblance in human brain is carried out by combination of existing neurocomputational architecture [4]. However, psychologists highlight that the cognitive processes associated analysis of facial resemblance among family members and family verification algorithms "have received little attention to date" [1].

Recently in the field of computer vision, researchers conducted experiments to verify the possibility of recognizing human kin members that are related within a family known as "family (kinship) verification" [5-7]. We limit our search for kinship to "immediate" family members similar to psychological studies [1,2]. The aim of family verification is to classify the query image to "family" or "non-family" members. One way for family (kinship) verification is to perform DNA test that is currently accurate. The DNA test is not suitable for mass screening and a very expensive test for crime scene investigations that takes days to get the results [8].

1.1 Motivation and applications

To the best of our knowledge, family verification hasn't been addressed in the field of computer vision as defined in this paper to benefit human being in critical applications. We summarize motivations of family verifications in two major categories but are not limited to,

Recognize absent genuine faces, face recognition aims to recognize a person while his/her genuine samples were utilized to train the system against imposters. It gets more challenging when we aim to recognize an individual when his/her face sample was captured long time ago or there is no sample available. As defined in this paper, family verification is a solution to finding missing children in shopping centers, train stations or airports as approximately 2185 children are being reported missing in united states [9].

Consumer products, most of digital cameras are able to focus on faces to capture human faces at camera lens focus point. However, it is possible to focus on family faces rather than other faces in the background in group photos. Moreover, albuming software and social robots may require distinguishing family members from imposters.

1.2 Our solution for family verification

The facial resemblance is the key solution to recognize family members. The similarity among family members varies in three ways:

- It depends on gender and individuals in the family, as diverse results on the resemblance of daughters, sons and their corresponding fathers or mothers are reported [10]
- Distinctive resemblance features and the degree of similarity differs in facial segments of a particular family [6]
- The kinship verification is not processed using overall spatial information in the human brain. The accuracy achieved by combining “masked” facial patches is higher than considering the full face [1,11]

As a result, the algorithm must exploit the *resemblance* of each family *member's* image *segment* to perform family verification. We illustrate the overall process of family verification in Figure 1. Figure 1.(a) illustrates the constructed average face of the family and the corresponding average facial patch resemblance of family members. The degree of resemblance is shown as the color map index in Figure 1.(a). Faces of each family member are shown in Figure 1.(c). We usually compare the resemblance among family members and recognize that in their facial patches when we meet a new family. This fact is the evidence that we are capable to estimate the resemblance depicted in Figure 1.(a) and (b). The color mapped resemblance of each member's facial patch to that of the average face is shown in Figure 1.(b). Finally, we fuse the information to recognize if the query person belongs to the same family. In summary, the key contributions of this research work are,

- Estimate the degree of resemblance among family members that differs from member to member and image segments
- Combine the estimated family members' facial resemblance based on the given member's image segment information to classify the query image for automated family (or kinship) verification

The rest of the paper is organized as follows; Section 2 provides a literature review of related family verification in psychological studies and the field of computer vision. Section 3 outlines the proposed match score fusion algorithm for family verification followed by the details of each step. The experimental results on human and object family verify the achieved improvements in Section 4. Section 5 then concludes the paper.

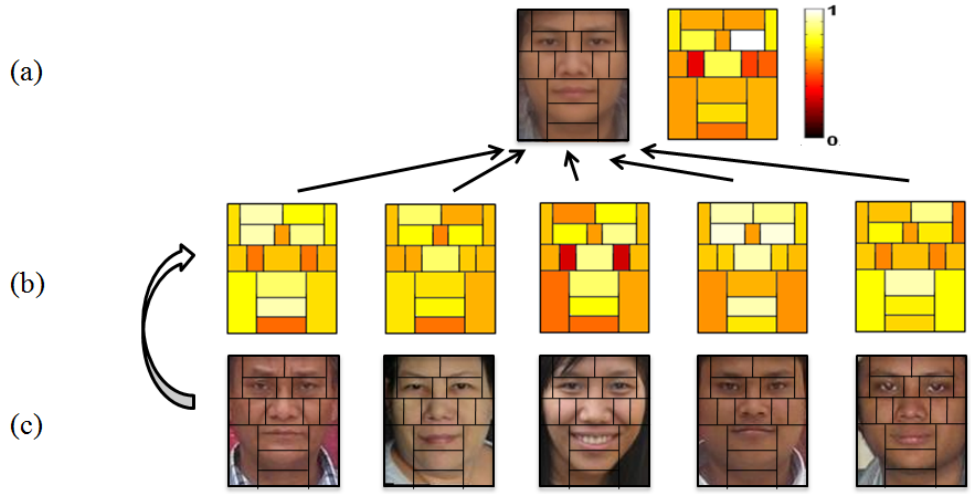

Figure 1 (a) The average face of family members and their overall facial patch resemblance [6] (b) each member's facial patch resemblance to be considered in the family verification algorithm (c) family members' facial patches split using the golden ratio mask template implemented in [6]

2. **Background and Literature review**

2.1 Family members' facial parts similarity in the field of psychology

Psychologists asked participants to assess facial pictures of samples of nonfamily individuals to obtain the resemblance between children and parents [10], among siblings [11] or adult faces [12]. It was discovered that other people's judgments about facial resemblance referred as "social mirror" affects individuals behaviors as in spouse/child abuse [13] or paternal investment [3]. There are interesting consensuses from psychological studies on facial parts resemblance for family verification as follows,

- **It depends on gender and members.** There is differential resemblance between the two parents, depending on children's gender that suggests the facial phenotype might be towards one parent as a reaction to costs and benefits of paternal investment [10]. Alvergne et al. deduced from the collected dataset that the facial resemblance inverts for boys, but not for girls [10]. However, the effect of children's age and gender for preferential resemblance needs to be investigated carefully in a large sample size, assuming it can be generalized.

