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# Human Verification System Based on Fuzzy Rule

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## Abstract

The integration of humans with computers is advancing biometric systems, particularly in utilizing DNA biometrics for human verification and identification, especially in forensic contexts. DNA analysis has significantly improved forensic examinations, aiding in detecting crimes such as murders and rapes and identifying unidentified corpses. Additionally, DNA profile analysis plays a crucial role in determining paternity. The main objective of this research is to develop a human identification system that is fast, cost-effective, error-free, and equipped with user-friendly graphical interfaces. The system aims to enhance accuracy in forensic applications, utilizing fuzzy logic to improve the identification process through the use of fuzzy inference. The proposed system employs fuzzy logic to enhance accuracy in DNA motif identification. Multiple experiments validate the system's performance, demonstrating its high accuracy and scalability in handling large datasets. The experiments conducted have shown that the proposed system offers essential functions for forensic applications, significantly contributing to genetic and forensic processes. The system demonstrated high accuracy and scalability, with an improvement of 27% in accuracy compared to pre-existing systems. The proposed system stands out for its speed, cost-effectiveness, and error-free operation, with a user-friendly graphical interface.

**Keywords:** DNA biometrics, DNA profiling, Fuzzy logic, Forensic identification, Human verification.

## 1. Introduction

A synergy occurs between biomedicine, namely forensic science, and information technology. The synergy is accomplished by applying information technology methods in several areas, such as DNA motif categorization and the identification of individuals [1], [2]. Fuzzy logic can be described as a set of numerical principles used for representing samples based on levels of association. It offers a method to denote variations or fuzziness in logic by considering that many attributes, such as height, color, and smell, rely on degrees. Fuzzy logic enables the use of natural language in logical reasoning [3], [4].

DNA possesses distinctive properties that can be harnessed to establish an individual's identity. DNA is ubiquitous in the human body. DNA identification involves the analysis of bio-samples until classifying them to a unique set of DNA markers known as Short Tandem Repeats (STRs). Subsequently, the DNA profiles of unidentified individuals, whether in the context of criminal investigations or natural disasters, are compared to reference samples to determine potential matches [5]. DNA finds diverse applications, including the diagnosis of defendants, the identification of criminals, and distinguishing suspects from individuals who have been accused or convicted of crimes, all with a high degree of accuracy. It also plays a crucial role in counter-terrorism efforts and national security by aiding in crime detection, suspect identification, and risk reduction [6]. Challenges arise when attempting to identify the root causes of problems with limited evidence, especially when the victim's body or the bodies of suspects are damaged. In these situations, the bulk of the victim and suspect samples' DNA profiles are used to create DNA profiles that are used for human identification [7]. Both biometric identification systems that stand for either an individual's physiology or behavioral traits are essential in many fields [8], [9]. The selection of identifying technology is based on security needs, with biometric technologies offering exceptional levels of protection that are hard to trick. Well-known biometric methods, including fingerprinting, iris identification, DNA analysis, hand geometry, signature verification, and voice recognition, have been used in previous research [10]-[12].

The present survey includes some research efforts related to this work the present survey includes some research efforts related to this work. Dutta and Banik [13] presented a fuzzy decision rules system to identify criminals based on DNA profiling. The system's effectiveness is evaluated by training and testing with real-world DNA profiles. The results confirm the benefits of using fuzzy logic to deal with the issues of ambiguous and insufficient DNA evidence.

Abigail [14] presented a biometric system using DNA markers, namely Short Tandem Repeats (STRs), which contain unique genetic information to identify individuals accurately.

Sadiq [15] focused on the integration of several biometric methods. They present a framework for building a multimodal identification system that combines facial features, iris patterns, fingerprints, and DNA analysis. The results indicate that the proposed integrated biometric system improves the accuracy of identification when applied in forensic investigations.

Sharma and Garg [16] investigated tandem patterns in DNA sequences using the integer period discrete Fourier transform (IPDFT) technique. The rapid development of genetics and informatics has led to the adoption of any work that requires trustworthy identification systems.

