A Combined DNA and Dental X-Ray Based Biometrics System for Forensic Human Identification

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Abstract: Recently, the relying on the biological and personal are adopted for the human identification purpose to produce a more reliable method. This method is the base of a biometrics system which is a measurement of the behavioral or physical attributes - such as scents, individual voice, fingerprints, facial structure, and others to identify or verify the identity of person. In this paper, we propose a biometrics forensic human identification system based on the valuable and reliable biometrics tools which are DNA and Dental X-Ray. The motivation of this work among the previous work is the combination of the DNA and Dental features for human identification. This is for two main reasons; firstly, to cover the lack in the stored database information and secondly, for cross checking verification. Sixteen Short Tandem Repeats (STRs) DNA and a bite-wing image, used to extract the dental information, are used. The goal of the proposed system is to introduce a forensic identification system based on a built database, which contains a real STR DNA profiles and an ante-mortem dental image features (AM) for Iraqi Diyala Province Population. The adopted AM dental features are Standard Deviation (STD), Euler number and Intensity, extracted from the bite-wing image through utilizing a three stages algorithm. These stages are image segmentation, classification and features extraction. The proposed system's algorithm utilizes MATLAB software to extract dental features from the AM image and uses SQL Server software environment to build the database. Moreover, the Visual Studio (VS) environment was utilized to design the Graphical User Interface (GUI) of the system which connects the MATLAB with SQL database in an attractive and useful manner. The achieved outcomes offer the outstanding performance of the proposed system for inserting, searching, updating and matching purposes and also for dental features extraction in a flexible and accurate manner..

Keywords: Human identification, Dental biometrics, DNA profile, SQL Server, STR markers.

1. INTRODUCTION

Historically and over the centuries, humanitarian norms on identification purpose was based on tangible things, such as a key, a passport or identity card, or relied on information such as a password or answer to a question to satisfy the need to confirm the identity. However, these methods are ineffective and can be up to the wrong person, leading to security breaches. Therefore, the biometrics technology has become a basic rule for secure identification which poses a front part of the systems that require precise identity. In addition, the proliferation of these systems is in a significant escalation not only for the security, but the friendly use. The biometrics technologies are generally divided into two main parts: Physiological and Behavioral [1]-[2]. Based on these technologies, everyone has the distinctive features, such as a fingerprint, shape of the hand, DNA, teeth imprint, facial image and eye imprint [3]. Most of these features can be determined through a biological reader, and then archived in a database to be used later in verification or identification purpose. The

verification process is based on comparing the biometrics features with referenced biometrics stored in the system database. While the identification process relies on a comparison of biometrics features with all biometrics references, stored in the system database [4]-[7]. The biometrics system is used in many spheres, such as, voting system, security systems, marketing, criminalistics …etc., because it is not cheatable and reliable system [7].

Wagner et al. [8]presented a face recognition system for access control purpose. Their system is fixed towards the common problems that faces the similar systems which are: image misalignment, partial occlusion and illumination variation by capture image under a practical conditions. The proposed system achieved a high performance in the investigated applications.

Shivanand [9]offered an overall survey about biometrics research that detect gender based on fingerprint technology. He proposed a method that

combines multiple methods and strategies which has been detailed to achieve a results with high precision.

On the other hand, the physiological characteristics and behavioral characteristics are used in identifying as well as verifying the individual in many fields, such as handwriting, keystroke and signature. Schomaker [10]considered the handwriting of the person as a significant biometrics tool for identifying and verifying the identity. While, Bulacu et al. [11] proposed a system with two levels method to identify and verify person based on handwriting with text-independent using textural and allography features. Moreover, Ribaric et al. [12] utilized the whole human hand as a biometrics tool. They presented a biometrics system for identification based on Eigen-finger and Eigen-palm.

Tripathi et al. [13]proposed a biometrics system for identification purpose by utilizing the DNA as a biometrics technology. He created a huge database that comprises a DNA profiles to use it later for retrieval. The presented system achieves a high accuracy using the STR loci as a DNA marker.

The teeth information or dental features also considered as a biometrics tool. Where the dental x- ray is used in forensic under the term "forensic dentistry" to identify and verify the identity of the unknown person. In 2013, Charbel et al. [14] presented a method for identification purpose utilizing the dental features extracted from the Orthopantomogram (OPG) dental image. They proposed to use a high resolution dental X-Ray to facilitate the segmentation of teeth and features' extraction.

It is important to note that all the biometrics tools (some of them mentioned above) are considered as a reliable and valuable technologies in authentication and identification purpose, but each one has a security level and a distinctive application. Forensically, the DNA was considered as an accurate and reliable evidence in courts for criminal cases. At the other hand, the teeth are considered as an important tool in forensic science. Some forensic cases demand a specific biometrics technology, for example, forensic dentistry that plays an important role in criminal cases. This is for dealing with a burned or decomposed bodies following the fact of that the other physiological characteristics are affected more than the teeth. The teeth show satisfactory resistant to the septic and combustion factors including high heating degree up to 500 degrees Celsius [15]. Moreover, a blood stains behind the crime scene enables investigators to use DNA as a tool for a reliable detection of criminals and identification of victim.

In this paper we automate the usage of the physiological characteristics for identification and verification purpose by proposing a biometrics system based on forensic human identification using the DNA and Dental X-Ray as biometrics tool. A sixteen Shorter Hypervariable Regions (STR) loci and the features of bite-wing images for Iraqi Diyala Province Population are used and saved in a database. The database is built using a SQL Server environment. The AM bite-wing image is processed by Matlab software with a three stages algorithm: Image enhancement, Image segmentation and features extraction. The extracted features are Standard Deviation (STD), Euler number and Intensity for a selected teeth. We select eight teeth (four from each jaw side) that are more practical in forensic cases. As a result, the AM dental features are formed in the database as a dental profile. A GUI of the system has been built using VS environment to provide an attractive and a simple interface. The outcomes of the proposed system show the reliability and efficiency in database management, human identification and image processing terms.

2. THE PROPOSED SYSTEM

The proposed forensic identification system considers the DNA and dental X-Ray as metrics to satisfy the identity of the human. From DNA, we utilize a sixteen STR loci where the human genome contains a shorter hypervariable regions called STR which repeats in tandem. Moreover, the STR in 1990s was considered as markers for identify and verify the human identity [16], and then used as outstanding standard in paternity testing and any forensic cases [17]-[18]. Thirteen from the utilized loci are CODIS core loci. The considered STR Loci are (D3S1358, VWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, CSF1PO, D16S539, D19S433, D2S1338) plus Amelogenin (AMEL) to determine sex. The utilized loci are saved in the database as a DNA- profile for each individual. The adopted STR profiles are collected from the pre-stored STR loci of Iraq/Diyala Province population [16] following the steps of our previous works of [19]-[20].

