

# Fusion Method with Mean-discrete Algorithm in Feature level for Identical twins Identification



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## ABSTRACT

The study on twins is an important form of study in the forensic and biometrics field as twins share similar genetic traits. A biometric is one of the common types of pattern recognition which acquires biometric data from a person. From these data, a feature is established and extracted where these features can be used to identify individual. Existing works in biometric identification concentrate on unimodal biometric identification. The high similarity in a pair of twin's biometric may lead to miss performance. Hence, due to their great accurateness, multimodal biometric systems have become more favored than unimodal biometric systems in identical twins identification. However, these systems are highly complex. We proposed Mean-Discrete feature based fusion algorithm for Kurdish handwriting and fingerprint for identical twins detection. Its viability and advantage over the unimodal biometric systems are highlighted. This paper employed 800 images from 50 pairs of identical twins from Kurdistan Region to carry out the experiment.

**Index Terms:** Mean-discrete Algorithm, Multi-biometric, Feature Based Fusion, Twins Identification, Kurdish Handwriting-fingerprint.

## 1. INTRODUCTION

Biometric-based identification and systems of verification are among the integral technologies today [1-3], and their applications are rather common in access controls (e.g., building entry and computers), electronic commerce (elimination of fake transactions), as well as illegal immigration's reduction [4]. Notably, biometric identification system for identical twins poses greater challenge as opposed to that which identifies non-twins due to the considerable resemblance that twin individuals have with each other [4,5]. For this reason, researchers of pattern recognition and

computer vision have shown their interest in identifying the biometric of a twin. Furthermore, due to its high level of accurateness, in certain situation, this method was the one which could recognize a specific person's biometric pattern from a collection of individuals [6-8].

The unimodal biometric identification systems for identical twins are now significantly more accurate and reliable [9], and in this respect, good performance can be seen in a number of traits. Still, technological issues remain to be addressed. Among the available unimodal biometric systems include Wonder Ears (Identification of Identical Twins based on images of ear) [10], 3D face recognition (Identification of Identical Twins based on faces) [11], double trouble (Identification of Identical Twins based on Face Recognition) [12], analysis of facial marks [5], and aside from identification of identical twins based on handwriting individuality [13]; these systems have all been scrutinized. Nonetheless, it should be noted that these studies were

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all considering the physiological aspects [14] implying the unlikely occurrence of change.

Sharing one zygote causes identical twins to have similar genetic composition, increasing the difficulty in identifying them [15]. More than one biometric trait would thus be used in identifying these twins, making multimodal biometric system suitable due to the use of both physical and behavioral traits in its application [16]. Multimodal biometric system combines many biometric traits from multitude of sources. In the context of enrolment, the use of this system enables the enrolment of users even though they have no identified biometric identifier. Such ability becomes a solution to the problems of enrolment, and these abilities therefore prove the universality of multimodal biometric system. To affirm sound performance in a twin's biometric identification, good and thorough features have to be used as input to a classifier. Accordingly, in a multi-biometric system, an individual is represented by various features. For this reason, a single feature extracted directly for the multi-biometric itself is not representative of a unique feature for a twin biometric.

There are countless of representations in multi-biometric systems, which have led to the presence of vast variance between features for one individual. Somehow, there is small variance in the context of twins' comparison, making it necessary to engage one more process. This is to enable the unique features to be represented from the pool of multi-biometric features. During the process, many representations obtained from multi-biometric representations of a twin are merged and converted into a uni-representation. The merging and conversion are done before the execution of the identification task. As a result, the level of variance in the data between the twins is decreased. However, the majority of past researches were focusing on the discrete feature extraction methods of each twin's biometric. Hence, this study presents the application of Mean-Discrete feature based fusion algorithm to combine these features with twins' Kurdish handwriting-fingerprint.

## 2. RESEARCH FRAME WORK

Features extracted from a feature extraction method comprise an ensemble of global features. In the context of this study, the features, which are usually classed individually, are representatives of the twin's Kurdish handwriting-fingerprint particularly, with respect to word and shape. Furthermore, the individual classification of features allows the identification of an individual within a twin or a group of individuals.

Accordingly, this study presents the feature-based fusion that the performance of identification in the arena of twin biometric identification can be improved.

For the purpose, twin's exclusive individual features would be needed, whereas the extracted features are often in multi-representations. For this reason, individual features for each individual within a set of twins are employed together. Arguably, such usage will increase the performance of twin identification. These are called a Mean-Discrete feature vector and this method is used following the process of feature extraction. Mean-discrete feature vector carries the generalized features of global features possessed by individuals. In the model of twin identification, the features are generalized before the classification task. This generates better outcome. Relevantly, the framework proposed in this study is shown in summarized form in Fig. 1.

## 3. FEATURE EXTRACTION

Aspect United Moment Invariant (AUMI) allows the extraction of global features from the region and boundary (word or shape) in a separate and continuous manner to represent an individual [17]. Here, the fusion embedded scaling factor of aspect [18] into the United Moment Invariant [19], as shown in Fig. 2.