- **Consider the whole face for facial resemblance analysis?** the question was firstly raised by Maloney & Dal Martello as "Where are kin recognition signals in the human face" utilizing children's facial segments without considering their genders [11]. In reality, the performance of family verification improved when face regions were analyzed instead of the "full-face" as examined by Dal Martello and Maloney [11]. They inferred that the lower half of children's faces including mouth and chin shape carries less useful information about genetic family resemblance, probably due to growth through childhood. Debruine et al. investigated finding facial similarities of family members in adult faces in [12] as the continuation of [11]. They concluded "combination of kinship information from the two halves of the face can be treated as *optimal combination* of *independent cues*" [11].

- **What are the mechanisms and algorithms for assessment of family facial patches similarities?** It has been highlighted that algorithms and feature types of kinship recognition signals are poorly known [12,10]. Based on studies, recognizing faces may result from facial organs arrangement processing ability [14]. Research works on family facial resemblance [1] reveal that the resemblance extraction is not processed using overall spatial information such as ratio of the distance between face organs as in [7].

Similarly, when humans observe family members, we usually hear e.g. "this family is all blond. These sayings also suggest that resemblance in a family is related to facial parts and varies with the members of other families. In other words, it is member and patch specific. As a result, the family verification strategy should consider facial resemblance of each individual family member's image segment (facial patch) to the whole family to satisfy the assumptions and important findings above.

2.2 Recognizing family members by artificial intelligence

In this part, we review some previous works related to family verification in the field of computer vision. Not only family verification encounters all variations found in face recognition but also there are family specific changes such as mixed ethnicities, unbalanced datasets, various age groups and high aging effect. Das et al. developed a system for automatic grouping of digital albums including snapshots from family photos [15]. The minimum Euclidean distance of clusters to the query image is chosen as the closest similar face. One of the disadvantages is that similar faces of family members were classified as the query person. Holistic face processing was among the first solutions for the face recognition due to low computational power [16]. Another research work that experimented with the immediate relationship of people, employed mostly holistic approaches e.g. facial parts ratios and concluded the left pupil gray-value is the most accurate feature with the total error equal to 29% [7]. They collected a database of 150 pairs of a single sample of a parent and the corresponding child to from a dataset of 300 faces. However, psychological studies disprove features utilized by Feng et al. [7] as similarity features. Xia et al. collected the UB KinFace database [17]. However, these databases suffer from multi-samples of members of the family and only one of the parents and one of the children are available. Thus, studies and conclusion on previous family databases can not be generalized.

To benefit from boosting classifiers, discrete fusion rules were investigated on family verification results of members' extracted features in [5]. They showed that it can reach acceptable accuracy using strong classifiers such as SVM and AdaBoost [5]. In another research work, Ghahramani et al. investigated the fact that family datasets contain larger intra-class variation compared to face recognition [18]. To solve the problem of excess redundant Gabor wavelets selected by the AdaBoost classifier, they incorporated Genetic Algorithm to optimize the likelihood ratio of decision results of every wavelet to tune Gabor wavelet parameters.

The overall resemblance between family members was first addressed in [6]. Faces were divided to several parts based on the golden ratio mask for beauty analysis [19] as shown in Figure 2. The facial resemblance was incorporated for family verification and the top *'t'* informative patches were selected to reduce the computational load through diversity analysis. The diversity calculation of patches' classification results revealed the amount of useful information embedded in every patch of the face image [6]. In summary, the key problem of recognizing family members is to extract the resemblance of family members' faces.

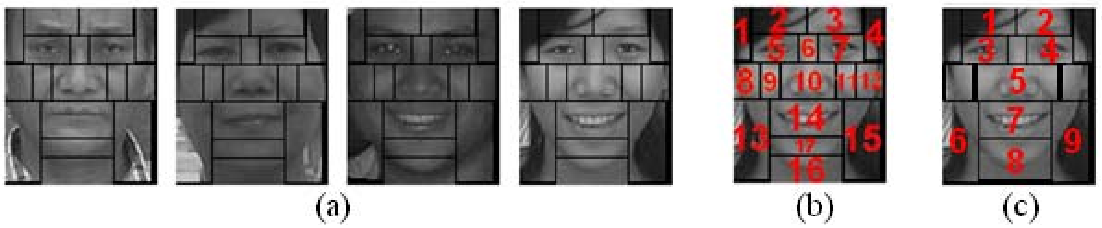

Figure 2 (a) Aligned and Cropped family faces are split into regions (b) the golden ratio mask template indexing implemented in [6] (c) modified patches selected in this work