In addition, a set of Bite-wing dental image are considered and processed using a three stages MATLAB algorithm that enhances, segments and extracts features from them. A distinctive features are extracted from the fifth and sixth tooth of the lower and upper jaws for both sides. The adopted numbering system of teeth is the Palmer Notation Method as shown in Fig. (1) [21]. The extracted dental features are saved as a dental-profile for each individual. As a result, these are archived in the database to retrieval in matching process with the query PM features.

The system offers a high ability in performing the database activities, such as insert, update and search the physiological characteristics (i.e. STR DNA and/or dental features). Moreover, the matching process is performed at a time of presence the query PM physiological characteristics with these the saved information. The GUI provides the

ordinary users a high flexibility and simplicity dealing with the system without need to pre-knowledge about the internal procedure [22].
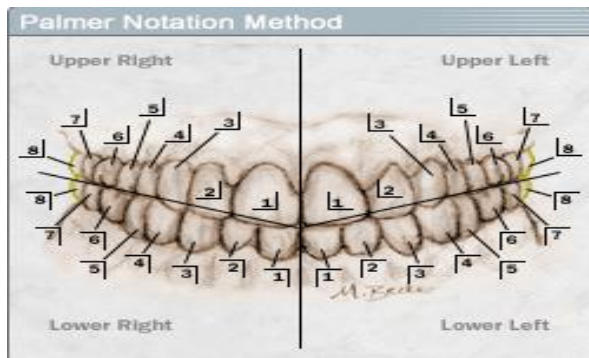

Figure 1. Palmer Notation Numbering System [22]

3. The Proposed Algorithm

The proposed algorithm comprises of four operations under two main processes which are: Image processing and Human Identification. The algorithm can be summarized as follows:

I. **Image Processing:** involves an algorithm which is interested in the processing of the bite-wing images in order to extract features [23]. Fig. (2) shows the flowchart of the image processing method. At this process, a three stages MATLAB sub-algorithms are considered. These stages are: image enhancement, image segmentation and feature extraction, where each one is complementary to other. At the first stage (image enhancement), an enhanced image is achieved that can provide a better result from the next stage in comparison with the original image. In this stage, the Histogram Equalization is used to equalize the brightness level of the image which has an uniformly distributed histogram. The histogram equalization for an image is computed as [24]:

$$s_k = T(r_k) = (L-1)\sum_{j=0}^{k} p_r(r_j) = (L-1)\sum_{j=0}^{k}\frac{n_j}{M\times N}$$

$$= \frac{(L-1)}{M\times N}\sum_{j=0}^{k} n_j \qquad k=0,1,2,\ldots,L-1 \qquad (1)$$

Where, r = input image, sk = processed image (equalized image), T = an operator on r, L = gray level, pr = histogram value, nj= gray intensity of the corresponding gray level and N, M = dimension of image matrices.

In addition, the two steps thresholding is employed to convert a gray scale image to a binary image. The Contrast-Limited Adaptive Histogram Equalization (CLAHE) is utilized. Later on, Global image threshold (Otsu's method) is adopted which is operating on the gray level histogram to convert the input image to a binary image as shown in Fig. (3). The main process of the Otsu's method is to compute a threshold level (T) over which all gray scale pixels are considered white (i.e. foreground) and the rest considered black (i.e. background). The main goal of this method is to minimize the error of classifying the foreground as a background and vice versa. Therefore, the threshold which *minimizes the weighted within-class variance* must be calculated as:

$$\sigma_w^2(t) = q_1(t)\sigma_1^2(t) + q_2(t)\sigma_2^2(t) \qquad (2)$$

Where, q_1 (t) and q_2= the class probabilities which are estimated by the equation (3), and (4) respectively.

$$q_1(t) = \sum_{i=1}^{t} P(i) \qquad (3)$$

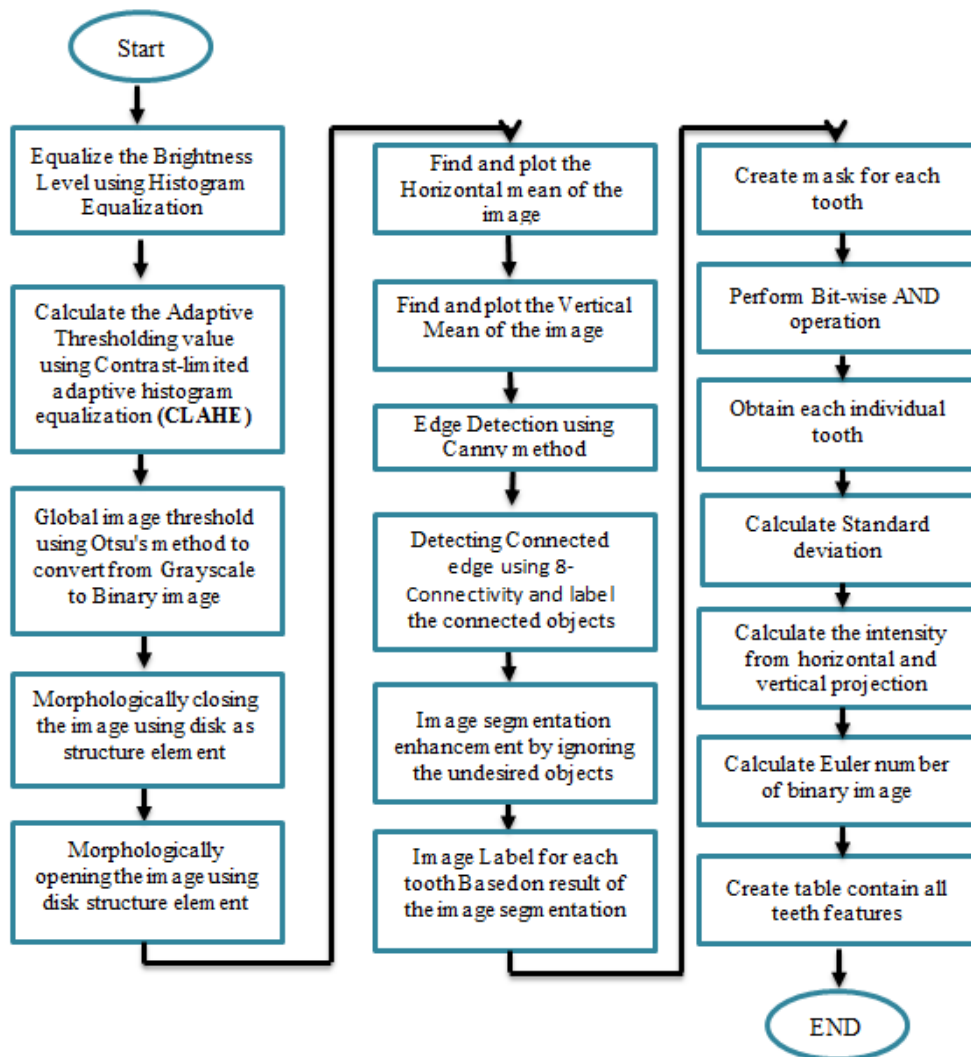$$q_2(t) = \sum_{i=t+1}^{I} P(i) \qquad (4)$$