This instantly combines the capacities of these two functions of moment into the proposed AUMI. The [19] United Moment Invariant has an association with the geometrical representation that considers the normalized central moment equations of Geometric Moment Invariant (GMI) [20] and the boundary representation of Improved Moment Invariant (IMI) [21]. Finally, [17] AUMI comprises eight features with the construction of the [19] United Moment Invariants (UMI), as shown below:

$$\theta_1 = \frac{\sqrt{\phi_2}}{\phi_1} \tag{1}$$

$$\theta_1 = \frac{\sqrt{\phi_2}}{\phi_1} \tag{2}$$

$$\theta_3 = \frac{\sqrt{\phi_5}}{\phi_4} \tag{3}$$

$$\theta_4 = \frac{\phi_3}{\phi_2 \phi_4} \tag{4}$$

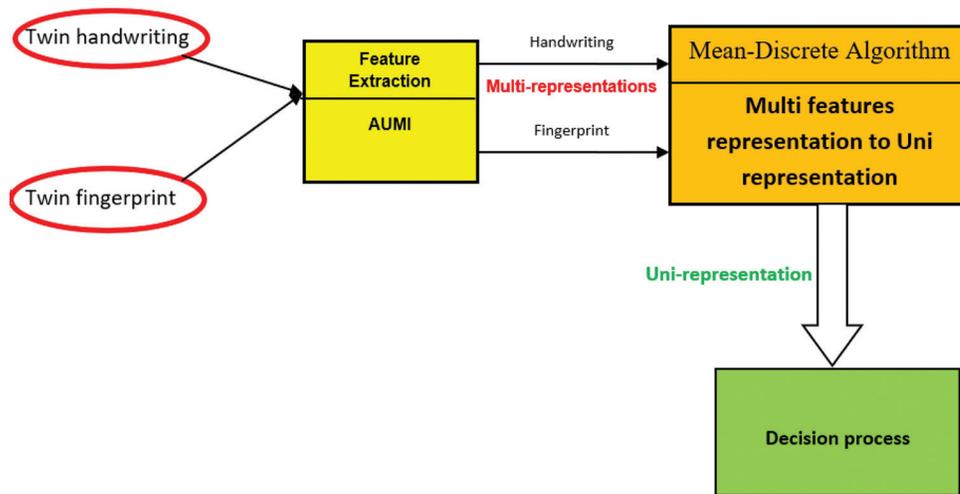


Fig. 1. Proposed framework for twin multi-biometric.

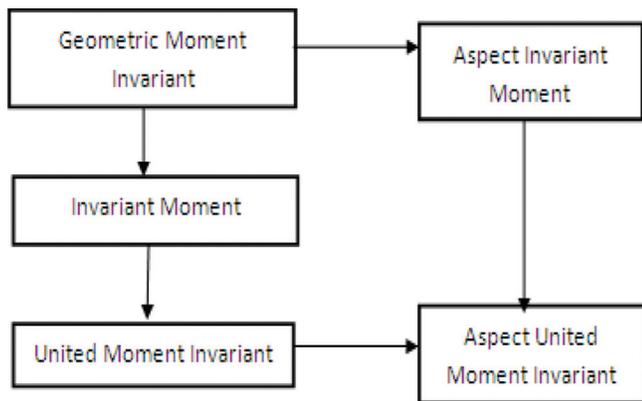


Fig. 2. Aspect united moment invariant structure by Mohammed and Shamsuddin [14], Hu [20].

$$\theta_5 = \frac{\phi_1 \phi_6}{\phi_2 \phi_4} \quad (5)$$

$$\theta_6 = \frac{(\phi_1 + \sqrt{\phi_2}) \phi_2}{\phi_6} \quad (6)$$

$$\theta_7 = \frac{\phi_1 \phi_5}{\phi_3 \phi_4} \quad (7)$$

$$\theta_8 = \frac{\phi_3 + \phi_4}{\sqrt{\phi_5}} \quad (8)$$

As  $\phi_i$  denotes large values, the natural logarithm is employed. As such, below is obtained for  $i = 1$  to  $7$ ;  $\theta_i \leftarrow \log_{10} \phi_i$

The features of the AUMI satisfy the individuality of the concept of the twin’s handwriting-fingerprint [22,23], and the outcomes demonstrate a lower intra-class value for the variance between features for the mean absolute error (MAE) in comparison to the value for the inter-class. This is the reason why the features of the AUMI were explored and employed in the domain of twin biometric identification in this study. The AUMI presents the striking individual features in the extracted invariant feature. In the context of a twin’s biometric identification, getting features that denote the twin’s handwriting-fingerprint from numerous writing styles and shapes are the main purpose [23,24]. The AUMI is primarily concerned with obtaining the twin’s handwriting-fingerprint’s unique features. The purpose of employing algorithms is to extract individual features. Eventually, such use accurately reflects the handwriting-fingerprint of the twin. Conversely, for a multi-biometric representing an individual belonging to a twin, the directly extracted individual features do not directly represent the unique features of a twin biometric. As such, before the measurement task, additional processes should be included. This study proposes use of the Mean- Discrete feature based fusion algorithm before the identification task.

