EVOLUTIONARY ALGORITHM FOR SELECTING DYNAMIC SIGNATURES PARTITIONING APPROACH

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Abstract

In the verification of identity, the aim is to increase effectiveness and reduce involvement of verified users. A good compromise between these issues is ensured by dynamic signature verification. The dynamic signature is represented by signals describing the position of the stylus in time. They can be used to determine the velocity or acceleration signal. Values of these signals can be analyzed, interpreted, selected, and compared. In this paper, we propose an approach that: (a) uses an evolutionary algorithm to create signature partitions in the time and velocity domains; (b) selects the most characteristic partitions in terms of matching with reference signatures; and (c) works individually for each user, eliminating the need of using skilled forgeries. The proposed approach was tested using Biosecure DS2 database which is a part of the DeepSignDB, a database with genuine dynamic signatures. Our simulations confirmed the correctness of the adopted assumptions.

Keywords: identity verification, dynamic signature, hybrid partitions, partitions' selection, evolutionary algorithm.

1 Introduction

In the verification of identity, the aim is to increase the effectiveness and reduce involvement of verified users. A good compromise between these issues is ensured by the dynamic signature verification as the signature is a socially acceptable biometric attribute and its acquisition does not require the use of advanced devices. The typical devices for the acquisition of dynamic signatures include a graphics tablet, often used, for example, in banks. In some applications, a device with a touch screen is sufficient for the acquisition of signatures. The dynamic signature is represented by signals describing the position of the stylus in time along the abscissa and ordinate axes. This position is read discreetly with a certain sampling frequency depending on the technical capabilities of the used device. From the stylus position signals, for example, velocity or acceleration signals can be obtained, which are also discrete signals. Some features that can be easily compared are sometimes determined from these discrete signals [34, 35]. In the case of a static signature, it is only its shape that is available. It is a subject of geometric transformations and adjustments. Despite this, the shape of the signature is easier to reproduce than its dynamics. On the other hand, the discrete values of the signals describing the signature dynamics can be analyzed. The purpose of such an analysis is, for example, to select the most characteristic fragments. Then, such fragments can be associated with the signature shape fragments, and next interpreted, verified, and compared. This usually results in the creation of different signature descriptors. Descriptors aggregate certain properties, have their own interpretation and are used in the practical use phase of the method. The signature descriptors can be partitions created in the domains of time, velocity, pressure, etc. [31, 32]. In the designing and creating of dynamic signature descriptors, the aim is to ensure that they are matched to the reference signatures of the user and are possibly different from the descriptors created for the signatures of other users.

It is worth emphasizing that the advantage of biometric systems is the ability to analyze dynamic signals individually for each user. There are several reasons. First, the biometric system must work properly even for a single user from the user database. Second, it eliminates the need to use skilled forgeries during the verification phase. This is important because the quality of such forgeries prepared by skilled forgers determines the effectiveness of the verification. Third, the ability to analyze dynamic signals individually for each user can reduce the problem of accuracy loss when verifying machine-forged signatures, for example with CNC devices. Such machine tools can reproduce the dynamics of a signature based on its shape. The control algorithms of these machine tools can take into account the rules linking the signature shape with its dynamics and can be extracted, for example, from the available dynamic signature databases. Moreover, the possibility of an individual analysis of each user's signatures decomposes the problem into sub-problems, which increases the scalability of the method.

In this paper, we propose an approach that uses the capabilities of an evolutionary algorithm to create and select dynamic signature partitions. This is a hybrid problem because it consists in determining the boundaries between partitions and selecting a subset of partitions to use them in the signature verification process. The problem is therefore a combination of two problems, i.e. a continuous one (creating a partition) and a combinatorial one (selecting a partition). For this reason, the use of an evolutionary algorithm seems to be an interesting solution. The evolutionary algorithms belong to the group of population-based algorithms (Population-Based Algorithms, PBAs [10, 11, 16, 19, 36, 38]). They are widely used to solve problems in which the evaluation function may be non-differentiable [18].

1.1 Related work

In the literature, various approaches to dynamic signature processing are proposed. Some of them are summarized in this section.

The purpose of dynamic signature verification methods is most often the extraction of certain characteristic features in order to increase the effectiveness of verification. In [1] the authors proposed an approach to the verification of dynamic signatures in which the velocity signals are interpolated from the stylus displacement data, and the frequency components of the signals are calculated using a continuous wavelet transform. This allowed them to focus in the verification process on dominant frequencies as barcodes.