Figure 2. The Flowchart of The Image Processing Method
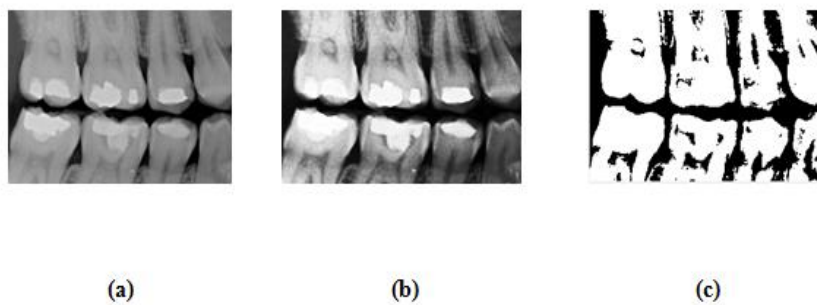

(a)   (b)   (c)

Figure 3. (a) Original Image (b) Equalized Image (c) Binary Image

The class means are computed by this formula:

$$\mu_1(t) = \sum_{i=1}^{t} \frac{iP(i)}{q_1(t)} \qquad (5)$$

$$\mu_2(t) = \sum_{i=t+1}^{I} \frac{iP(i)}{q_2(t)} \qquad (6)$$

Then the individual class variances are calculated by the following equations:

$$\sigma_1^2(t) = \sum_{i=1}^{t} [i - \mu_1(t)]^2 \frac{P(i)}{q_1(t)} \qquad (7)$$

$$\sigma_2^2(t) = \sum_{i=t+1}^{I} [i - \mu_2(t)]^2 \frac{P(i)}{q_2(t)} \qquad (8)$$

To select the optimal t value, the full range of t is used to determine which of them can minimize the $\sigma w2(t)$. Moreover, the morphological operation is utilized in this stage. At the other hand, image segmentation is the second stage of image processing. Separating the teeth

from the background and other tissue is the aim of this stage that can be achieved by detecting the valley between each tooth and jaw. Therefore, the vertical and horizontal projection are calculated in order to satisfy these valleys that ease the segmentation process as shown in Fig. (4). These projections are computed as [25]:
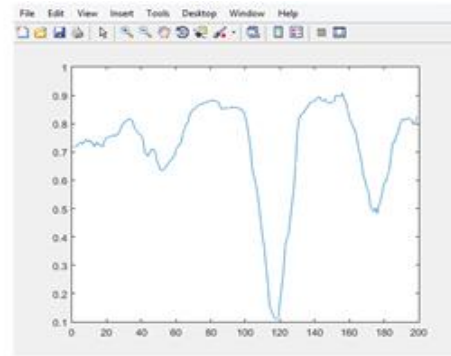
$$H[i] = \sum_{j=0}^{m-1} B[i,j] \qquad (9)$$

$$V[j] = \sum_{j=0}^{n-1} B[i,j] \qquad (10)$$

Where the $[i,]$ is a binary image, Hi is the projection of a binary image along the rows (horizontal projection). And the Vj is the projection of a binary image along the columns (vertical projection).
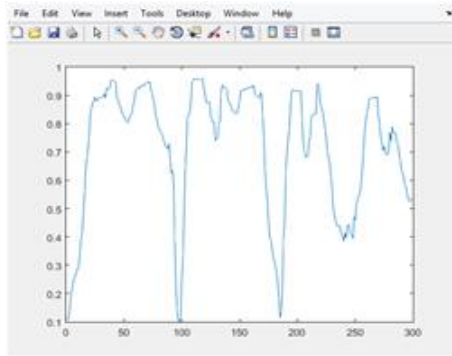
Figure 4. (a) Vertical Projection (b) Horizontal Projection

Edge detection is achieved using Canny algorithm. It works in five separate steps, which are Smoothing, Finding gradients, Non-maximum suppression, Double thresholding and Edge tracking by hysteresis. The results of the Canny edge detection is shown in the Fig. (5). To detect each teeth in the resulted image, the connected edges are detected using the 8-connectivity in which each teeth is considered as an object ready to extract features as shown in Fig. (6). Fig. (7) shows the segmented teeth. At the feature extraction stage (third stage of the algorithm), three features are considered to be extracted from the adopted four teeth at each jaws side. The selected teeth are: (fifth Upper Left, sixth Upper Left, fifth Lower Left, sixth Lower Left, fifth Upper Right, sixth Upper Right, fifth Lower Right and sixth Lower Right). The extracted features are: (STD, Euler number and Intensity) of the selected teeth. The AM features are stored in the built database to be used later in human identification process.
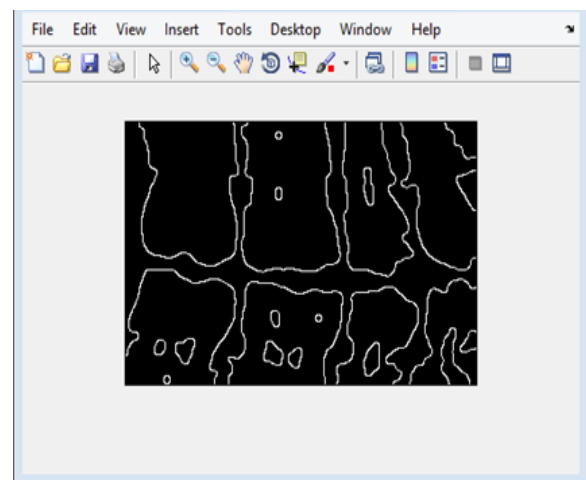

Figure 5. Edge Detection By Canny Algorithm

Figure 6. The Detected Objects

Figure 7. Segmented Teeth

II. **Human Identification:** it is the most important process in the proposed system. After the image processing is completed and the DNA profiles are available, The next stage is to archive the DNA and the

Dental profiles in the database. The database (as mentioned previously) is built using SQL Server with the consideration of the SQL Server Management Studio (SSMS). The SSMS provides the SSQL Server for an integrated environment to manage all server components [26]. The built database involves four tables which are: "IndividualInfo ", "indivDNAprofile", "indivFSDental" and "indivSSDental" table. The fist table, "IndividualInfo ", contains a personal information to each physiological profile. This table help the investigator to hold more information about the required profile. The second table, "indivDNAprofile", comprises the DNA profiles of the Iraqi Diyala Province Population. As mentioned, a sixteen STR are utilized where each locus has two alleles so the total number of columns are 32 in addition to the ID column. The last two, "indivFSDental" and "indivSSDental", tables comprise the dental profiles (i.e. dental features) which are extracted from the AM bite-wing image through the image processing as explained earlier. The extracted features are saved in the "indivSSDental" table. It is important to note that each tooth has a code (weight) that is computed from the first three feature for each tooth and stored in the "indivFSDental" table. Fig. (8) shown the Entity Relationship diagram (ER) of the built database's tables and their relations.