#### 4. PROPOSED MEAN-DISCRETE FEATURE-BASED FUSION

Due to the performance of the collective process on the task of identification, Mean-Discrete Algorithm is dubbed as global combination as well. Furthermore, due to its reliance on each attribute for each feature within the dataset, the Mean-Discrete Algorithm also becomes part of the global

characteristic class. Such reliance allows the calculation of Mean-Discrete value for each attribute for each multi-biometric of twin. The application of Mean-Discrete feature vector leads to improved representation of data for the twin's Kurdish handwriting-fingerprint's individuality. Accordingly, the Mean-Discrete algorithm methodologies are presented in this section. Mean-Discrete algorithm is used at the feature level and it entails a blend of twins' multiple features for the concluding decision making. In the task of feature extraction for the multi-biometric of each twin, AUMI is used in producing the columns of eight feature vector, and for the process of Mean-Discrete, eight features are generated from the twin's Kurdish handwriting-fingerprint. For this reason, it is not impossible to keep the initial amount of invariant feature vector columns within the moment function that is utilized within the feature extraction task. Accordingly, the following section provides the elaboration of the process of Mean-Discrete feature-based fusion, and Fig. 3 details the flowcharts of the Mean-Discrete algorithm proposed in this study.

The feature value of Mean-Discrete is computed alongside both biometrics for a twin. This is in line with the class of the individual due to the fact that within a twin set, every individual has distinctive style of writing and shape of fingerprint. Hence, there is individuality of handwriting-fingerprint in twin identification. Using the individual's class, computation is made to the feature value of Mean-Discrete. The application of this method affirms the

protection of the characteristic's uniqueness or individuality. In addition, the supervised method demonstrates its aptness for twin's handwriting-fingerprint particularly with respect to individuality. This is because this method maintains the individual features of each twin. In this context, if the two twins have a close or indistinguishable feature vector, then the two classes will be regarded as possessing indistinguishable or nearly indistinguishable Mean-Discrete feature. For this reason, the Mean-Discrete feature will be identical or nearly identical as well.

Moreover, the obtained information and the characteristics of each twin will not be altered by the algorithm proposed. Rather, it denotes the initially extracted multi-biometric feature vector within the Mean-Discrete feature vector of a uni-representation. The process of Mean-Discrete will provide a clear elucidation on the linkages between features, while the characteristics of the features remain the same. For this reason, Mean-Discrete algorithm is appropriate while also fulfilling the individuality of the twin's handwriting-fingerprint in the context of twin identification. Fig. 4 presents the terms as well as the Mean-Discrete process.

The process of Mean-Discrete feature-based fusion entails the labeling of the person's class, and the conversion of the multi-representation features into uni-representation features. In the line of Mean-Discrete, first concatenate twins Kurdish handwriting-fingerprint then the intervals are computed using the minimum ( $F_{e_{min}}$ ) and maximum ( $F_{e_{max}}$ ) feature vectors ( $j/v$ )

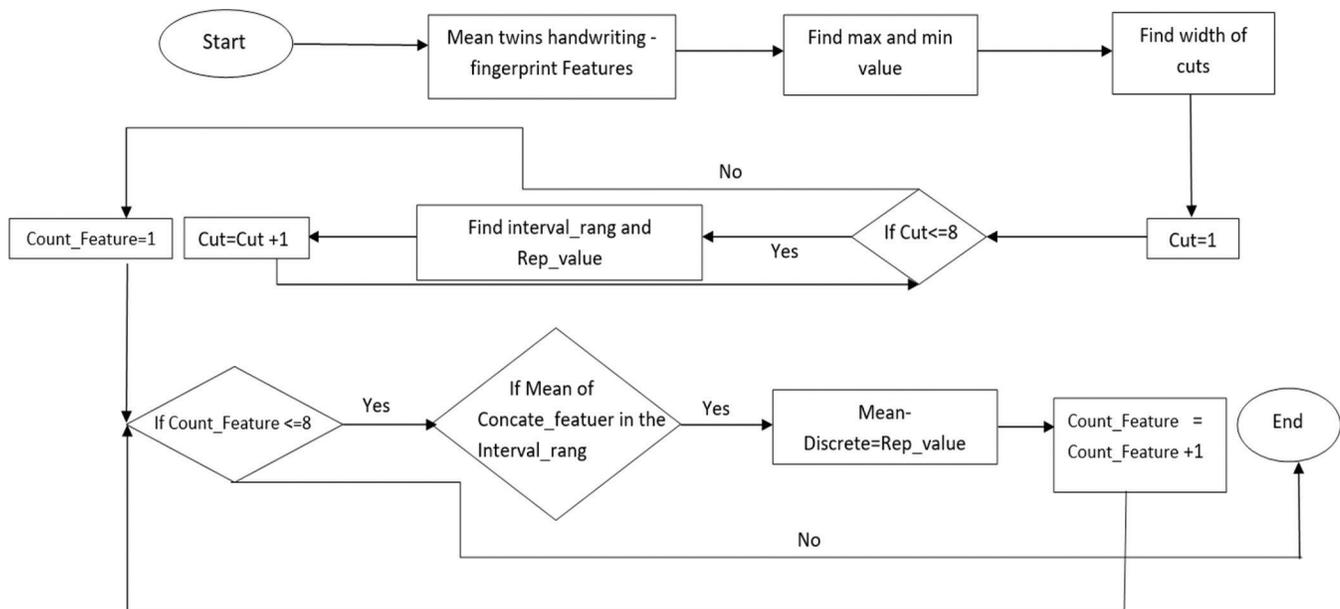


Fig. 3. Flowchart of Proposed Mean-Discrete Algorithm.