In [24] the authors proposed a dynamic signature verification system based on the so-called critical segments. They identify unchanging parts of signatures independently for each user. The proposed system distinguishes functions describing the geometric arrangement of the signature, its behavioral and physiological features. This approach also uses the assessment of signatures in the context of the possibility of their effective verification.

In [15] the authors proposed an approach based on the use of one reference signature and a dedicated calculation method called the curve similarity model. This model is based on the analysis of geometric similarity in order to eliminate differences in sizes, positions and angles of rotation of the compared signatures. The matching of the similarity curves is performed in an evolutionary way and uses extraction of local fitness functions.

In [4] the authors proposed to verify the dynamic signature with the use of a hybrid wavelet transform and a hidden Markov model classifier. The hybrid wavelet transform is generated using the Kronecker product on the basis of two selected orthogonal transforms. The following transform methods were considered: Discrete Cosine transform, Discrete Hartley transform, Discrete Walsh transform, and Discrete Kekre transform.

In [13] the authors proposed to verify the dynamic signature in which the curvature and torsion feature were used. They were associated with Hausdorff distance measure which is used in the verification process. A set of curvature and torsion value of the extreme point is computed from both x coordinate and y coordinate, and a pressure feature so that the dimension of the curve is reduced. In the considered approach, the signature curve is created independently for each user, and the distance between the test signatures and the signature template is determined in an eight-dimensional space.

If authors take into account skilled forgeries or signatures of other users, then they can take advantage of deep learning methods. In [17] the authors proposed a stroke-based bidirectional RNN architecture for the dynamic signature verification. The main idea is to split the signature into multiple patches using strokes. Concatenation of query and reference signature pairs are used as input. The proposed method uses two LSTM RNN networks to extract different features. One extracts the fea-

tures of the strokes and the other extracts the global features of the whole signatures.

In [29] the authors proposed writer-independent on-line signature verification systems based on Recurrent Neural Networks (RNNs) with a Siamese architecture whose goal is to learn a dissimilarity metric from the pairs of signatures. The tests include skilled forgeries and random signatures treated as forgeries. This reduces the verification of signatures to two-class classification and eliminates the problem of designing one-class classifiers. Paper [28] is a continuation of the research described in [29]. It is a summary of solutions in the field of the use of deep learning methods in the verification of dynamic signatures.

1.2 Motivation

Partitioning of dynamic signatures is an effective way of identity verification. A single partition is usually a subset of the signals describing the signature dynamics that correspond to the discretization points. Partitioning can be done in different ways: in the time domain [5], in the velocity domain [6], in the pen pressure domain [6], and their combination [7], etc. In addition, partitions can be interpreted differently, for example: as subsets of distributed discretization points or occurring after each other [6, 5, 7].

The basis of velocity partitioning in most methods is the arithmetic mean of the values of partitioned signals. However, this approach may not be beneficial for a certain class of signatures. This applies, for example, to a signature in which the signer creates the final underline faster than in the case of the main part of the signature. In this case, using the arithmetic mean causes the loss of important information, which might lower the accuracy of the verification. Therefore, in this paper, we use an evolutionary algorithm to partition signals. It belongs to a group of population-based algorithms that perform well in a variety of application areas [26, 37]. We assume that this algorithm will perform appropriate partitioning of the signature template, taking into account the adopted evaluation function, and then select the partitions most characteristic for the signatures of the considered user.

1.3 Contribution of the paper

In this paper, we propose a new approach to identity verification based on the dynamic signature partitioning. It uses an evolutionary algorithm to create partition in time and velocity domains. The goal of the evolutionary algorithm is also to select the most characteristic partitions in terms of matching to the reference signatures. These actions are performed individually for each user, which eliminates the need of using skilled forgeries. Therefore, the evolutionary algorithm aims at solving a continuous and discrete problem.

An interesting issue considered in this paper is also the comparison of the non-evolutionary approach to dynamic signatures verification (proposed by us earlier) with the evolutionary approach. In this comparison, real dynamic signatures from the Biosecure DS2 database were used (which is a part of the DeepSignDB, see [12, 21, 22, 30]).

1.4 Structure of the paper

In Section 2 we describe the proposed approach to the evolutionary selection of the dynamic signatures partitioning. In Section 3 we present simulation results. In Section 4 we summarize the most important conclusions and plans for future research.