Figure 8. Database ER Diagram

The proposed system offers four operations for managing the built database. These operations facilitate the dealing with system from the ordinary users as follows:

a) **Inserting**: A new record (profile) is created in this stage and saved in the "IndividualInfo" table after generating the universal ID number. This ID is considered as the primary key for DNA and X-Ray dental profiles. Some notes must be taken to the consideration:

- All fields that marked with * must be filled.
- At the DNA profile insertion, all alleles have to be filled.
- If the user selects the automatically insertion of the DNA or Dental X-Ray profile, the uploaded file should be in a CSV file extension.

b) **Updating**: The editing of the existing records can be performed in this process using the ID, Full Name or Mother Name of the required record.

c) **Searching**: The ID, Full Name or Mother Name can be utilized for searching of a desired records.

d) **Matching**: This is the most important operation in the proposed system for forensic human identification. The PM features for both DNA and Dental X-Ray profiles are inserted for searching and matching over the saved AM records with acceptable matching ratio. This operation composes two stages: *Filtering* and *Finding*.

In the Filtering stage, the DNA records that have similarity with at least one allele of the D2S1338 locus are selected. This locus is adopted due to low frequently appearance in human [16]. Whilst, the X-Ray dental records that have a similarity to the average feature (weight) of the corresponding tooth are chosen. This stage can reduce the consumed time and memory size for matching and searching processes over the available. Then the selected DNA and Dental records are passed to the next stage.

The next stage is the Finding stage. The passed records from the first stage are examines over the underlying profile to find out the similar records with matching ration equal or greater than the ratio dedicated by the user.

4. GUI Design

The graphical user interface (GUI) of the proposed system are accomplished using the VS environment for introducing flexibility and friendly interfaces that can be used by even unskilled users. The home page of the system involves four main buttons that are dealing with the database and human identification processes as shows in Fig. (9).

The "Profile Inserting" button allows the user to create a new record in the "IndividualInfo" table to a person who have a DNA and Dental Profile. By clicking on this button, a multiple fields which dedicated to the personal information is appeared. After filling all the compulsory fields, the inserted information with a unique ID are archived as a record in the IndividualInfo table.

Afterwards creation an ID to the new profile, the physiological characteristics profiles can be inserted separately. From the DNA profile side the user has two options in the insertion operation. These are: Insert and Upload. The Insert option provides the user the ability of entering the STR loci manually and to fill all allele's fields. While the Upload option allows the user to upload the DNA-profile CSV file. The csv file must involve 32 columns, each of which is with two columns, dedicated to one locus. The sequence of the STR loci must be taken under the consideration.
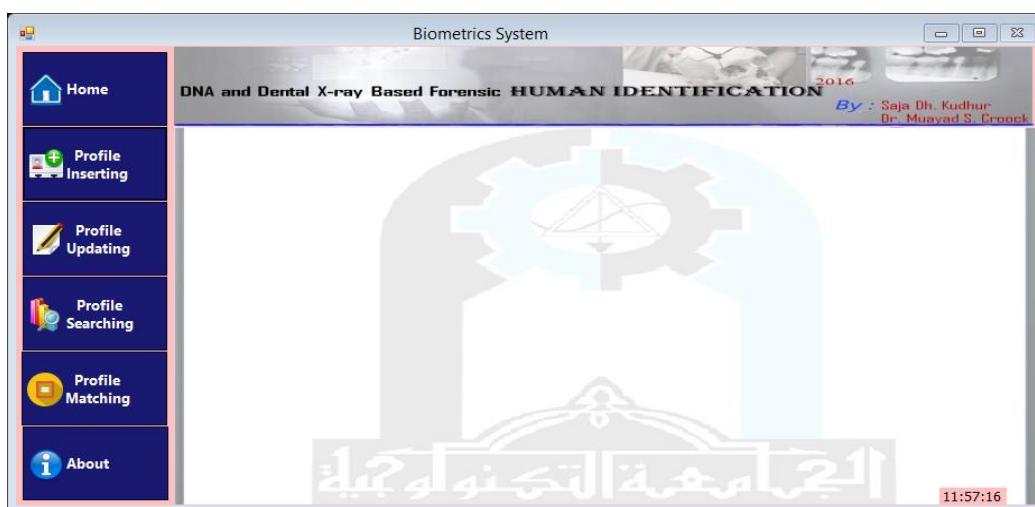

Figure 9. The Home Page of The Proposed System

Later on, the user is turned to insert the Dental-profile, where the user has many options in the insertion operation which are: Upload File, Manual Insertion and Upload X-Ray. The first option, Upload File, allows the user to upload the Dental-profile file in a CSV format and with a specific structure. The CSV file must compose 24 columns where each three columns are STR, Euler, Intensity features for each tooth. As a highlight note, the synchronization of the features with the tooth is a very restricted and important. The second option, Manual Insertion, allows the user to enter the dental features manually. The last option, named Upload X-Ray, gives the user a possibility to upload the bite-wing images of each jaw side for each individual. When the user uploads the bite-wing images, the uploaded images are redirected to the MATLAB for implementing the considered three stages algorithm to extract the distinctive features of the selected teeth. The system brings the features automatically to the corresponding fields. Fig. (10) shown the flowchart of the profile inserting process.

The "Profile Updating" button composes the updating process that gives a user the ability to edit the information of selected profile. Fig. (11) shows the flowchart of the profile updating process. The "Profile Searching" button allows the user to inspecting for a specific profile. The searching procedure is done in the same manner as the updating procedure. This process is explained as a flowchart in Fig. (12). Moreover, the "Profile Matching" button comprises the most important process in the proposed system which is the matching process. At the first time, the investigated DNA and Dental profile is inserted following the same insertion procedure explained above. This algorithm has two stages which are: Filtering and Finding followed as clearly explained earlier.

It is important to note that the proposed system can performing the whole processes partially. i.e. either both biometric sides (DNA and dental X-Ray) or one of them. The internal procedure of this process is explained in Fig. (13).