3. The proposed approach

Our goal is to enhance the family verification accuracy based on family resemblance assumptions discussed in Section 2. As aforementioned, the dependence of family resemblance *to gender and facial image segments* and the method to *benefit from such a priori information* are missing in previous studies. Hence, our proposed approach is to,

- Estimate similarity of individual member's image segments
- combine the estimated resemblance based on the a priori information

We utilize the a priori information of "member" and "the corresponding image segment" in verifying whether a person belongs to a particular family. To achieve this goal, we used the face mask developed in [6] which is modified from the original facial beauty analysis [19] to split the face regions as shown in Figure 2.(c). The main steps of our proposed algorithm are as follows:

1. Split the face to regions based on the developed facial mask as in Figure 2.(c)
2. Extract features from the face patches
3. Process features extracted from each patch to get the match score
4. During the training stage:
    a. Compute similarity of every present member's patch to the whole family
    b. Adjust the threshold to perform fusion of selected patches' match scores by incorporating similarity measurement of every member's patch
5. During the testing stage, match scores of each patch are computed and used as the input to the proposed fusion rule
6. The decision from the combined output determines if the face image belongs to the family.

3.1 Facial segments

There are various types of information in the human face that could contribute to the family verification. Genetic similarities in the family include skin and hair color, face shape, face organs and minute features of the face. We opt for the developed facial mask in [6], designed based on the face golden ratio to select regions containing the genetic similarities of the face. However, there are patches as shown in Figure 2.(b), which do not carry much face texture. Moreover, the informativeness analysis in [6] shows that the information carried by patches 1, 4, 6, 8 and 12 was previously captured by other patches. Hence, we do not consider patches 1, 4, 6, 8, 12 and merge patch 9, 10 and 11 to form the nose region. Patch 16 and 17 are also merged to form the chin region to get the final mask as shown in Figure 2.(c).

3.2 Facial Feature Extraction

A local appearance-based feature space, such as Haar [20], Gabor wavelet-based features [21] and local binary pattern (LBP) [22] can be employed on the image to overcome the non-linearity of face manifolds [23]. Dense Scale Invariant Feature Transform (DSIFT) features are known to be robust against illumination changes, slight misalignment and scale changes as they are investigated to enhance the recognition performance in [24]. It has been reported that Gabor features are robust to small variation in illumination and alignment [21] compared to Haar features. Therefore, we select Gabor [21], LBP [22] and DSIFT operators [24].

3.3 Classification and Match Score Computation

This is an important stage of which a classification algorithm is implemented to find margins for classes. Linear algorithms e.g. PCA and holistic approaches are not accurate enough to find non-linear boundaries of face manifolds in the face space particularly in family verification. On the other hand, kernel methods may not perform well on the unseen data [23] which occurs in family verification. We select AdaBoost [25] as it is a widely used feature selection and learning algorithm that combines many weak classifiers to form a strong classifier by adjusting the weights of training samples at each iteration. AdaBoost has been used successfully to handle the feature selection and nonlinear classification problems [26]. The code provided in [27] selects features and employs the AdaBoost algorithm to generates match scores.

3.4 Consolidation of family resemblance

Among fusion methods at different stages of recognition, score fusion is usually preferred due to the balance between information possession and the fusion complexity [28]. It is complicated to include minimization of error types in classification based algorithms [29]. It occurs in case of missing member which is very critical to fail to spot a genuine sample (*minimize* P_{miss}). In transformation-based approaches match scores are converted to a normalized common domain which require large amount of data for evaluation [30]. Though, in the application of family verification, we encounter unbalanced and small number of training datasets.

Therefore, we choose the density-based classifier fusion approach as it achieves the minimum False Negative Ratio (FNR) at the desired False Positive Ratio (FPR) that suits family verification. It guarantees optimal performance if the match scores densities are known and well estimated. An extensive test on the large NIST database concluded that the density-based method could achieve the highest accuracy among other selected algorithms [31]. The genuine and imposter match score densities were estimated in [32,28] for score fusion as they are unknown in most cases. The estimation complexity of the kernel density approach was then reduced by modeling the Probability Density Function (PDF) as the finite Gaussian Mixture Model (GMM) of joint PDFs in [28]. Their proposed method slightly outperformed the Support Vector Machine (SVM) classifier on the output scores [28].

Family verification is a two class problem. We need to formulate the family verification problem to derive the fusion rule based on the similarities of human family members' facial parts. Parameters and variables used in this part are described in Table I in details.