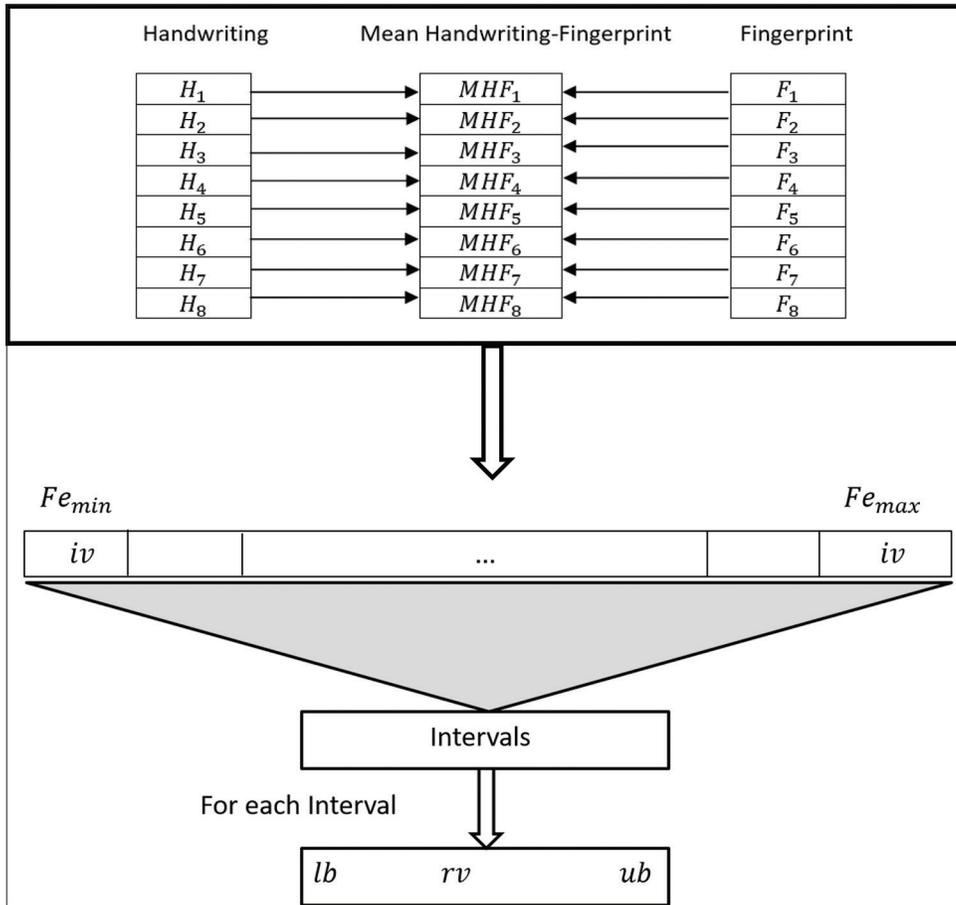


Fig. 4. Mean-discrete (uni-representation) features.

for an individual. The line of Mean-Discrete line entails a line of invariant feature vectors. This line begins from the minimum ( $Fe_{min}$ ) invariant feature vector value and finishes with the maximum ( $Fe_{max}$ ) invariant feature vector value for an individual twin. An interval encompasses the average of the line of Mean-Discrete apportioned by the number of columns within the invariant feature vector. The following is the calculation of the width ( $wd$ ) of an interval:

$$wd = (Fe_{max} - Fe_{min}) / f \tag{9}$$

where

$Fe_{min}$ : Minimum value of invariant feature vector for a person in a twin.

$Fe_{max}$ : Maximum value of invariant feature vector for a person in a twin.

$f$ : Number of columns in the invariant features vector.

The width describes the interval's cut points. It also computes the value of representation value. The " $p$ " value denotes eight

for the number of columns of the feature from AUMI. Meanwhile, the cut point denotes the intervals' divider ( $iv$ ) within the line of Mean-Discrete. For invariant feature vectors with similar interval, they have the exact value of representation. For each interval, the value of representation ( $rv$ ) comprises the average of an interval computed using the following formula:  $rv = \frac{ub - lb}{2}$ . The value of representation

value for all intervals (1-8) denotes the invariant feature vector that is in the following range: if  $MHF \geq lb$  and if  $MHF \leq ub$ . Meanwhile, mean features ( $MHF$ ) for each twin are computed using the invariant feature vectors of the twin's handwriting ( $H_{ij}$ ) and fingerprint ( $F_{ij}$ ).

Eight features were created in this study, which represents the number of columns for the number of features of the AUMI applied for the twin's multi-biometric. These features are called the Mean-Discrete feature vector. This vector symbolizes the individuality of the twin's handwriting-

fingerprint to the person. Tables 1 and 2 exemplify the transformation of the twin’s multi-biometric feature vector into the Mean-Discrete feature vector.

Tables 1 and 2 exhibit a total of eight columns. These columns signify the eight columns of the invariant feature vectors in the AUMI. The Mean-Discrete process is then performed using these data. Fig. 5 shows the Mean-Discrete process for twin number a1.

Table 3 shows the Mean-Discrete feature vector produced from the Mean-Discrete algorithm process. The Mean-Discrete features vector includes the generalized features of a twin individual. These features clearly represent the general individual features for each individual in a twin.