The algorithms of Filtering and Finding stages for the DNA side are illustrated in our previse work of [19].
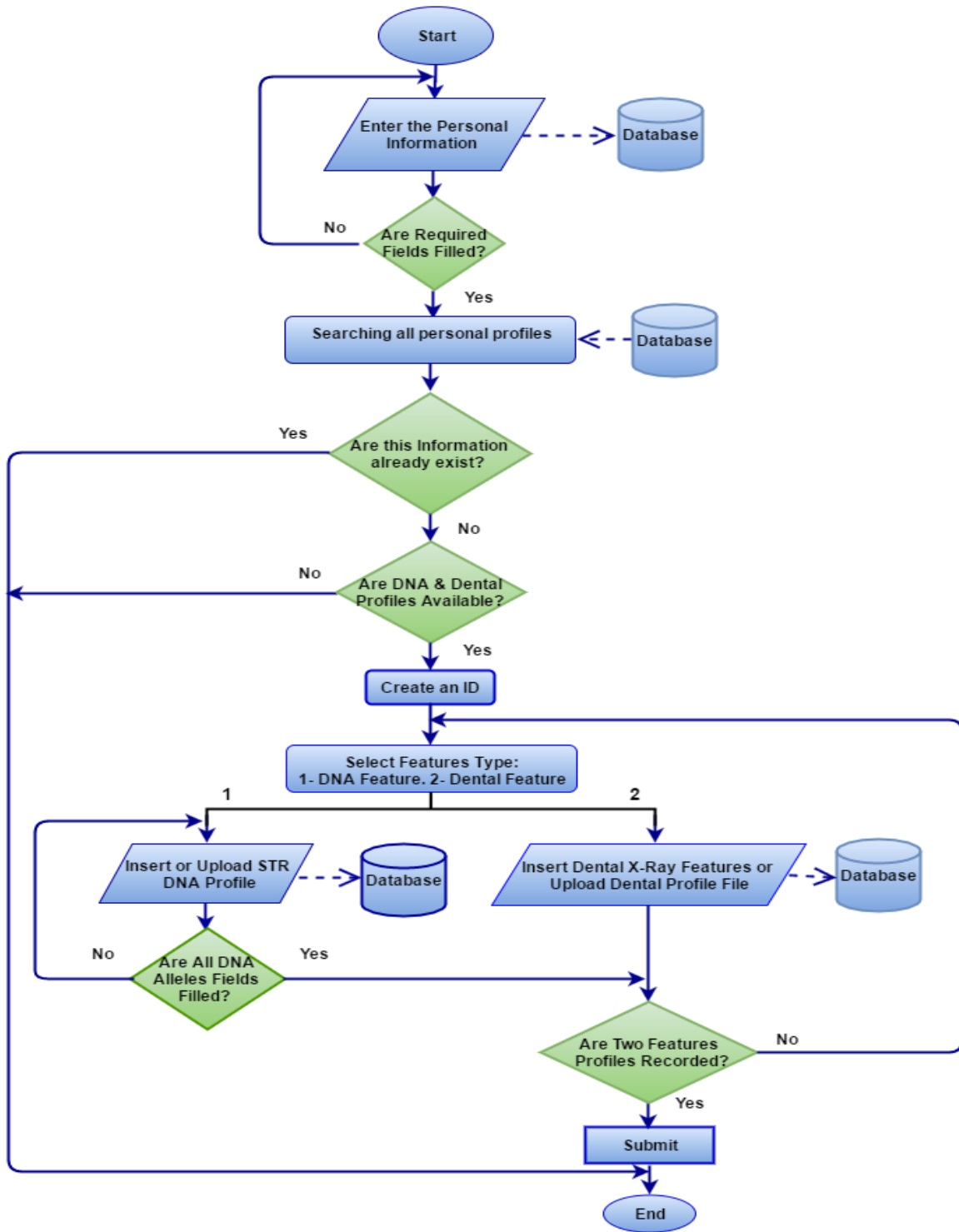
Figure 10. Flowchart of The Profile Inserting Process

At the other hand, the algorithms of Filtering and Finding stages for the dental side are established by the Filtering stage. At this stage, all records with a similar proportion of tooth code for the selected teeth are filtered from the "indivFSDental" table to be used in the next stage to decrease the consumed time. The matching distance for each tooth is computed by calculate the differences between the each feature of the corresponding tooth in the PM profile with the corresponding feature of the AM profile by the following formula:

$$D = \frac{PM\ feature - AM\ feature}{AM\ feature} \times 100\% \qquad (11)$$

Where *D* is the differences.