TABLE I. DETAILED DESCRIPTION OF PARAMETERS AND VARIABLES

Variable	description
F_p	*p-th* family
M_p	Members of *p-th* family
n_{pq}	number of total images for *q-th* member from *p-th* family
X_{pq}	face sample of *q-th* member from *p-th* family
L	Number of regions Faces are divided into
$S = [S_1, \ldots, S_L]$.	vector of all patches' match scores
$f_{g,p}(S)$	the conditional joint density of L match scores for *p-th* family
$f_i(S)$	the conditional joint density of L match scores for imposter samples
H_0	the hypothesis of belonging to non-family members
H_1	the hypothesis of belonging to *p-th* family
η	threshold
U_q	the set of all samples belong to *q-th* member
$\hat{f}_{p,r,q}(Y \in F_p)$	the estimated marginal density function of the genuine *q-th* member's *r-th* patch samples of *p-th* family

The task is to verify if the query (Y) belongs to *p-th* family, F_p or ($Y \in F_p?$). Each dataset has parents and at least one child (not infant). Each family dataset is labeled and annotated to M_p members where n_{pq} is the number of total images for *q-th* member from *p-th* family. The face sample of *q-th* member from *p-th* family denoted as X_{pq} is divided into L regions. Features of each region are extracted and given to AdaBoost matcher to calculate the match score. The vector of all patches' match scores is S = [S_1, …, S_L]. Let $f_g(S)$ be the conditional joint density of L match scores given the *p-th* family genuine samples, and $f_i(S)$ be the conditional joint density of L match scores given the imposter samples. According to Bayes decision theory, we should decide $Y \in F_p$ if

$$P\left(Y \in F_p \middle| X_Y\right) \;>\; P(Y \notin F_p | X_Y) \tag{1}$$

or,

$$\frac{P\left(Y \in F_p \middle| X_Y\right)}{P(Y \notin F_p | X_Y)} \;>\; 1 \tag{2}$$

where X_Y is a face sample belonging to person Y. According to Bayes theorem,

$$P\left(Y \in F_p \middle| X_Y\right) = \frac{P\left(X_Y \middle| Y \in F_p\right). P(Y \in F_p)}{P(X_Y)} \tag{3}$$

and

$$P\left(Y \notin F_p \middle| X_Y\right) = \frac{P\left(X_Y \middle| Y \notin F_p\right). P(Y \notin F_p)}{P(X_Y)} \tag{4}$$

By substituting equations (3) and (4) in equation (2), the decision rule can be simplified to decide $Y \in F_p$ if

$$\frac{P\left(X_Y \middle| Y \in F_p\right). P(Y \in F_p)}{P\left(X_Y \middle| Y \notin F_p\right). P(Y \notin F_p)} \;>\; 1 \tag{5}$$

We assume equal prior probabilities, (i.e. $P\left(Y \in F_p\right) = P\left(Y \notin F_p\right) = \frac{1}{2}$) then the decision rule depends only on the likelihood ratio, which is defined as

$$LR_p(X_Y) = \frac{P\left(X_Y \middle| Y \in F_p\right)}{P\left(X_Y \middle| Y \notin F_p\right)} \tag{6}$$

Based on the Neyman-Pearson theorem, T(S) is the optimal test such that

$$T(S) = 1 \quad if \quad \frac{f_{g,p}(S)}{f_i(S)} \geq \eta \tag{7}$$

We define the False Positive Ratio, (FPR) equal to number of non-family samples that are recognized as family divided by total number of non-family samples as

$$P(T(S) = 1 \,|H_0) = FPR \tag{8}$$

where H_0 is the hypothesis of belonging to non-family members. The Neyman-Pearson (N-P) theorem guarantees that, given the desired FPR, the optimal test for deciding whether the match score vector S is a genuine user or an impostor is given by equation (7). We adjust the threshold η for a fixed FPR such that the likelihood ratio test minimizes the False Negative Ratio, FNR, given by number of samples of family members that are not recognized as family divided by the total number of family members' samples. Here, we need to estimate the joint density functions $f_{g,p}(S)$ and $f_i(S)$. We select the Gaussian Mixture Model (GMM) estimation [28,33]. Hence, the N-P test T(S) is performed on the GMM estimated PDFs as,

$$T(S) = 1 \quad if \quad \frac{\hat{f}_{g,p}(S)}{\hat{f}_i(S)} \geq \eta \tag{9}$$

Dal Martello and Maloney observed that the kinship information obtained from the two halves of the face can be considered as "optimal combination of independent cues". Among selected patches patch 1 and 2 are usually altered by hair particularly in ladies faces that reduces the correlation between them, significantly. The only similar patches are patch 3 and 4 that include eyes. However, since the dependence characteristics among genuine and imposter left and right eyes do not differ, the independence assumption of eyes patches' match scores does not alter the fusion performance [33]. Nandakumar et al. showed that in this condition, embedding the dependence information to the fusion scheme will not lead to significant performance improvement [33]. They also indicated, as estimation of each marginal density is more accurate and efficient than estimation of the complex, multi-dimensional joint density function of the combined random variables, the independence assumption would ease the match score fusion, especially when we encounter *lack of genuine data as in family verification*. Hence, we extend equation (9) to the product of marginal density functions,

$$\frac{\hat{f}_{g,p}(S)}{\hat{f}_i(S)} = \frac{\prod_{r=1}^{L} \hat{f}_{g,p,r}(s_r)}{\prod_{r=1}^{L} \hat{f}_{i,r}(s_r)} = \prod_{r=1}^{L} \frac{\hat{f}_{g,p,r}(s_r)}{\hat{f}_{i,r}(s_r)} \tag{10}$$