Faleh and Karidi [17] presented a system for identifying individuals' DNA profiles accurately. They exploit fuzzy logic and association rule mining techniques in order to enhance the accuracy and reliability, as well as address the intricacy and diversity of human DNA profiles. The study demonstrates the system's efficiency when tested on real DNA datasets. This system uses fuzzy-based data extraction, while the system is a fuzzy-based modification, improving the data accuracy to 27%.

Despite the rapid advancement of DNA-based biometric systems, several limitations persist in current human identification approaches. Traditional DNA matching techniques often rely on deterministic or exact comparisons between STR loci, making them highly sensitive to missing data, degraded samples, and noise caused by environmental factors or laboratory conditions. In real forensic scenarios, DNA samples are frequently incomplete or contaminated, which introduces uncertainty that conventional methods are not well equipped to handle. Furthermore, many existing similarity measures fail to capture the gradual or partial resemblance between alleles, especially in cases involving familial relationships where exact matches are not expected. Another key limitation is the insufficient integration of intelligent decision-making frameworks. While fuzzy logic has been widely recognized for its ability to model uncertainty, and association rule classification has shown promise in pattern recognition, their combined application in DNA-based human verification remains limited. Additionally, many prior studies focus primarily on theoretical models without offering scalable, user-friendly systems that can be applied in real forensic environments.

To address these gaps, this study proposes a hybrid intelligent framework that integrates fuzzy logic with association rule classification to enhance the accuracy and robustness of DNA-based human identification. The novelty of this work lies in the development of a modified fuzzy similarity approach specifically designed for STR DNA profile comparison, combined with a Fuzzy Association Rule Classification (FARC) mechanism for decision-making. Unlike conventional methods, the proposed system incorporates fuzzy inference to model uncertainty in allele matching, allowing for more flexible and realistic similarity assessment. Moreover, the integration of fuzzy reasoning with classification techniques provides a unified framework capable of improving identification performance under uncertain and incomplete conditions. The study also contributes a practical implementation using a database-driven system, making it applicable for real-world forensic use.

The primary objectives of this research are to develop a reliable human verification system based on DNA biometrics, design a fuzzy-based similarity measurement method for STR profiles, and integrate fuzzy inference with association rule classification to improve decision-making accuracy. Additionally, the study aims to evaluate the performance of the proposed system using real forensic DNA datasets and to enhance the reliability of identifying individuals and biological relationships.

The main contributions of this work include the development of a modified fuzzy similarity algorithm that accounts for uncertainty in DNA matching, the integration of fuzzy inference with association rule classification into a unified framework, and the design of a practical system implemented using Visual C# and SQL Server. The proposed approach demonstrates an improvement in identification accuracy compared to existing methods and extends its application to familial relationship classification through threshold-based evaluation. Overall, this study provides a more flexible, accurate, and practical solution for DNA-based human verification in forensic applications.

## 3. The Methodology

Visual C# with SQL Server is used practically to create a reliable and efficient system that allows for easy interaction with a variety of applications and database systems. It also offers user-friendly graphical interfaces, enabling non-technical users to interact with the database effectively, without requiring prior knowledge of data storage and organization mechanisms. The database comprises tables with 31 fields/columns, including the individual's name and 30 locus values of 15 DNA profiles (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, VWA, TPOX, D18S51, D5S818, and FGA). This segment presents a practical solution for the classification of DNA motifs. The proposed system adopts a human identification system based on Classification, which stands for Fuzzy Association Rules, which employs techniques for identifying DNA motifs. This system is connected to a vast database.

### 3.1. Preprocessing Module

Its function is to extract allele values from the STR DNA profiles of the query victim and reference individuals in the DB, as well as manage the comparison method between alleles. This part comprises 3 primary components:

- Fetching the DNA profile unit: This unit is dedicated to retrieving data from the SQL Server database. Initially, a connection is established with SQL Server.
- Check the missing value unit: This unit is devoted to checking the incompleteness of any missing alleles in the DNA profile.