2 Description of the proposed approach

The approach proposed in this paper operates in two phases: learning and action (testing). These phases are described later in this section.

2.1 Training phase description

Learning is performed once for each user according to the algorithm presented in Figure 1. The remarks regarding this algorithm can be summarized as follows:

– The algorithm performs the initial rejection of $Ndisprej$ (in %) discretization points related to the highest and the lowest pen velocity. This is performed in order to eliminate information about accidental pen movements, which should not have a significant impact on the verification of signatures.

Table 1. The formulas used in the learning and testing phases by the algorithms shown in Figures 1-4.

No.	Description and formula
1.	User index: i
2.	Signature index: $j \in \{1,...,J\}$
3.	Pen trajectory: $a \in \{x,y\}$
4.	Dynamic signal: $s \in \{velocity, pressure, ...\}$
5.	Horizontal partition index: $p \in \{1,...,P\}$
6.	Vertical partition index: $r \in \{1,...,R\}$
7.	Discretization point index in partition (p,r): $k \in \left\{1, ..., Kc_{i,p,r}^{\{s,a\}}\right\}$
8.	template of the signature: $\mathbf{tc}_{i,p,r}^{\{s,a\}} = \left[tc_{i,p,r,k=1}^{\{s,a\}}, ..., tc_{i,p,r,k=Kc_{i,p,r}^{\{s,a\}}}^{\{s,a\}}\right]$, where $tc_{i,j,p,r,k}^{\{s,a\}} = \frac{1}{J}\sum_{j=1}^{J} a_{i,j,p,r,k}^{\{s\}}$.
9.	Descriptor of the signature: $d_{i,j,p,r}^{\{s,a\}} = \frac{1}{Kc_{i,p,r}^{\{s,a\}}} \sum_{k=1}^{Kc_{i,p,r}^{\{s,a\}}} \left| a_{i,j,p,r,k}^{\{s\}} - tc_{i,p,r,k}^{\{s,a\}} \right|$
10.	Weights of importance of the partitions used in the classification: $w_{i,p,r}^{\{s,a\}} = 1 - \dfrac{\bar{\sigma}_{i,p,r}^{\{s,a\}}}{\max\limits_{\substack{p=1,2,\ldots,P^{\{s\}} \\ r=1,2}} \left\{\bar{\sigma}_{i,p,r}^{\{s,a\}}\right\}}$
11.	Parameters used to determine fuzzy sets used in the classification process: $d\max_{i,p,r}^{\{s,a\}} = \sigma_i \cdot \max\limits_{j=1,...,J} \left\{ \frac{1}{Kc_{i,p,r}^{\{s,a\}}} \sum_{k=1}^{Kc_{i,p,r}^{\{s,a\}}} \left| a_{i,j,p,r,k}^{\{s\}} - tc_{i,p,r,k}^{\{s,a\}} \right| \right\}$

– The algorithm works on the basis of the template of model signatures. This template is one of the reference signatures submitted by the user before the learning phase. It is the reference signature for which the Euclidean distance between its discretization points and discretization points of other reference signatures is the smallest. Thus, the template is not created by averaging the corresponding discretization points from the reference signatures - the use of averaging discretization points may result in losing information.
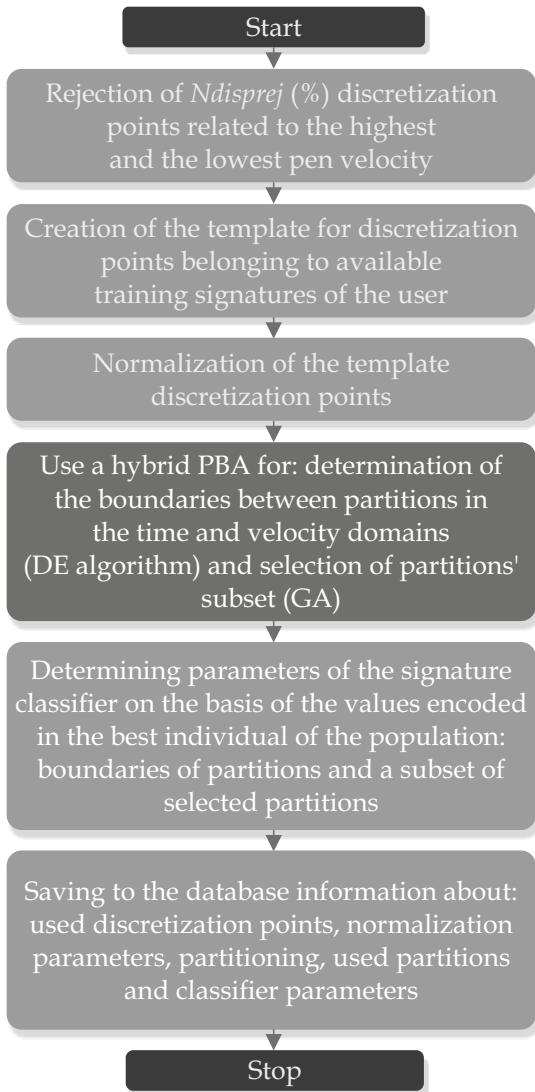
Figure 1. Learning phase for a single user. The operation of the HPBA is shown in Figure 3.