The numerator of equation (10) estimates the marginal density functions of the genuine samples regardless of the given patch scores but we know that the family resemblance of each patch differs from member to member. To deploy the dissimilar resemblance among members' facial patches, we propose to extend the nominator of equation (10) based on the *Total probability* and Bayes formula as,

$$\frac{\hat{f}_{g,p}(S)}{\hat{f}_i(S)} = \frac{\prod_{r=1}^{L} \hat{f}_{g,p,r}(s_r)}{\prod_{r=1}^{L} \hat{f}_{i,r}(s_r)} = \prod_{r=1}^{L} \frac{\sum_{q=1}^{Mp} \hat{f}_{g,p,r,q}\left(s_r \mid Y \epsilon\, U_q\right) * P_g(Y \epsilon\, U_q)}{\hat{f}_{i,r}(s_r)} \tag{11}$$

where U_q is the set of all samples belonging to *q-th* member and Y is the given face. We know that $\hat{f}_g(S)$ and $\hat{f}_i(S)$ are the short forms of conditional density functions $\hat{f}_p\left(S \mid Y \epsilon\, F_p\right)$ and $\hat{f}\left(S \mid Y \notin F_p\right)$ where F_p is *p-th* family. Hence, the estimated genuine density function is given by,

$$\hat{f}_p(S \mid Y \epsilon F_p) = \prod_{r=1}^{L} \hat{f}_{p,r}(s_r \mid Y \epsilon F_p)$$
$$= \prod_{r=1}^{L} \sum_{q=1}^{Mp} \hat{f}_{p,r,q}(s_r \mid \{Y \epsilon U_q\}, \{Y \epsilon F_p\}) * P(Y \epsilon U_q \mid \{Y \epsilon F_p\}) \tag{12}$$

Therefore, the final test is to calculate equation (13),

$$\frac{\hat{f}_p(S \mid Y \in F_p)}{\hat{f}(S \mid Y \notin F_P)} = \frac{\prod_{r=1}^{L} \hat{f}_{p,r}(s_r \mid Y \in F_p)}{\prod_{r=1}^{L} \hat{f}_r(s_r \mid Y \notin F_p)}$$
$$= \frac{\prod_{r=1}^{L} \sum_{q=1}^{Mp} \hat{f}_{p,r,q}(s_r \mid \{Y \epsilon U_q\}, \{Y \in F_p\}) * P(Y \epsilon U_q \mid \{Y \in F_p\})}{\prod_{r=1}^{L} \hat{f}_r(s_r \mid Y \notin F_p)} \tag{13}$$

The degree of similarity between *q-th* member's *r-th* patch and the whole family is now deployed in equation (7). Next, we illustrate how to estimate the degree of similarity for each member's facial patch.

3.5 Estimation of similarity

We propose to estimate similarity of each member's patch by computing the probability of *q-th* member's *r-th* patch samples belonging to family P. Given all training *q-th* member's *r-th* patch samples, the GMM marginal density function of the genuine $\hat{f}_{p,r,q}(s_r \mid \{Y \epsilon U_q\}, \{Y \epsilon F_p\})$ and imposter $\hat{f}_{i,r}(s_r)$ samples are estimated. A Baysian classifier is utilized to calculate the probability of recognizing the given sample belonging to family *p*. The parameters of the Bayesian classifier and estimated $P(Y \epsilon U_q \mid \{Y \epsilon F_p\})$ are stored for the test stage. The overall proposed method to utilize family resemblance based on valid assumptions discussed in Section 3.4 is summarized in the following pseudo code in Figure 3.

Consolidation of facial resemblance

Split the given face into L patches
Extract features of the patches
Obtain the match scores from each patch $S = [S_1, \ldots, S_L]$
$A=0; M=1;$
for patch $r=1:L$
  for member $q=1:M_p$
    read the similarity measurement $P(Y \epsilon U_q \mid \{Y \epsilon F_p\})$ from training
    compute $sum = \hat{f}_{p,r,q}(s_r \mid \{Y \epsilon U_q\}, \{Y \epsilon F_p\}) * P(Y \epsilon U_q \mid \{Y \epsilon F_p\})$
    $A = sum + A$
  End for
  $Ratio = A / \hat{f}_{i,r}(s_r)$
  $M = Ratio * M$
End for
Compare M with the threshold obtained in training

Figure 3 Pseudo code of the proposed method to utilize similarity of individual member's facial patch

4. Experimental results

To the best of our knowledge, there is no comprehensive publicly available dataset for family verification comprising photos of family members taken over a period of time. Recently, Gallagher's database [34] used for clothing co-segmentation is published online which is not practically collected for family verification. The dataset provided by [7] does not allow us to implement feature based algorithms that require training stage and the face size is rather small, about 60×70. Therefore, it necessitates collecting a representative database of multiple families with diverse characteristics present in human family such as, twin children, adult or adolescence children or parents with high aging effect from various ethnicities.