The *D* for each feature is multiplied by its priority which is illustrated in results section, to produce a matching percentage for each tooth. Finally, the average value of the matching percentage for the eight teeth is produced as a final proportion of congruence between the AM and PM dental profile.
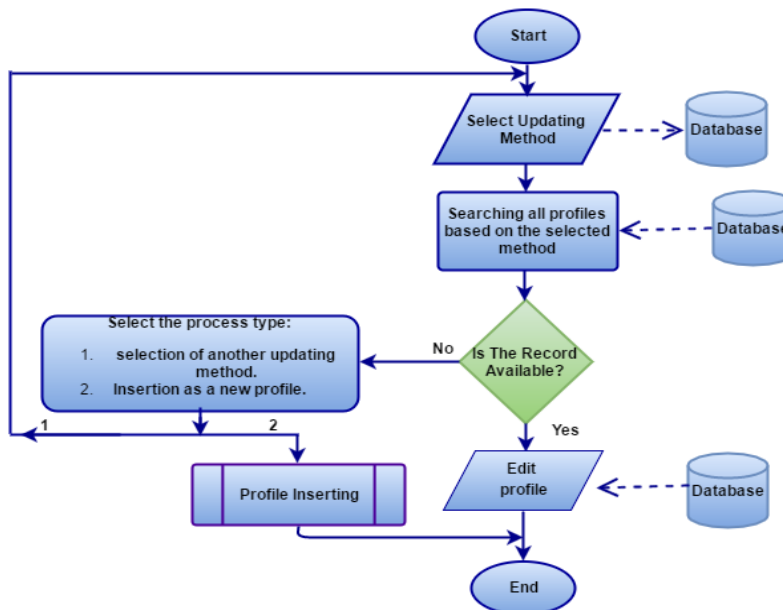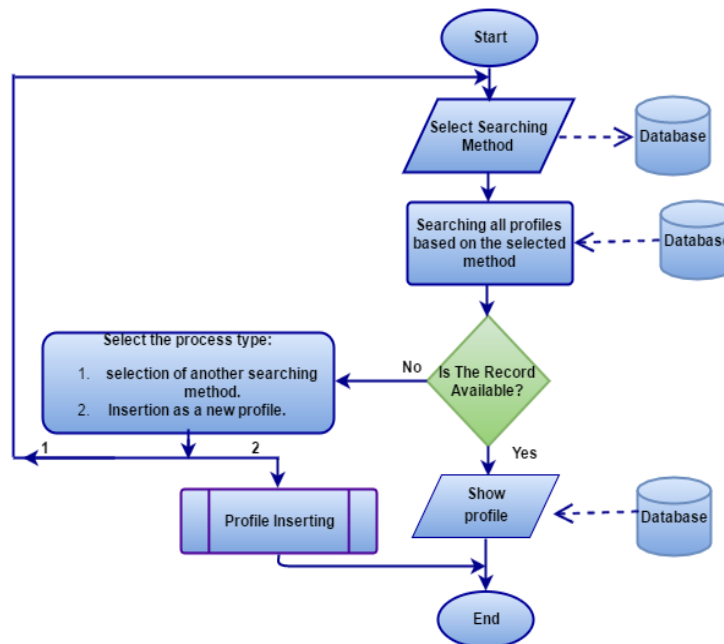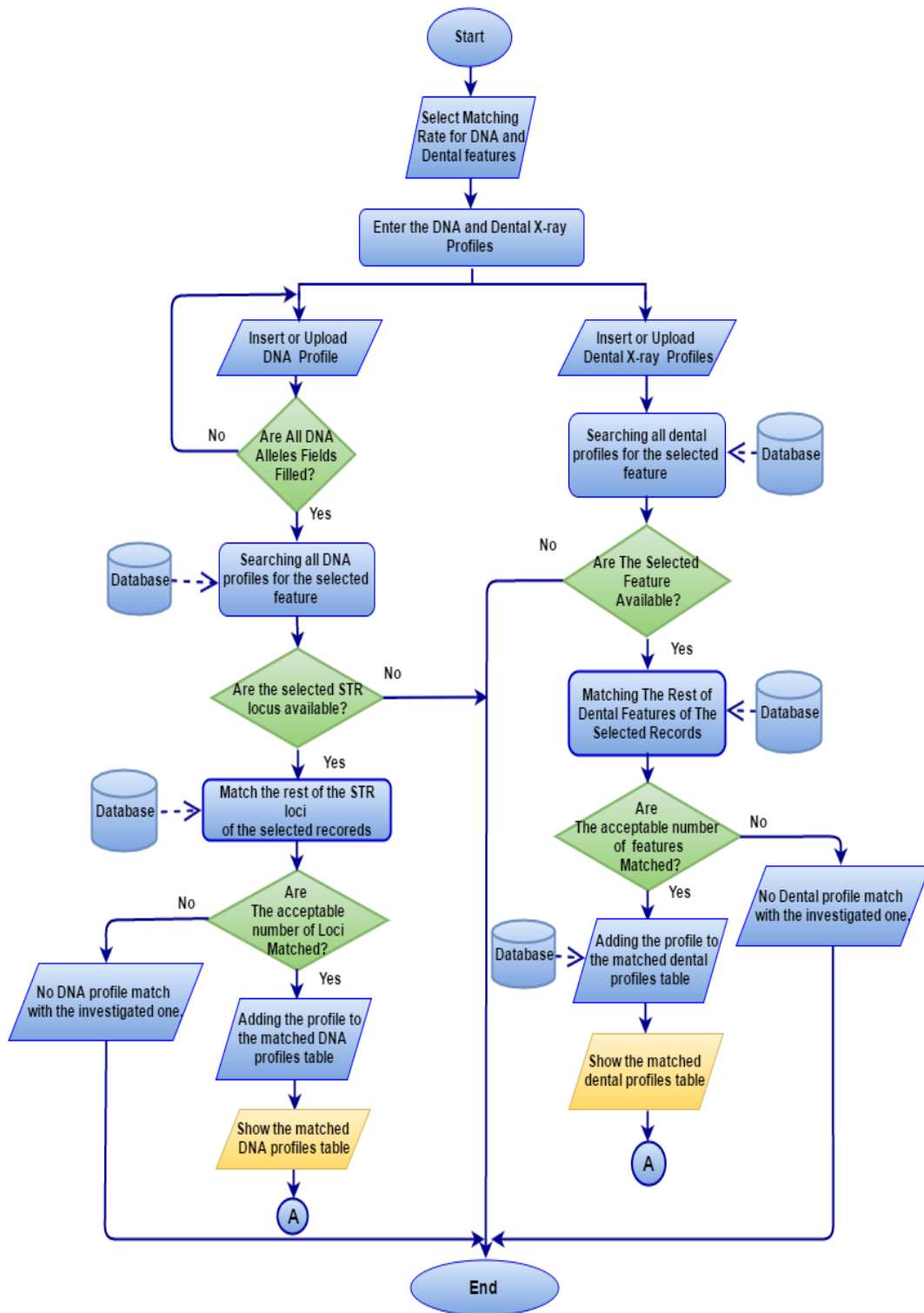

Figure 11. Flowchart Updating Process

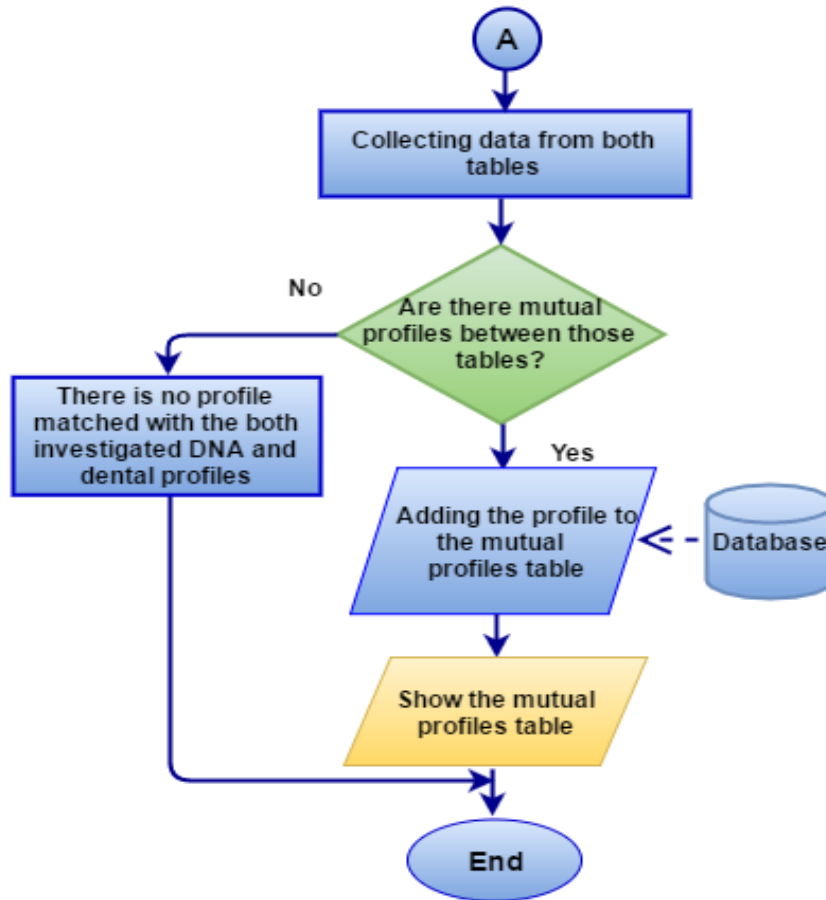Figure 12. Flowchart Searching Process

(continued)