ified. The formulas are analogous to those we have described in detail in [33]. They are briefly summarized in Table 1. The basic structure of the classifier can be easily modified [2].

– The learning phase ends with storing in the database the parameters individually set for the user. They include used discretization points, signature template normalization parameters, information determining the partitioning, information indicating used partitions (see Figure 2), and the classifier parameters.
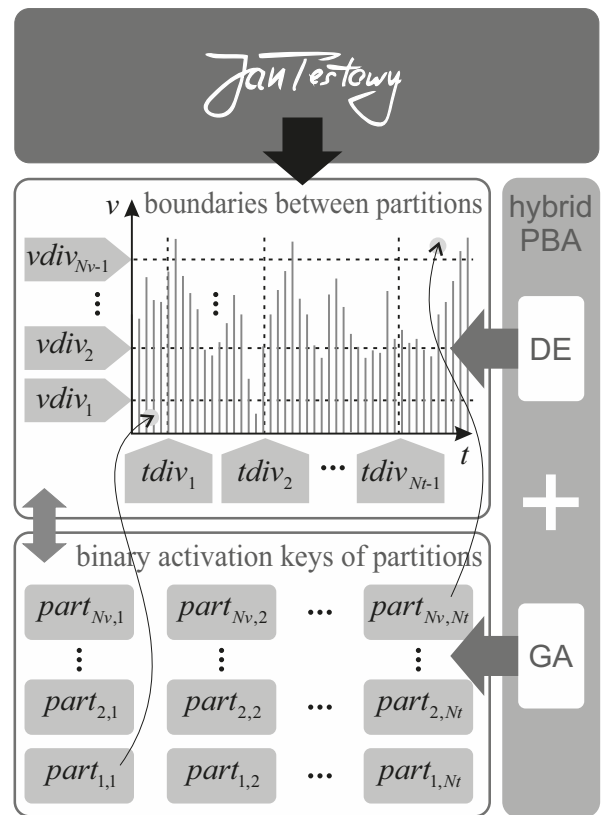

Figure 2. The idea of using HPBA in the learning phase for a single user.

2.2 Description of the use of the population-based hybrid algorithm (HPBA)

The use of the HPBA is an important stage in the learning phase (see Figure 1). As an HPBA, you can use an algorithm that can be created by combining two methods that look for a solution in a continuous and discrete spaces. These methods affect the individuals of the population according to the rule shown in Figure 2. In the simulations we used a

– The main step in the learning phase is to use a population-based hybrid algorithm (Hybrid Population Based Algorithm, HPBA) to: (a) determine the boundaries between partitions in the time and velocity domains and (b) find a subset of partitions. The algorithm is hybrid in nature because its task is to find a solution in the continuous and discrete domains. The details of the use of the algorithm are described in Section 2.2.