For our experiment, we collected a family dataset containing 45 families with an average of 120 face samples per family (overall 5400 samples) from the available digital albums. Thus, photometric changes such as lighting, background, camera lens and sensor variation exist in the collected digital albums as in other family databases [7] and [17]. The dataset has families of different ethnicities and includes 18 families with high aging effect in the parent's face images, 16 families with adolescences, 5 families with twins or quadruplets and 6 families with single child. In addition, 800 frontal face samples are collected from other people in family photos but didn't belong to the family. These samples were considered as the dataset for non-family members. All faces are cropped with respect to their eyes' position extracted using the Active Appearance Model (AAM) [35]. As our current work does not consider significant pose variation, only faces with near frontal pose are used in the database. Finally all face samples are resized to 80×95 pixels.

4.1 Experiment scenarios

We conduct challenging experiments to compare our proposed approach with the state-of-the-art algorithms. Inspired by test designs in psychological studies in section 2.1, we define 3 different tests of family verification to explore the possible situations in the real world:

Test 1: All family members are present in both training and test datasets
Test 2: One of the family members is missing. There are two possible scenarios:

> Test 2.a: the child is missing. We simulate this scenario by removing the child with the largest number of samples from the training dataset [9]
>
> Test 2.b: one of the parents is missing. We simulate this scenario by removing the parent with the largest number of samples from the training dataset.

The family member with the largest number of samples is chosen as the omitted member as this gives the largest error. In test 2.b the other parent samples are also omitted from the training stage due to very low genetic similarities of parents. For each family, 2/3 of the family dataset and 2/3 of the non-family dataset are used for training and the remaining for testing. For test 2a and 2b, 2/3 of all the family members' samples, except the omitted member, are used for training together with 2/3 of the non-family members. For the test set, all samples of the omitted member and the remaining non-family members are used.

Firstly, we need to determine distinctive feature operators for facial patches and then implement the fusion rule on the rendered match scores for family verification. Hence, to compare feature's discrimination power, we utilized AdaBoost as the matching algorithm and set the threshold to default value '0'. We compare Gabor [26], LBP [22] and DSIFT [24] operators, due to their robustness against illumination changes and acceptable feature size for large face sample processing [21]. To extract Gabor features, the bank of 40 Gabor wavelets with 5 scales and 8 orientations are convolved with the image and the magnitude of the complex value is represented as the Gabor feature. We select 16 sample points around center pixel on radius equal to 2 to extract LBP features [22]. DSIFT features were extracted using the finest settings for feature extraction based on the image size with block size equal to 10 pixels. Features of each patch are separated for each facial region shown in Figure 2.c. The Total Error (Err) given by the total of all misclassified samples divided by the whole number of samples and FNR of selected features for every patch in Test 1, 2a and 2b are shown in Figure 4, after 25 iterations of AdaBoost classifier training. The results show that Gabor features outperform other selected features in most patches in terms of total error and FNR.