### 3.2 The Measurement of DNA Similarity

The similarity between STR DNA profiles can be calculated by assessing the likeness of alleles. This involves computing the similarity by following the steps below:

```
Input: DNA Dataset
Output: Similarity and Cross-Similarity DNA Dataset
Begin:
    Step 1: Calculate the maximum difference within each locus in the database
    FOR each locus j in the dataset:
        $D(j) = max(valueatlocusj) - min(valueatlocusj)$   (1)
    Step 2: For each allele in the dataset: Initialize $S_1$ and $S_2$ for the current allele to 0
    Step 3: Calculate the symmetric similarity $S_1$:
        FOR each allele i in the dataset: $S_1$(i) = calculated symmetric similarity value for allele i
    Step 4: Calculate the cross-similarity$S_2$: FOR each allele i in the dataset: $S_2$(i) = calculated cross similarity value for allele i End
```

### 3.3. Fuzzy Inference Subsystem (FIS)

It is the part that is responsible for assigning inputs to outputs through the use of fuzzy logic. There are two main approaches within FIS: the Sugeno way and the Mamdani way. In the Mamdani approach, fuzzy inputs are processed by the fuzzy inference engine, which generates fuzzy outputs based on predefined rules. On the other hand, the Sugeno approach in the fuzzy inference subsystem takes fuzzy inputs and produces crisp outputs. In the proposed system, the Sugeno fuzzy approach is chosen as it is considered the most suitable method. When identifying individuals or establishing biological family relationships through DNA profiling, it is possible for alleles of a DNA profile locus to be incorrectly identified. Various factors, such as climate change, temperature fluctuations, or sample contamination with other substances, can contribute to erroneous results and inaccurate readings in the PCR tool. These errors pose significant challenges to the accuracy of human identification processes. To mitigate and minimize these errors, the comparison of DNA profiles among individuals will be performed using a Fuzzy Inference sub-System in conjunction with the classification algorithm based on Association Rule. This combined approach aims to enhance the accuracy and reliability of the identification process.

Fig. 1 shows a block diagram for finding the highest similar sample from the database to the input sample.