– As a result of the HPBA operation, we obtain information on the performed partitioning which is encoded in the best individual of the population (see Section 2.2.1). On its basis, the parameters of the signature classifier should be spec-

genetic algorithm (GA) [27] and a differential evolution algorithm (DE) [23]. In this paper, we do not describe the widely known rules of operation of these algorithms, but focus on their use in the considered problem (see Figure 3 and Figure 2). The remarks on the hybrid algorithm can be summarized as follows:
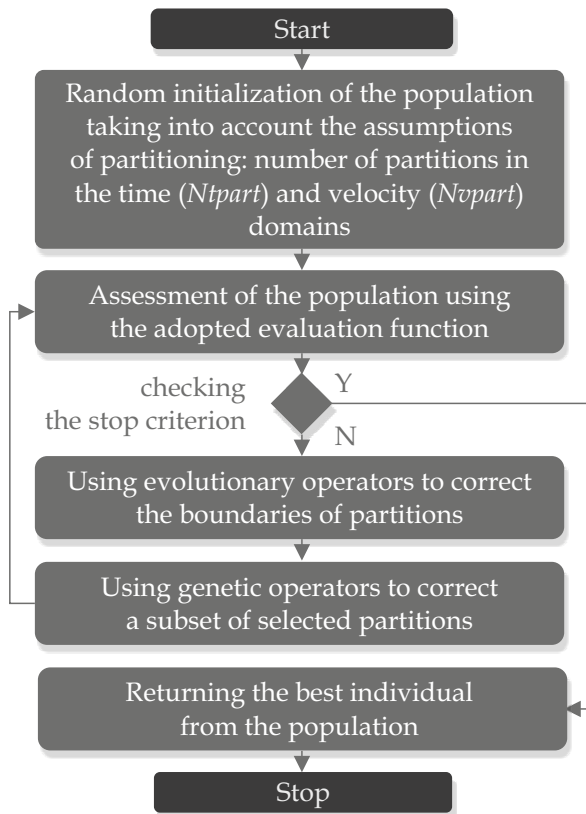

Figure 3. Mode of operation of the HPBA used in the learning phase for a single user.

– Its operation begins with a random initialization of the population. For each parameter of each individual, its domain is taken into account. The interpretation of the parameters encoded in a single individual of the population is shown in Figure 2, and a description is presented in Section 2.2.1.

– Assessing a population consists in evaluating each individual in the context of the partitioning expectations. These expectations take into account, among others, similarity level of the user reference signatures within the partitions defined in the population individual in accordance with Figure 2. The definition of evaluation function is presented in Section 2.2.2.

– The HPBA stop condition check may take into account the allowable number of steps, the permissible number of calls to the evaluation function, or the threshold value of the evaluation function.

– The use of evolutionary and genetic operators is typical for the component algorithms used in the construction of the HPBA. The GA and DE methods use mutation and crossover operators. Their mode of operation is typical and will not be considered in this paper.

– Returning the best solution consists in returning the best individual of the population in terms of the evaluation function. It encodes the method of partitioning the dynamic signature of the considered user (see Section 2.2.1).

2.2.1 Encoding of individuals

Each individual of the population encodes one possible solution of the considered problem - a proposal for partitioning the template of the reference signature of the user i. Each individual $\mathbf{X}_{i,ch}$ is a set of two components:

$$\mathbf{X}_{i,ch} = \{\mathbf{Xdiv}_{i,ch}, \mathbf{Xsel}_{i,ch}\}, \quad (1)$$

where ch is an index of the individual in the population. Each component $\mathbf{X}_{i,ch}$ is processed by a different component algorithm (see Figure 2). This is due to the specificity of the used algorithms, one of which seeks a solution in the continuous domain, and the other in the discrete domain.

Component $\mathbf{Xdiv}_{i,ch}$ is processed by the DE algorithm, which encodes boundaries between partitions and has the following structure (see Figure 2):

$$\mathbf{Xdiv}_{i,ch} = \left\{ \begin{array}{l} tdiv_1, tdiv_2, \ldots, tdiv_{Nt-1}, \\ vdiv_1, vdiv_2, \ldots, vdiv_{Nv-1} \end{array} \right\}, \quad (2)$$

where $tdiv_p$ is a boundary between partitions p and $p+1$ in the time domain ($p = 1, 2, \ldots, Nt - 1$; Nt is the number of partitions in the time domain); $vdiv_r$ is a boundary between partitions r and $r+1$ in the velocity domain ($r = 1, 2, \ldots, Nv - 1$; Nv is the number of partitions in the velocity domain). For a better readability of formula (2) and Figure 2 user index i was omitted in the notation of the components $\{vdiv_r, tdiv_p\}$.