Figure 13. Flowchart of The Matching Process

5. Results

The presented system is evaluated in terms of image processing and database activities for forensic human identification processes. From the image processing side, the MATLAB three stages algorithm is implemented for 80 Bite-wing images considered as AM information. The proposed algorithm provides promising results in terms of enhancing the original image, segmenting each tooth from other and detecting the missing tooth as well as extracting the distinctive features from the selected teeth. In order to test the proposed algorithm for feature extraction of dental X-Ray in terms of identifications and the limitation, Gaussian noise is added to the original images. This is to show the accepted distortion ration of received images as well as to dedicated which feature should has an important probability than anther features. This is done by presenting a study of images with adding Gaussian noise as an expected distortion with a range of variance values of (0.0040 – 0.3972). Gaussian noise is statistical noise having a probability density function (PDF) equal to that of the normal distribution, which is also known as the Gaussian distribution [24] and [27]. The variance value (σ) is computed by applying Signal-to-Noise Ratio

(SNR) value ranged between (-10) – (10) dB. The SNR is a measure used in science and engineering that compares the level of a desired signal to the level of background noise. It is defined as the ratio of signal power to the noise power, often expressed in decibels [25].

$$SNR_{dB} = 10 \log_{10} \left(\frac{P_{signal}}{P_{noise}} \right) \qquad (12)$$

Where P_{signal} is the power of the signal and P_{noise} is the power of the noise.

From the obtained result, we conclude that the applying a priority to each one of the extracted features can reduce the consumed time and increase the testing accuracy. The intensity feature is considered with priority ratio of 60 %, because it is the less effected features by the distortion from the obtained result. The STD feature has been allocated with priority ratio of 30% while the priority ratio of Euler number is 10% because it is the most effected feature by the distortion from the obtained result. Table (1) shows the features of the nominated four image (sample) without applying noise. While the Table (2) shows the total percentage

change for four teeth for the first sample in Table (1) after adding Gaussian noise to the original images. It is notes from these two tables that the applied noise does not change the features extremely due to the enhancement procedure of our algorithm.

TABLE 1. Dental Features For Four Bite-wing Image

Sample	Standard Deviation STD	Euler Number E	Intensity I
1	58.11733	-1	1283552
	67.69546	2	699287
	63.67708	-9	880771
	62.6763	3	467901
2	49.23657	4	606134
	40.35853	0	340979
	42.92113	1	674072
	34.01621	0	232767
3	64.73191	1	662677
	59.02893	1	747452
	63.32574	6	1043457
	71.62955	4	788677
4	60.24108	1	488999
	63.82001	-1	859434
	55.0328	2	962325
	77.09814	9	467530

TABLE 2. Total Percentage Change For Four Teeth (First Sample)

	Percentage Change		
σ	STD	E	I
0.0040	4.814%	23.97%	0.51%
0.0063	8.656%	26.625%	1.7575%
0.0100	9.154%	28.225%	2.7775%
0.0158	10.366%	29.015%	2.97%
0.0251	11.05%	34.32%	3.5225%
0.0397	12.204%	42.695%	4.045%
0.0630	12.498%	49.905%	4.69%
0.0998	13.012%	54.7175%	5.7175%
0.1581	14.978%	65.9825%	7.2525%
0.2506	15.952%	77.6325%	8.9225%
0.3972	16.558%	79.1425%	9.9025%

All the extracted features are saved in the built database for future utilizing in forensic identification processes. These features are exported from the MATLAB automatically to the corresponding field as well as to a Microsoft Excel and CVS file.

To test the performance of the proposed system in term of database activities, we entering the 139 DNA profiles for Diyala Province-Iraq and all the AM dental features using the Profile Inserting operation. The insertion is done in high accuracy and flexibility without recording any problems. It is highlighted that the difference in the number of DNA and Dental X-Ray profiles gives the option of missing one side of the adopted biometrics.

Moreover, the updating and searching processes are tested. The updating process gives the user the freedom to edit any fields in both physiological profiles as well as the personal information profile. Also, the user has a flexibility to print, save as a pdf file format and screen capture of the obtained profile from both updating and inserting processes.

In term of evaluating the scalability of the system database, random DNA and dental X-Ray profiles are generated. We utilized the allelic ladder fetched from the GeneMapper1 v. 3.2 software (Applied Biosystems, Foster City, CA, USA) to generate up to ten million records based on the specific rang of each locus. Table (3) shows the time consumed with the corresponding records number. From the obtained results, we verify the scalability of the proposed system to handle a huge amount of records. Also the system proves its accuracy in human identification as well as the security level that was fetched by presenting the username and password within the connection string of the SQL server.

Finally, the ability of the proposed system to identify humans is evaluated over a profiles set of the DNA and bite-wing features as AM physiological features. The matching process takes the PM physiological features as a query. This query is used for searching of a profile or profiles amongst the saved records. The output of this process is three tables. The first table shows the DNA profiles that have a matching ratio equals to or greater than the requested ratio. In addition, the second table shows the dental X-Ray profiles reached a matching ratio equals to or greater than the assigned ratio. While the last table shows the crossed mutual profiles between the previous tables as shown in Fig. (14).