## 5. EXPERIMENT AND RESULTS

Mean-Discrete algorithm generates more accurate results of identification task results, and for this reason, it is of value to the context of this study. Within the context of multi-representation analysis, the individuality of the twin’s handwriting-fingerprint is this study’s focal point. The twin’s multi-biometric identification has been improved using the Score Histogram which is based on false Non-Match Rate (FNMR) and False Match Rate (FMR),

and the improved aspect is its individuality. An example of the performance of identification with the current accuracy in twin identification task shows the feasibility of Mean-Discrete data in generating better performance. In other words, the prospect of attaining better level of individuality of a twin’s Kurdish handwriting-fingerprint with Mean-Discrete feature based fusion data utilization is proven in this work. Comparison was made between this study’s outcomes of the uni-representation analysis with the Mean-Discrete feature based fusion data and those from the analysis of multi-representation.

### 5.1. Matching Performance with Mean-discrete Algorithm

In this study, the matching performance is evaluated using Score Histogram which is based on false Non-Match Rate (FNMR) and False Match Rate (FMR). The number of multiple biometric such as the true and non-true match datasets, taken into consideration for the experimental purpose, is also included in the section.

In this study, the datasets used for the experimental purposes are summarized in Table 4:

#### 5.1.1. Score histogram

Here, the histogram illustrates the comparative probability distribution of score for both matches and non-matches over

**TABLE 1: Real data for handwriting and fingerprint for twins**

F1	F2	F3	F4	F5	F6	F7	F8	Twin
1.0318	0.1098	1.7241	0.3362	0.0117	83.1055	3.0619	5.7089	Ha1
1.0347	0.0976	1.7239	0.3362	0.0103	93.6710	3.4440	5.7071	Ha1
1.0299	0.1026	1.7241	0.3362	0.0109	88.7336	3.2760	5.7082	Ha1
1.0300	0.1024	1.7241	0.3362	0.0109	88.9304	3.2831	5.7082	Ha1
1.0178	0.1602	1.7237	0.3363	0.0175	56.1404	2.0994	5.7059	Fa1
1.0142	0.1418	1.7242	0.3361	0.0156	63.2681	2.3703	5.7100	Fa1
1.0305	0.0901	1.7238	0.3363	0.0096	101.105	3.733	5.7062	Fa1
1.0178	0.1021	1.7239	0.3362	0.0110	88.8608	3.2916	5.7073	Fa1
1.0315	0.1087	1.7242	0.3362	0.0116	83.9064	3.0919	5.7091	Hb1
1.0325	0.0988	1.7240	0.3362	0.0105	92.4349	3.4045	5.7078	Hb1
1.0311	0.1046	1.7241	0.3362	0.0111	87.1319	3.2127	5.7087	Hb1
1.0322	0.1076	1.7242	0.3362	0.0114	84.8370	3.1241	5.7091	Hb1
1.0564	0.0629	1.7239	0.3363	0.0064	148.405	5.3458	5.7064	Fb1
1.0490	0.0616	1.7240	0.3363	0.0063	150.580	5.4608	5.7070	Fb1
1.0644	0.0611	1.7239	0.3362	0.0061	154.040	5.5053	5.7070	Fb1
1.0305	0.1353	1.7248	0.3359	0.0144	67.4441	2.4819	5.7149	Fb1

**TABLE 2: Mean handwriting and fingerprint for Twin a1**

F1	F2	F3	F4	F5	F6	F7	F8
1.0248	0.1350	1.7239	0.3362	0.0146	69.623	2.5807	5.7074
1.0244	0.1197	1.7241	0.3362	0.0130	78.4695	2.9071	5.7085
1.0302	0.0963	1.7239	0.3362	0.0102	94.9196	3.5048	5.7072
1.0239	0.1023	1.7240	0.3362	0.0110	88.8956	3.2874	5.7077

the full range of possible score. This histogram is computed using the relative equations in (10, 11).

$$\text{Relative matches} = \frac{\text{Number of tru trail}}{\text{Total number of trails}} \quad (10)$$

$$\text{Relative non\_marches} = \frac{\text{Number of false trial}}{\text{Total number of trials}} \quad (11)$$

Fig. 6 thought 14 shows the significant difference for Mean-Discrete, Min, Max, Produced, Weight-Sum, Sum-Produced, Handwriting, Fingerprint, Sum and Concatenate methods and the following Figs. 6-14 shows the characteristics of the whole methods with matched score distribution after the matching process, respectively. Based on the scores distribution, it can be observed that the match score are

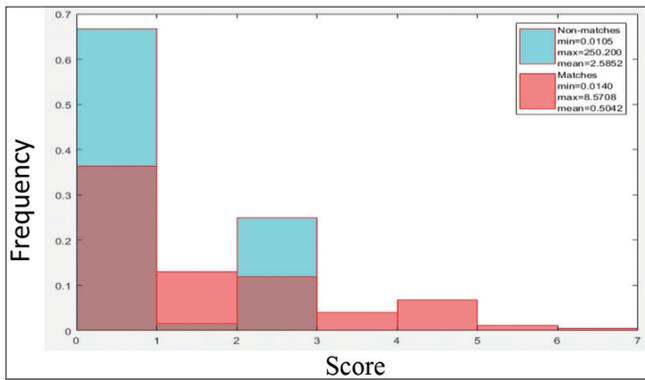
lower than [48.5700, 99.7900, 32.7900, 8.5708, 44.1100, 99.7901, 86.9926 , 141.9000, and 103] and non-match score are higher than [0.0013, 0.0090, 0.0000299, 0.0105, 0.0122, 0.0061, 0.0020, 0.0154, and 4.2534], respectively. Thus, if a score is higher than [ 48.5700, 99.7900, 32.7900, 8.5708, 44.1100, 99.7901, 86.9926, 141.9000, and 103], it is definitely represented as false or non-match score with zero probability of error and if a score is lower than [0.0013, 0.0090, 0.0000299, 0.0105, 0.0122, 0.0061, 0.0020, 0.0154, and 4.2534 ], it is represented as true match score with zero probability of error. However, if the score value falls between scores [0.0013 , 0.0090, 0.0000299, 0.0105 , 0.0122, 0.0061, 0.0020, 0.0154, and 4.2534 ] and [48.5700, 99.7900, 32.7900, 8.5708 , 44.1100, 99.7901, 86.9926, 141.9000, and