Component $\mathbf{Xsel}_{i,ch}$ is processed by GA and it encodes the information which partitions marked by indices $\{p, r\}$ ($p = 1, 2, \ldots, Nt$ i $r = 1, 2, \ldots, Nv$) are to be included in the verification of the signatures of a user who claims to be the user i (test phase). Component $\mathbf{Xsel}_{i,ch}$ has the following structure (see Figure 2):

$$\mathbf{Xsel}_{i,ch} = \left\{ \begin{array}{l} part_{1,1}, part_{1,2}, \ldots, part_{1,Nt}, \\ part_{2,1}, part_{2,2}, \ldots, part_{2,Nt}, \ldots \\ part_{Nv,1}, part_{Nv,2}, \ldots, part_{Nv,Nt} \end{array} \right\}, \tag{3}$$

where $part_{r,p} \in \{0, 1\}$ is a parameter determining whether the partition marked by indices $\{p, r\}$ is to be taken into account in the test phase. If $part_{r,p} = 1$, then partition $\{p, r\}$ is considered in the test phase, otherwise it is not. For a better readability of formula (3) and Figure 2 user index i was omitted in the notation of components $part_{r,p}$.

2.2.2 Individuals evaluation

Each individual (1) is evaluated in the procedure presented in Figure 3. The following fitness function is used for the evaluation:

$$\begin{aligned} \mathrm{FF}\left(\mathbf{X}_{i,ch}\right) = \\ = \frac{\sum\limits_{j=1, j \neq j*}^{J} \sum\limits_{p=1}^{Nt} \sum\limits_{r=1}^{Nv} \left(\begin{array}{c} \left| \mathbf{S}_{j*,p,r} - \mathbf{S}_{j,p,r} \right| \cdot \\ \cdot part_{p,r} \end{array} \right)}{(J-1) \cdot \sum\limits_{p=1}^{Nt} \sum\limits_{r=1}^{Nv} part_{p,r}}, \end{aligned} \tag{4}$$

where $\mathbf{S}_{j,p,r}$ is a fragment of the reference signature shape associated with partition $\{p, r\}$ and reference signature j ($j = 1, 2, \ldots, J$; J is the number of reference signatures created before the learning phase), $j*$ is the index of the reference signature treated as the template of the reference signatures, $\mathbf{S}_{j*,p,r}$ is the fragment of the reference signature shape associated with partition $\{p, r\}$, and $|\cdot|$ is the Euclidean distance.

Fragments $\left\{ \mathbf{S}_{j*,p,r}, \mathbf{S}_{j,p,r} \right\}$ are subsets of the corresponding discretization points allocated to partition $\{p, r\}$ on the basis of the information contained in the assessed individual $\mathbf{X}_{i,ch}$. These discretization points correspond to the signature shape signals represented by the pen movement signals on the ordinate and the abscissa, which we wrote about in detail in our previous papers [6, 5, 7].

Function (4) can be interpreted as the average match of the reference signatures template to the template within the partition. The goal of the HPBA is to minimize this function.

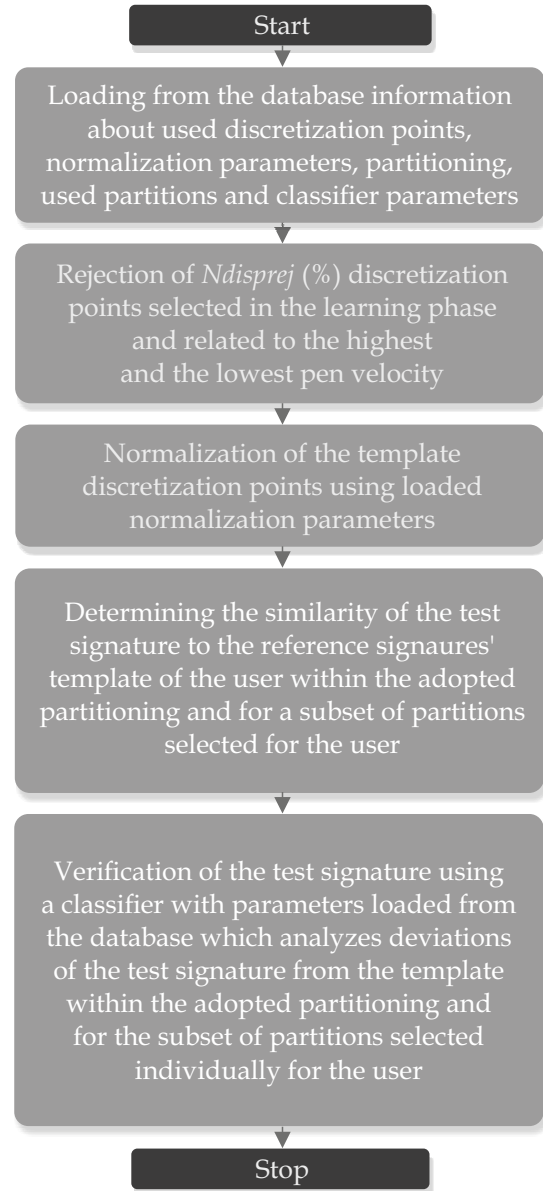### 2.3 Description of the test phase

Figure 4. Verification of a single test signature of a user claiming to be user i.