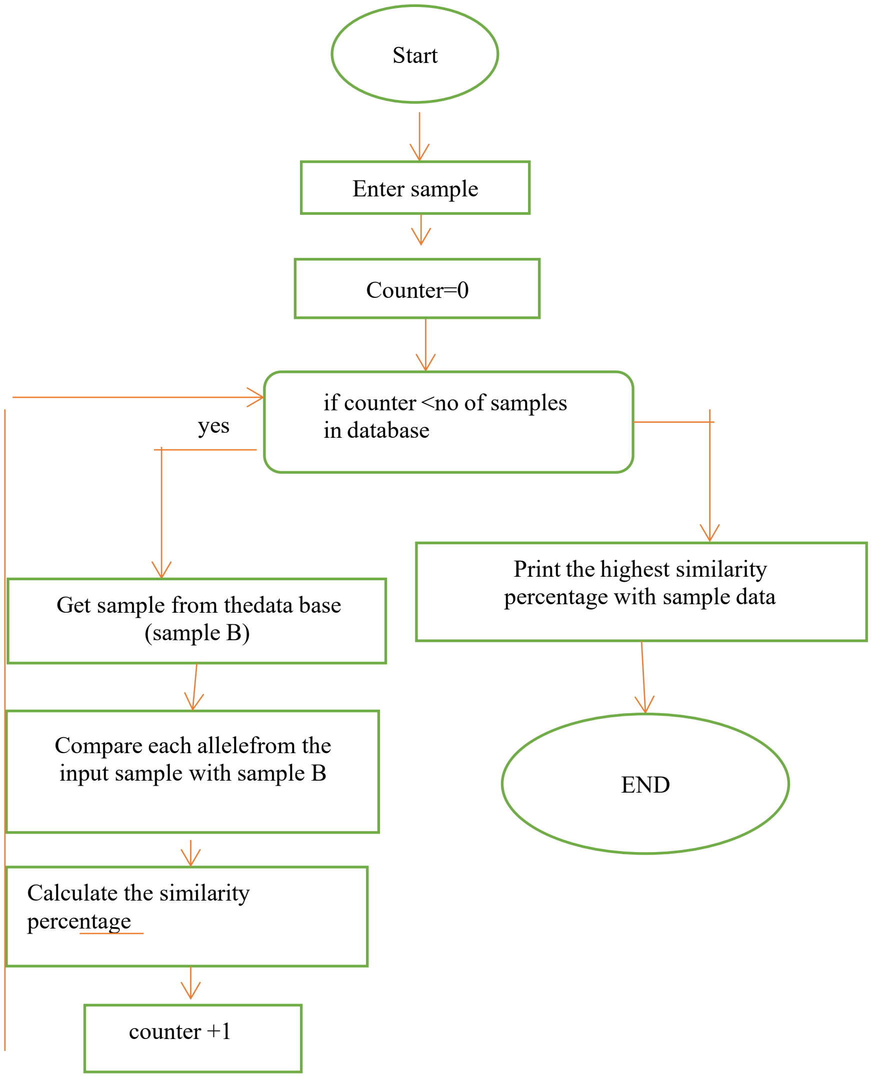

**Figure 1 :** Block diagram for finding the highest similar sample from the database with the input sample

## 4. Results and Discussion

The experimental tests were performed on a database of samples extracted from the Iraqi Forensic DNA Center Research and Training at Al-Nahrain University that includes a set of STR DNA profiles, in order to evaluate the proposed system's precision and efficiency. The DNA profiles were kept in a database that also held records of other people, even those who were related biologically.

The test's goals were to find out how close victim DNA profiles were to reference family relationship DNA profiles and how sure people were that the matches were real. 1063 sample DNA profiles made up the collection used in the tests.

To ensure precise findings, DNA profiles for people were first identified using just the Fuzzy rule Association Rules Classification Algorithm [17]. Afterward, the procedure was replicated utilizing an adapted Modified Fuzzy Rule Algorithm. The study showed that the modified Fuzzy rule Algorithm outperformed the others in terms of match percentage, and accuracy improved by 27%.

The use of the Family Association Rule Classification (FARC) was used to evaluate the degree of confidence in DNA profile matches. For every familial relationship type, predetermined criteria were used to conduct the comparison. Accordingly, the likelihood of a match and the existence of a family connection between the victim and the reference were assessed. The percentage values for the familial related thresholds are shown in Table 1 [18]-[20].

**Table 1.** Biological Family Relationship Threshold.

| Biological Family Relationship | Threshold |
|---|---|
| Same Person | 100% |
| Father, Mother, Son | 50% |
| Grandmother, Grandfather | 25% |
| Full-Sibling | 54-45% |
| Half-Sibling | 25% |
| Uncle, Aunt, Niece, Nephew | 25% |
| Cousin | 12.5% |

The results of our system and the previous system are shown in Table 2.

**Table 2.** Compare results.

| Family relationship | Accuracy rate in previous work | Accuracy rate in the current work |
|---|---|---|
| Between mother and son | 60% | 93.98% |
| Poor family relationship | 17% | 18% |
| Between the victim and the son | 60% | 94% |
| Same person | 100% | 100% |

## 5. Conclusions

A number of conclusions were obtained when adopting the proposed system, which shows hopeful results in the field of human identification. Its objective is to provide a forensic human identification system that is easy, automated, accurate, and reliable. The system utilizes the Modified Fuzzy Similarity Algorithm with STR DNA markers for forensic identification purposes. It has shown satisfactory outcomes in terms of accuracy and efficiency in both time and capacity. To enhance the system's performance further, STR markers are adopted as a trusted human identity tool. The presented system encompasses multiple modules based on the combined use of the Modified Fuzzy Rule Algorithm for biometric identification. This integration ensures better flexibility and uniqueness through the cross-checking of samples collected from latent prints. In order to attain better accuracy rates, FARCS is employed to reduce errors produced by various parameters such as humidity, temperature variations, and potential contamination of victim samples with other substances. This approach helps mitigate inaccuracies that may arise during PCR instrument readings and improves the overall reliability of the system.

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## Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this manuscript.

## Author Contribution Statement

Hiba Abdulelah Dawood and Mustafa Dhiaa Al-Hassani proposed the research idea. Hiba Abdulelah Dawood developed the theory and performed the calculations. Mustafa Dhiaa Al-Hassani and Majeed Arsheed Sabbah reviewed the methods and results and supervised the research. All authors discussed the results and contributed to writing and revising the manuscript.

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