**TABLE 3: Example of mean- discrete feature for twins**

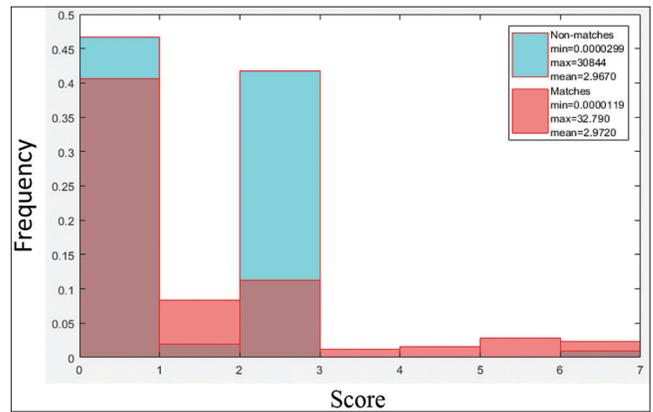
a	5.9554	5.9554	5.9554	5.9554	5.9554	53.5161	5.9554	5.9554
	5.9554	5.9554	5.9554	5.9554	5.9554	77.2965	5.9554	5.9554
	5.9554	5.9554	5.9554	5.9554	5.9554	65.4063	5.9554	5.9554
	5.9554	5.9554	5.9554	5.9554	5.9554	65.4063	5.9554	5.9554
b5	6.7749	6.7749	6.7749	6.7749	6.7749	60.9026	6.7749	6.7749
	6.7749	6.7749	6.7749	6.7749	6.7749	74.4346	6.7749	6.7749
	6.7749	6.7749	6.7749	6.7749	6.7749	74.4346	6.7749	6.7749
	6.7749	6.7749	6.7749	6.7749	6.7749	74.4346	6.7749	6.7749
a9	5.4436	5.4436	5.4436	5.4436	5.4436	70.6327	5.4436	5.4436
	5.4436	5.4436	5.4436	5.4436	5.4436	70.6327	5.4436	5.4436
	5.4436	5.4436	5.4436	5.4436	5.4436	81.4976	5.4436	5.4436
	5.4436	5.4436	5.4436	5.4436	5.4436	59.7679	5.4436	5.4436
b9	6.9559	6.9559	6.9559	6.9559	6.9559	76.4268	6.9559	6.9559
	6.9559	6.9559	6.9559	6.9559	6.9559	62.5326	6.9559	6.9559
	6.9559	6.9559	6.9559	6.9559	6.9559	90.3210	6.9559	6.9559
	6.9559	6.9559	6.9559	6.9559	6.9559	76.4268	6.9559	6.9559
a20	16.5356	16.5356	16.5356	16.5356	16.5356	49.5981	16.5356	16.5356
	16.5356	16.5356	16.5356	16.5356	16.5356	49.5981	16.5356	16.5356
	16.5356	16.5356	16.5356	16.5356	16.5356	49.5981	16.5356	16.5356
	16.5356	16.5356	16.5356	16.5356	16.5356	181.8482	16.5356	16.5356
b20	5.4474	5.4474	5.4474	5.4474	5.4474	59.8109	5.4474	5.4474
	5.4474	5.4474	5.4474	5.4474	5.4474	59.8109	5.4474	5.4474
	5.4474	5.4474	5.4474	5.4474	5.4474	70.6836	5.4474	5.4474
	5.4474	5.4474	5.4474	5.4474	5.4474	59.8109	5.4474	5.4474
a24	7.9487	7.9487	7.9487	7.9487	7.9487	103.3018	7.9487	7.9487
	7.9487	7.9487	7.9487	7.9487	7.9487	39.7331	7.9487	7.9487
	7.9487	7.9487	7.9487	7.9487	7.9487	71.517	7.9487	7.9487
	7.9487	7.9487	7.9487	7.9487	7.9487	71.5174	7.9487	7.9487
b24	10.0104	10.0104	10.0104	10.0104	10.0104	130.0586	10.0104	10.0104
	10.0104	10.0104	10.0104	10.0104	10.0104	110.0505	10.0104	10.0104
	10.0104	10.0104	10.0104	10.0104	10.0104	90.0425	10.0104	10.0104
	10.0104	10.0104	10.0104	10.0104	10.0104	70.0345	10.0104	10.0104