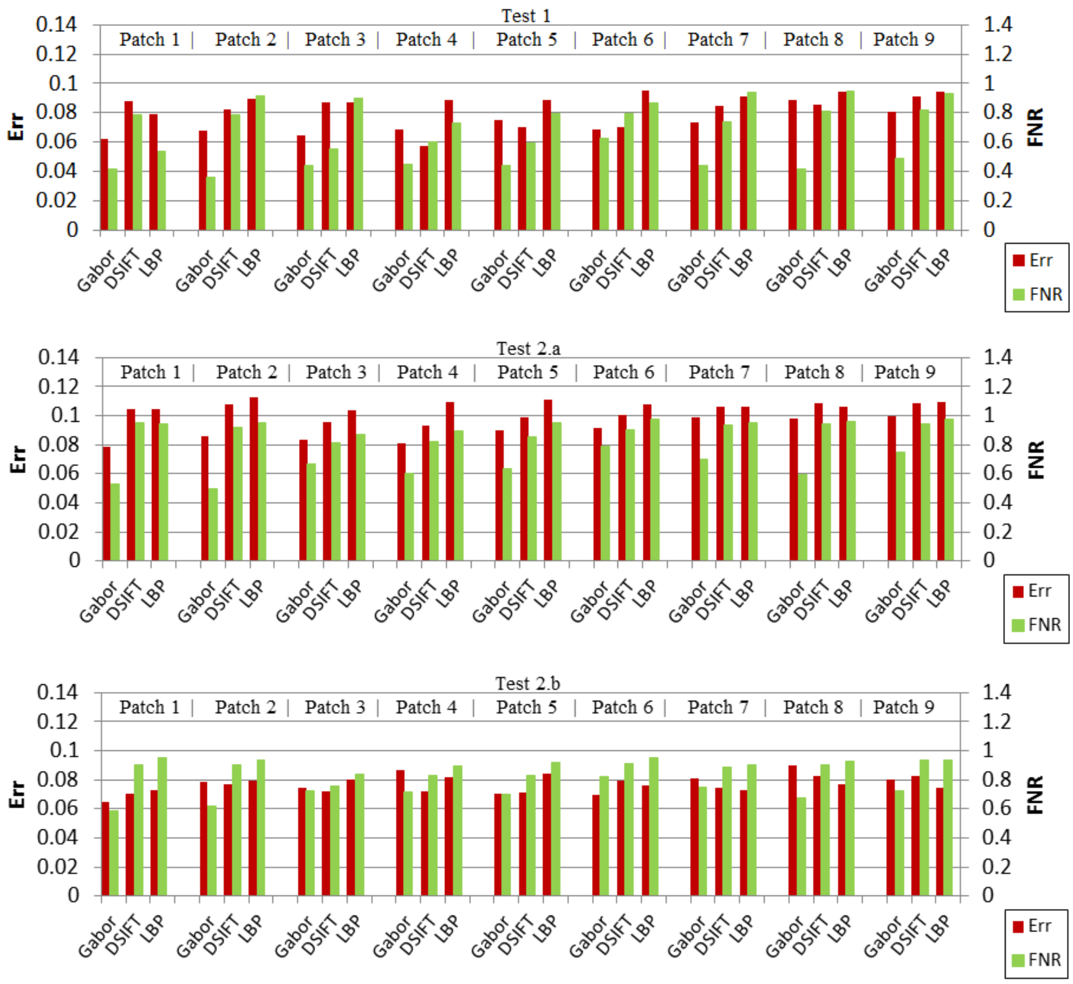

Figure 4 The average family verification total error (Err) and False Negative Ratio (FNR) of selected features for Test 1, Test 2.a and Test 2.b on facial patches

4.2 Score fusion results

In this section, the performance of the proposed method to fuse the match scores obtained from AdaBoost matchers is compared with the state-of-the-art GMM fusion rule [33]. We use the provided MATLAB code provided in [36] to estimate the density functions. The algorithm automatically estimates number of components and their parameters [36]. For every family, the training data match scores rendered by AdaBoost are utilized to estimate their density functions. The AdaBoost selects features and the classifier produces confidence score for each facial part [27]. The Baysian classifier is trained for each member's patch to adjust parameters for the testing stage. The Receiver operating characteristic of Genuine Positive Ratio (GPR) versus FPR, ROC, curve is the most representative curve to compare fusion algorithms performance. The ROC curves of the proposed fusion rule show the achieved improvements in Figure 5.a, 5.b and 5.c for Test 1, 2.a and 2.b, respectively. The proposed method outperforms the state-of-the-art score fusion rule at FPR=0.004 by 17%, 12% and 10% in Test 1, 2.a and 2.b, respectively.