After the learning phase has been completed, the method can be tested. Testing of signatures can be performed repeatedly in accordance with the algorithm presented in Figure 4. The remarks regarding this algorithm can be summarized as follows:

– In the first step, the algorithm reads from the database individual parameters characterizing the reference signatures of user i and the way of their partitioning. Then, it is prepared to verify the authenticity of the signatures of the user who claims to be user i.

– The next two steps of the algorithm are: (a) rejection of discretization points corresponding to those that were rejected in the learning phase; (b) normalization of the remaining discretization points. These steps are the same as in the learning phase.

– Verification of the test signature depends on its similarity to the reference signature. It is determined independently for each of the partitions set and selected in the learning phase. This leads to the determination of descriptors, the number of which corresponds to the number of partitions (see Table 1, row 1).

– The test signature descriptors are put to the inputs of the fuzzy signature similarity evaluation system. Its parameters are selected individually for each user. They take into account the stability of signing the reference signatures. The method of determining these parameters is shown in Table 1 (row 2) and described in our previous papers [6, 7, 33].

3   Simulations

In the simulations the BioSecure DS2 database (which is a part of the DeepSignDB, see [12, 21, 22, 30]) was used to test the algorithm for the verification of the dynamic signatures using HPBA proposed in this paper. Details on the number of users and signatures used in simulations are presented in Table 2. In the learning phase, the reference signatures were taken into account, while in the testing phase, the test signatures and skilled forgeries were used (they were not included in the learning phase). The remarks on the simulations can be summarized as follows:

– The parameters of the proposed approach are given in Table 3. Parameters 1-8 are related to HPBA, therefore their meaning will not be considered in this paper. Parameter 9 concerns the learning and testing phases (see Figure 1 i 4).

– The simulations were performed in several variants described in Table 4. The BASC11 variant does not perform partitioning and it is the base variant. Variants AVCO31, AVCO13, AVCO33, and AVCO55 relate to non-evolutionary determination of partition boundaries without selecting them. They are variants that can evaluate: (a) the impact of partitioning in time and velocity domain, and (b) the impact of increasing the number of partitions on the accuracy of signature verification. Variants DECO33 and DECO55 are related to partitioning with evolutionary partitions' boundary selection, but do not use partitions' selection. They are variants that allow to assess the influence of the evolutionary selection of partitioning boundaries on the accuracy of signature verification. Variants AVGA33 and AVGA55 are related to non-evolutionary partitioning with genetic partition selection. They are variants that allow to assess the impact of partition selection on the accuracy of signature verification. Variants DEGA33 and DEGA55 implement evolutionary partitioning with genetic partition selection. Therefore, they concern the full version of the algorithm proposed in this paper.

– The results obtained in the simulations are presented in Table 5. They concern the variants summarized in Table 4. They contain accuracies expressed by typical errors used in biometrics: FAR (False Acceptance Rate), FRR (False Rejection Rate), and average error value.

– The comparison of the best simulation results with the results of other methods is presented in Table 6. This table takes into account several popular dynamic signature partitioning methods and compares them with the best variant of the partitioning method proposed in this paper.

The conclusions from the simulations can be summarized as follows:

– Partitioning is an effective mechanism to support dynamic signature verification (see rows BASC11 and the other ones, Table 6).

– Time and velocity domain partitioning works better than time or velocity domain partitioning (see rows AVCO31/AVCO13 and AVCO33/AVCO55, Table 6).

Table 2. The number of users and signatures from BioSecure DS2 database used in the simulations.

No.	Description and value
1.	number of users: 140
2.	number of reference signatures for the user: 4
3.	number of genuine test signatures for the user: 15
4.	number of forged test signatures (skilled forgeries) for the user: 15

Table 3. Parameters of the proposed approach to the dynamic signature partitioning.