TABLE 3. Processing Time Consuming Table

Process		Time consuming		
		Not found	**Average**	**Random**
Matching process	For 140 records	539 ms	563 ms	568 ms
	For 1000 records	632 ms	740 ms	647 ms
	For 1000000 records	3056 ms	3124 ms	3201 ms
	For 10000000 records	5035 ms	15305 ms	12900 ms
Searching process	For 140 records	514 ms	728 ms	700 ms
	For 1000 records	628 ms	854 ms	953 ms
	For 1000000 records	919 ms	3318 ms	3921 ms
	For 10000000 records	1012 ms	13154 ms	15019 ms

* ms = millisecond

Figure 14. Output of The Matching Process

6. Conclusion

A biometric based forensic human identification system has been presented using DNA and dental X-Ray features profiles. These profiles were saved in the database that was built using the SQL Server 2012 software. The features of the dental bite-wing X-Ray images were extracted using a MATLAB three stages algorithm. The GUI of the system has been built utilizing the Visual Studio environment (C#). The presented system includes numerous processes which are: image enhancing, image segmenting, features extracting for dental X-Ray images. Moreover, profile inserting, updating, searching and matching activities have been performed for both DNA and dental X-Ray parts. The system GUI characterized with a high flexibility and without need to a skilled users. In adiition, the performance of the system was tested in terms of capacity, limitation and consumed time. The outcome results proved the efficiency and reliability of the system in terms of accuracy and run time. Finally, we guarantee that the physiological characteristics are the reliable tools for human identification especially in forensic cases because there are cannot cheated as well as cannot duplicated between people.

REFERENCES

[1]   Abhilash K. Sh., Ashish R. and Vijay K. Sh., "Biometrics System- A Review", International Journal of Computer Science and Information Technologies (IJCSIT), Vol. (6), No. (5) , 2015, pp. 4616-4619.

[2]   Zhang and David D., "Automated Biometrics: Technologies and Systems", Springer US, 2000; pp. 1-21.

[3]   Faisal R., M. Usman A., Naveed R. and F. Kunwar, "A Sharp Comparison of Biometrics Techniques and Dental Biometrics", Proceedings of the 2nd International Conference on Engineering & Emerging Technologies (ICEET), Superior University, Lahore, PK, 26-27 March, 2015.

[4] Rafael M.L., David E., Ezequiel L., Esteban J.P. and Tim W., "Assessment of geometric features for individual identification and verification in biometrics hand systems", Expert Systems with Applications, Vol.(40), No. 9, July 2013, PP. 3580–3594.

[5] Biometrics Update. Explainer: Verification vs. Identification Systems Accessed 6/3/2016.

[6] CSI. Identification vs. Verification Accessed 6/3/2016.

[7] http://www.theseus.fi/bitstream/handle/10024/44684/Babich_Al eksandra.pdf?sequence=1.

[8] A. Wagner, J. Wright, A. Ganesh, Z. Zhou, H. Mobahi and Y. Ma, "Toward a Practical Face Recognition System: Robust Alignment and Illumination by Sparse Representation", in IEEE Transactions on Pattern Analysis and Machine Intelligence, vol. 34, no. 2, pp. 372-386, Feb. 2012.

[9] Shivanand. S.G., "Fingerprint Based Gender Classification for Biometrics Security: A State Of-The-Art Technique", published by International Association of Scientific Innovation and Research (IASIR), USA (An Association Unifying the Sciences, Engineering, and Applied Research).

[10] Schomaker, L., "Advances in Writer Identification and Verification", in Document Analysis and Recognition, 2007. ICDAR 2007. Ninth International Conference on , vol.2, no., pp.1268-1273, 23-26 Sept. 2007.

[11] Bulacu, M. and Schomaker, L., "Text-Independent Writer Identification and Verification Using Textural and Allographic Features", in Pattern Analysis and Machine Intelligence, IEEE Transactions on , vol.29, no.4, pp.701-717, April 2007.

[12] Ribaric, S. and Fratric, I., "A biometrics identification system based on eigenpalm and eigenfinger features", in Pattern Analysis and Machine Intelligence, IEEE Transactions on , vol.27, no.11, pp.1698-1709, Nov. 2005.

[13] Tripathi, Vijay Adam, "The Effects of Forensic DNA Typing on the FRR and FAR of a Biometric System" (2015). *South Carolina Junior Academy of Science*. 107.

[14] Charbel F. and Mireille F., "Tooth-Based Identification of Individuals", International Journal of New Computer Architectures and their Applications (IJNCAA), vol:3, no:1, pp: 22-34, 2013.

[15] Mischa W., Adrian L., Anders P. and Christian J., "Fire Victim Identification By Post-Mortem Dental CT: Radiologic Evaluation of Restorative Materials After Exposure to High Temperatures", European Journal of Radiology, vol:80, pp : 432-440, 2011.

[16] AL-Zubaidi, M.M., Al-Awadi, S.J., Namaa, D.S., Saleh, T.Y., Shehab, M.J., Hameed, S.N, and Abd- Alatief, A, "Genetic Variation of 15 Autosomal Short Tandem Repeat (STR) Loci in The Diyala-Iraqi Population", International Journal of Biological & Pharmaceutical Research, Vol. 5, No. 3, pp.131-135, 2014.

[17] Butler, J.M., "Review: Genetics and Genomics of Core STR Loci Used in Human Identity Testing", J. Forensic Sci, in press, Mar 2006.

[18] Kashyap A., Kumar, A., and Awadhanam S., "Investigating contributors of the mixed DNA samples by forensic Bioinformatics; Uncertainty to certainty for Crime laboratories", Helix, Vol. 1, No. 2, pp.101-108, 2012.

[19] Saja D.K. and Muayad S.C., "Biometrics System Based Human identification Using STR DNA Marker", International Journal of Computer Applications, Volume 138, No.7, March 2016.

[20] Saja D.K., Muayad S.C. and Mohammed M. A., "DNA-Profile Database Building Using STR DNA Marker For Diyala Province Population", International Journal of Advanced Research in Computer Engineering & Technology (IJARCET), Volume 5, Issue 3, March 2016.

[21] "Dental Dictionaries and Tooth Charts", Dental Fear Central, Available http://www.dentalfearcentral.org/resources/tooth-charts/ [Accessed 27th April, 2016].

[22] Saja Dheyaa Khudhur and Muayad Sadik Croock, "Dental X-Ray Based Human Identification System for Forensic," Engineering and Technology Journal, Vol. 35, No. 1, pp. 49-60, 2017.

[23] Muayad Sadik Croock, Saja Dheyaa Khudhur and Ali Kamal Taqi, "Edge Detection and Features Extraction for Dental X-Ray," Engineering and Technology Journal, Vol.34,Part (A), No.13,2016.

[24] R. C. Gonzalez and P. A. Wintz, "Digital image processing", Reading, Mass.: Addison-Wesley, **(1987).**

[25] R. Jain, R. Kasturi and B. G. Schunck, "Binary Image Processing", in MACHINE VISION, **(1995)**.

[26] Nahla A., "Developing a Database System for the Laboratory Tests", Eng. & Tech. Journal, vol. 31, part (A), no.18, pp 52-67, 2013.

[27] A. Ajaz and D. Kathirvelu, "Dental biometrics: Computer aided human identification system using the dental panoramic radiographs," Communications and Signal Processing (ICCSP), International Conference on, Melmaruvathur, PP: 717-721, 2013.

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