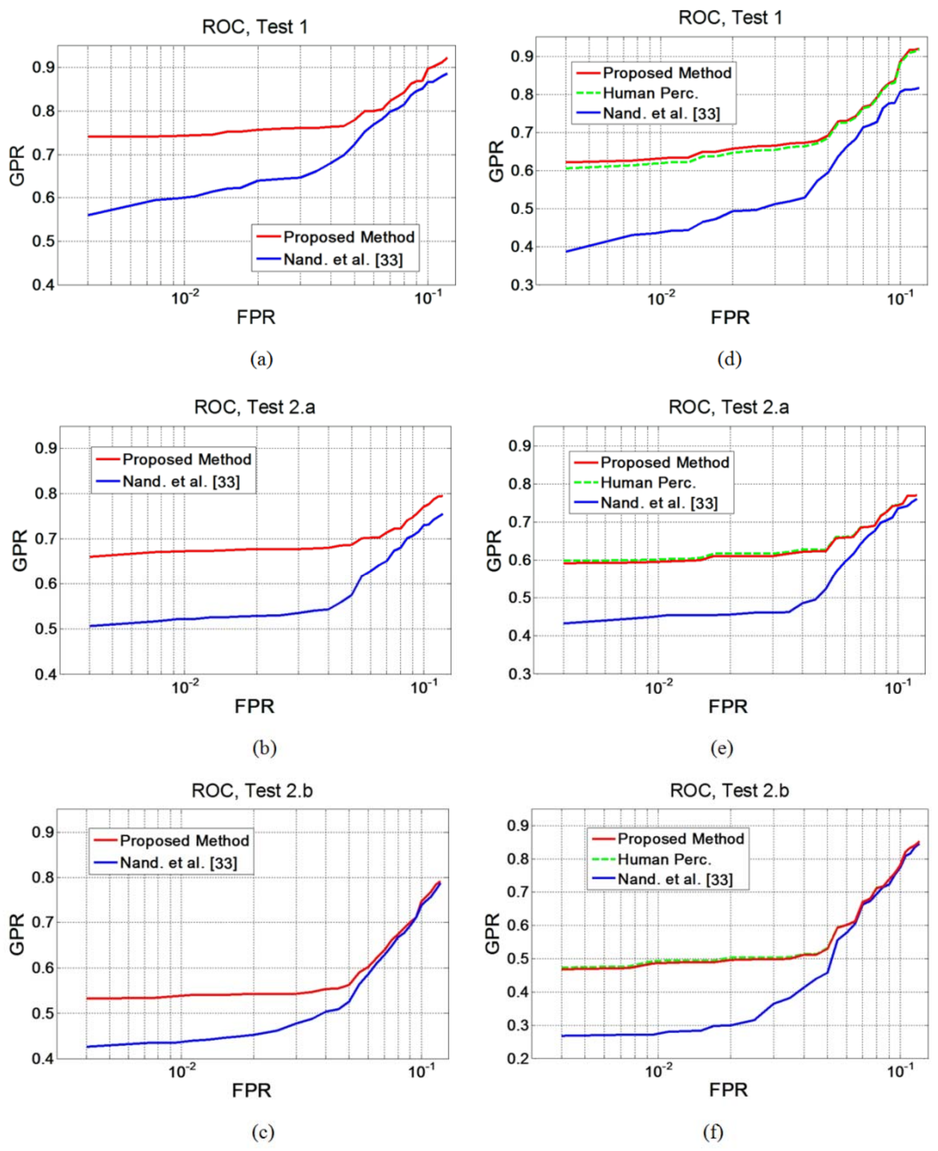

Figure 5 The ROC curves for the proposed fusion approach and the fusion rule by Nandakumar et al. [33] for (a) Test 1, (b) Test 2.a (c) Test 2.b. Incorporating human perception on family datasets provided in the survey for (d) Test 1, (e) Test 2.a (f) Test 2.b

The family verification performance of the proposed fusion rule is also compared with the SVM as also was utilized as the state-of-the-art methods in [33]. The (Radial Basis Function) RBF kernel SVM parameters need precise adjustment which cannot be accurately calculated on the available training dataset based on the criteria given in [37]. Hence, we employed the linear SVM on the match scores from facial patches. The SVM algorithm is implemented using the code provided in [37]. The results obtained at equal FPR are tabulated in Table II. We select the minimum average FPR achieved by the SVM algorithm to compare the GPR achieved by the algorithms. As we expected, algorithms employing kernel functions may not perform well in case of unseen data [23]; as in Test 2.a and 2.b GPR of SVM algorithm is less than the proposed method, particularly it is the least accurate in Test 2.b.

TABLE II. PERFORMANCE COMPARISON OF THE SVM CLASSIFIER, THE PROPOSED METHOD AND THE ALGORITHM SUGGESTED BY NANDAKUMAR ET AL. [33]

		Test 1		Test 2.a		Test 2.b	
		FPR	GPR	FPR	FNR	FPR	FNR
Algorithm	Proposed method	0.042	**77%**	0.04	**67%**	0.036	**58%**
	Linear SVM	0.042	76%	0.04	59%	0.036	44%
	Nand. et al. [33]	0.042	73%	0.04	57%	0.036	54%

4.3 Utilizing human perception

We asked 30 participants to rate the similarities for 10 selected families. They answered how much family members resemble each other in their forehead, eyes, nose (including cheeks), mouth and chin. Using the designated online survey to analyze the human perception of each member's patch resemblance to the whole family, we can incorporate human understanding of similarity estimation of members' facial patches. In the survey conducted, it allows participants to guess accurately the resemblance of the missing member's patches, since there are samples of the missing member in the provided album. However the algorithm just uses the information of available members. The choices of similarity amount were provided as “a lot”, “very”, “so so”, “a bit” and “No idea” in the survey and mapped to the quantized vector [4, 3, 2, 1, 0] respectively. The average mapping is calculated for the similarity measurement of member's facial patches for each family in the survey.

We substituted the human perception of similar regions in equation (13) to compare the performance of family verification results in Test 1, 2.a and 2.b. ROC curves of the proposed method fusion rule, human perception of family resemblance and the score fusion rule proposed in [33] are plotted in Figure 5.d, 6.e and 6.f, respectively. The estimated similarity of member's facial patch is comparable to human perception on all test cases. We include selected images of the provided genuine samples of the 3 different scenarios for further illustration in Table III. The output of the proposed method is compared with the approach suggested by Nandakumar et al. [33].

TABLE III. OUTPUTS OF THE PROPOSED METHOD AND THE ALGORITHM SUGGESTED BY NANDAKUMAR ET AL. [33] ON SELECTED SAMPLES FOR 3 DIFFERENT SCENARIOS

Random genuine training samples provided	Test type	Genuine query samples	True class	proposed method Output	Nand. et al. [31] Output
	Test 1		Family	**Family**	Imposter
			Family	**Family**	**Family**
	Test 2.a		Family	**Family**	**Family**
			Family	**Family**	Imposter
	Test 2.b		Family	**Family**	Imposter
			Family	Imposter	Imposter

5. Conclusions

We propose a novel method to consolidate the resemblance information estimated from every member's image segment for the problem of family verification. The proposed fusion technique was incorporated at the match score level due to its information richness of the input pattern. We enhance the performance by incorporating the fact that family resemblance is member and patch specific. Experiments were conducted based on real life scenarios on the collected family database. Our aim was to provide multiple samples of every member in the family to describe within-class variations. We believe that the public availableness of this database may advance the development in this domain. The results show that on the average 14% improvement is achieved using our proposed algorithm compared to the-state-of-the-art fusion rule at lowest FPR. We also conducted an online survey to obtain the human perception of the resemblance among family members. The results obtained utilizing human perceived similar regions are comparable to the proposed automated facial resemblance measurement. Future works include further improvement based on the similarity information of the missing member's facial patch to raise the bar in case of missing and unknown member verification.

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