**TABLE 4: Size and characteristic of the multimodal datasets obtained from Kurdistan Reign used in experimental**

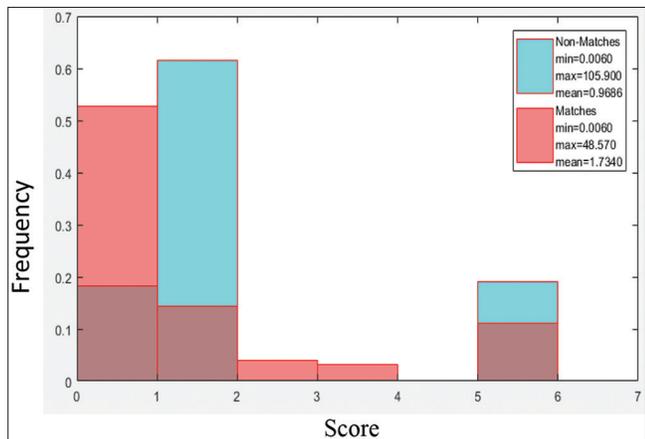
Total Individuals	50 twins (100) individuals			
	Matching		Non-Match	
Type of matched score	Handwriting		Handwriting	
Type of modality	Fingerprint		Fingerprint	
Total Samples	200		200	
Number of modalities per individual	4		4	



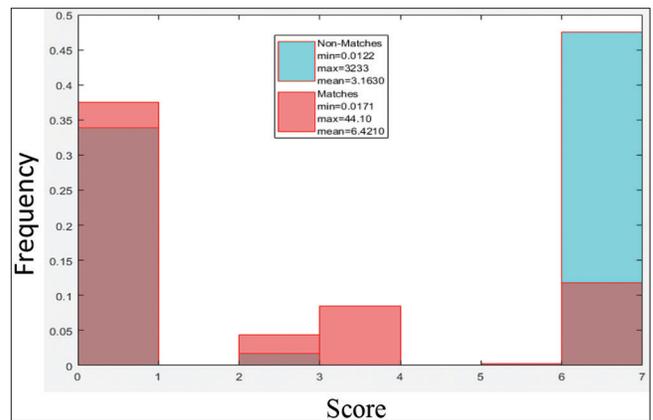
**Fig. 8.** From histogram for weight-sum matching score where true matches are on range [0.0140 , 8.5708] and non-match score is on range [0.0105, 250.2000].



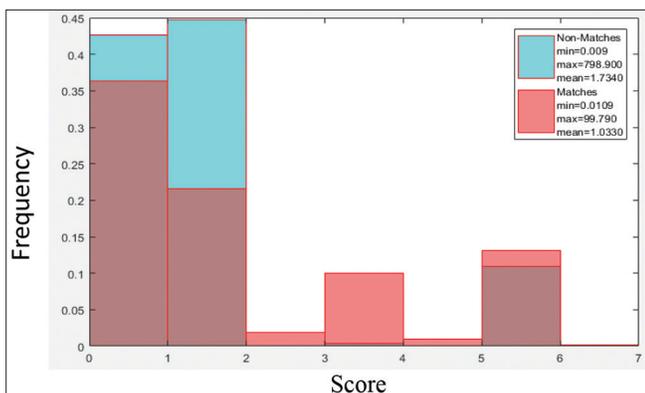
**Fig. 7.** From histogram for product matching score where true matches are on range [0.0000119, 32.7900] and non-match score is on range [0.0000299, 30844].



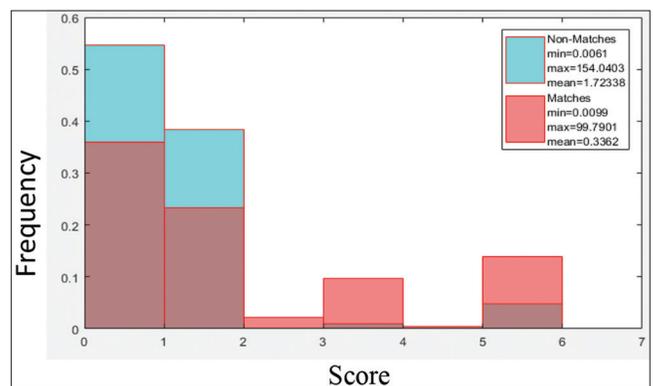
**Fig. 5.** From histogram for Max matching score where true matches are on range [0.0109, 99.7900] and non-match score is on range [0.0090, 798.9000].



**Fig. 9.** From histogram for sum-product matching score where true matches are on range [0.0171, 44.1100] and non-match score is on range [0.0122, 31233].



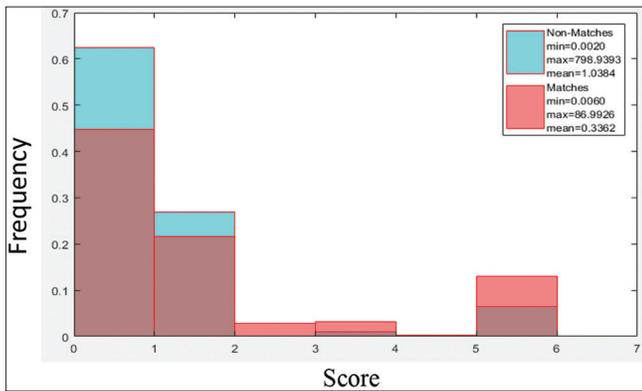
**Fig. 6.** From histogram for Min matching score where true matches are on range [0.0060, 48.5700] and non-match score is on range [0.0013, 105.9000].