No.	Description and value
1.	mutation probability in GA: 0.02
2.	crossover probability in GA: 0.80
3.	parameter F [23] value in DE: 0.50
4.	parameter CR [23] value in DE: 0.90
5.	population size: 1000
6.	selection method in GA and DE: roulette wheel
7.	allowable number of steps: 1000
8.	number of repetitions of each simulation: 50
9.	number of rejected discretization points $Ndisprej$: 5%

Table 4. Considered variants of the simulations.

Nota- tion	Nt	Nv	Select- ion of $\mathbf{Xdiv}_{i,ch}$	Select- ion of $\mathbf{Xsel}_{i,ch}$
BASC11	1	1	-	= 1 (constant)
AVCO31	3	1	avg	= 1 (constant)
AVCO13	1	3	avg	= 1 (constant)
AVCO33	3	3	avg	= 1 (constant)
AVCO55	5	5	avg	= 1 (constant)
DECO33	3	3	DE	= 1 (constant)
DECO55	5	5	DE	= 1 (constant)
AVGA33	3	3	avg	GA
AVGA55	5	5	avg	GA
DEGA33	3	3	DE	GA
DEGA55	5	5	DE	GA

Table 5. Obtained simulation results averaged within the performed repetitions. The best results are shown in bold.

Variant	Average FAR [%]	Average FRR [%]	Average error [%]
BASC11	6.88	7.64	7.26
AVCO31	2.59	5.69	4.14
AVCO13	3.02	4.02	3.52
AVCO33	3.56	3.24	3.40
AVCO55	7.18	5.38	6.28
DECO33	3.34	3.26	3.30
DECO55	6.76	5.36	6.06
AVGA33	3.50	3.26	3.38
AVGA55	7.10	5.22	6.16
DEGA33	**2.92**	**3.04**	**2.98**
DEGA55	6.82	5.22	6.02

Table 6. Comparison of the best (averaged) simulation results with the results of other methods using BioSecure DS2 database. The best results are shown in bold.

Method	Average FAR [%]	Average FRR [%]	Average error [%]
Methods presented in [14]	-	-	3.48-30.13
Method based on TA-RNNs [30]	-	-	3.00
DEGA33	2.92	3.04	**2.98**

- Increasing the number of partitions does not necessarily increase the accuracy of the signature verification (see rows AVCO33 and AVCO55, DECO33 and DECO55, AVGA33 and AVGA55, DEGA33 and DEGA55, Table 6).

- Evolutionary partition boundary selection and genetic partition selection increases the accuracy of the dynamic signature verification (see DEGA*xx* / DECO*xx* / AVCO*xx*, Table 6). This proves the validity of using HPBA in the partitioning of signatures. DEGA33 was the best variant in the simulations.

- A comparison of the DEGA33 variant with other partitioning variants shows that it is a method that works with a high and satisfactory accuracy. It should be emphasized that the given accuracy

of DEGA33 is the accuracy resulting from averaging the simulation repetitions. This proves the stability of the proposed method.

– Variants using GA only, DE only, or HPBA (GA and DE) are more computationally complex than the methods that do not use evolutionary partitioning. This is due to the specificity of the operation of PBAs and is a disadvantage of the approach. However, it is worth emphasizing that the learning phase is carried out once, and its course does not depend on the number of users in the database. On the other hand, the advantage of the proposed approach is a greater precision of signature processing, which results in the stability of the method and a high accuracy.

4   Conclusions

In this paper, we propose a new method for the dynamic signature verification. It uses partitioning performed with a hybrid population-based algorithm. This algorithm finds the boundaries between partitions and selects partitions individually for each user. The operation of this algorithm has been tested and compared with other methods. The simulations show that evolutionary dynamic signature partitioning is more effective than non-evolutionary partitioning. This may be due to the evolutionary algorithm omitting the signature areas related to accidental stylus movements, for example, quick underlines. After comparing the accuracy of the proposed method with the accuracy of other partitioning methods, it can be concluded that it performs slightly better and more reproducibly.

Our future plans include developing a partitioning method supported by neural networks and deep learning methods [3, 9, 20], the use of various approaches to the selection of the fuzzy system structure [2], the use of other population-based methods in the implementation of partitioning [26], and formulation of various criteria for assessing the considered problem (modeled on [25]).

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