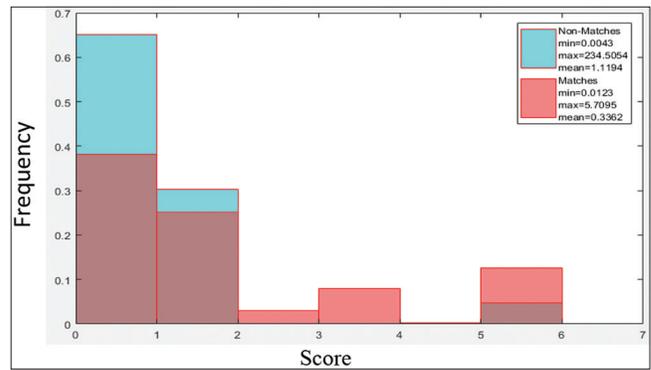
**Fig. 10.** From histogram for handwriting matching score where true matches are on range [0.0099, 99.7901] and non-match score is on range [0.0061, 154.0403].

103], it is known as undermined score because both true and false match score are in this range value [0.0013, 0.0090,

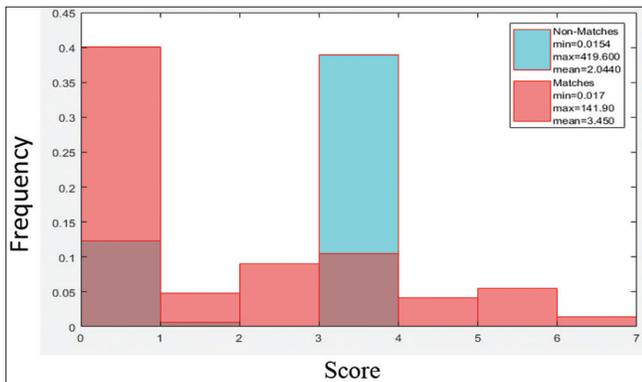
0.0000299, 0.0105, 0.0122, 0.0061, 0.0020, 0.0154, and 4.2534], [48.5700, 99.7900, 32.7900, 8.5708, 44.1100, 99.7901,



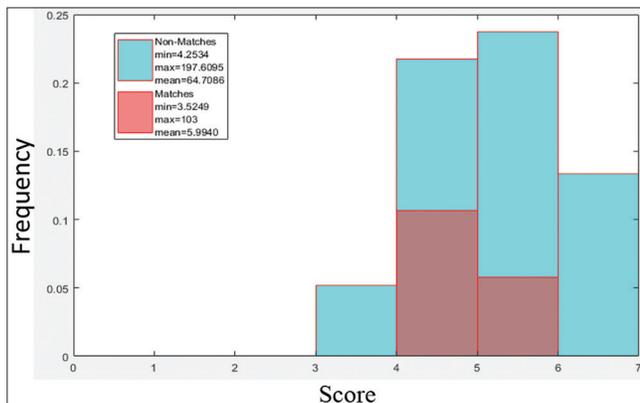
**Fig. 11.** From histogram for fingerprint matching score where true matches are on range [0.0060, 86.9926] and non-match score is on range [0.0020, 798.9393].



**Fig. 14.** Score histogram for Mean-Discrete matching score where true matches are on range [0.0123, 5.7095] and non-matches scores are on range [0.0043, 234, 5054].



**Fig. 12.** From histogram for sum matching score where true matches are on range [0.0170, 141.9000] and non-match score is on range [0.0154, 419.6000].



**Fig. 13.** From histogram for concatenate matching score where true matches are on range [3.5249, 103] and non-match score is on range [4.2534, 197.6095].

86.9926, 141.9000, and 103], respectively. This is where the case of miss-classification or probability of fusion error occurs. Fig. 6 though 14 shows the histogram of the Min,

Max, Produced, Weight-Sum, Sum-Produced, handwriting, fingerprint, Sum, and concatenate, respectively.

Fig. 14 shows the histogram of the Mean-Discrete feature matching score. The true Mean-Discrete matching score is lower than 5.7095, while the non-matching Mean-Discrete score is higher than 0.0043. Interestingly, from the figure, it can be seen that they have a very slightly little overlap between the true match and non-match scores [0.0043, 5.7095]. Thus, this technique can minimize the issues of miss-classification and probability of fusion error.

## 6. CONCLUSION

This study attempted to improve the individuality identical twin's handwriting-fingerprint through the demonstration of Mean-Discrete feature based fusion algorithm. Mean-Discrete method converts the multi-representations of individual features into a uni-representation with the technique of Mean-Discrete algorithm. The data representation signifies an individual's generalized features. The conventional approach and the proposed approach were compared with one another and then, the task of Score Histogram was executed. Using these approaches, the Kurdish handwriting-fingerprints produced by identical twins were identified. Then, the obtained outcomes were scrutinized. With the application of the Mean-Discrete feature, the individual features are represented in a manner that is systematic with representation that is more informative. Hence, better performance is generated with the application of the proposed method particularly with respect to accuracy. The application of the algorithm with the Mean-Discrete process is demonstrated in this study. Then, for biometric identification of a twin, the Mean-Discrete data, un-Mean-Discrete data, and

different fusion algorithms were compared in terms of usage outcomes. In this regard, it appears that using Mean-Discrete data enhance the individuality of a twin's Kurdish handwriting-fingerprint for get better performance with Score Histogram.

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