

Using Multi-Sets of Features to improve the Performance of Automatic Signature Verification Systems

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Abstract

For decades, published Automatic Signature Verification (ASV) works depended on using one feature set. Some researchers selected this feature set based on their experience, and some others selected it using some feature selection algorithms that can select the best feature set (bfs). In practical systems, the documents containing the signatures could be noisy, and recognition of check writer in multi-signatory accounts is required. Due to the error caused by such requirements and data quality, improving the performance of ASV becomes a necessity. In this paper, a new technique for ASV decision making using Multi-Sets of Features is introduced. The experimental results have shown that the introduced technique gives important improvement in forgery detection and in the overall performance of the system

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For the Arabic abstract in Arabic see page (11).

1 . Introduction

Off-line signatures are those we usually use in paper works like letters, contracts, and bank checks. The research introduced in this paper is related to this kind of signatures.

Ammar et al. reported in 1986 the first successful work on verification of skilled forgeries [1,2]. Their principle of extracting High Pressure Regions (HPRs) in signatures was adopted later by some researchers for further study [3,4], and motivated others to conduct further work on the same topic [5,6]. In 1989 they investigated the performance of using different types of features in ASV using a feature selection algorithm they developed [7,8]. Ammar used in 1990 a new type of features for ASV based on matching, and reached new results[9,10]. Later in 2006 and 2007, other researchers used these features in ASV with different decision making approaches [11,12]. During the same period (1980s), some other groups were active in this field [13,14]. Recently, some research works attempt to practically evaluate published approaches[15], and others are reattempting to explore the potential effectiveness in the gray level image [16]. The rest of ASV-related works can be found in related review papers [14,17, 18] and recent publications.

In 1995, Ammar et al. realized a portable software for off-line ASV usable with PCs under DOS, and tested it using a new signature data collected from the actual daily life activities like business documents, checks, correspondences, and actual caseworks, in which the signatures are written with complete spontaneity[19]. This data, to be explained in the next section, was used in the experiments of this paper. In 2002, Ammar reached an ASV system usable in *actual Interbank-Check-Imaging (I-C-I) environment in the USA* [20, 21]. In this new environment, the research faced more requirements like the necessity of using single reference signature, and handling the multi-signatory account ASV. The image data in this environment is always binary. It contains,

as well as the signature, a printed background, stamps, and sometimes special symbols. It may also be noisy. This new data quality made extracting clean signature from the check image a very hard task. Fig. 1 shows an example of such data. This environment affected negatively the overall performance of the ASV process so that searching for further improvements became a necessity. MSF technique explained in this paper was among the possible improvements investigated.

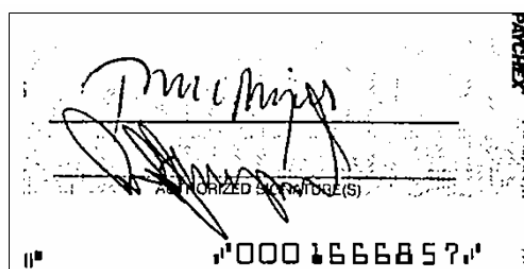


Fig. 1 An example of two-signatures noisy-check; (signature part of the check).

Ammar et al. [22] have shown that MSF can provide important improvement in detection of skilled forgeries. In this paper, the new MSF decision making technique for ASV, its motivation and experimental results in case of medium number of features are introduced in detail. The performance of the MSF approach in case of large number of features, and in case of using the bfs as well MSF are covered in detail in a different work[23]. This research done at Nagoya University, Nagoya , Japan during the sabbatical period of the author between Oct. 2009 and Feb. 2010, can be considered as a continuation to the previous works related to the same topic in the faculty of Information Engineering, Nagoya University.

2. Signature data

The signature data used in this research consists of 560 genuine and forgery signatures belong to 26 writers. The signatures are written in different languages by people of different nationalities including Arabic, Japanese, Koreans, Europeans, and Americans. The number of genuine

signatures and forgeries differ from one person to another. Moreover, the documents from which the signatures were extracted vary from white paper, business documents, to bank checks so that the signature data is naturally written under widely different conditions. Forgeries were created with a good attention in order to have convincing forgeries, and some forgeries are real ones obtained from actual caseworks. Fig. 2 shows the complete set of genuine and forgery samples of 2 persons.

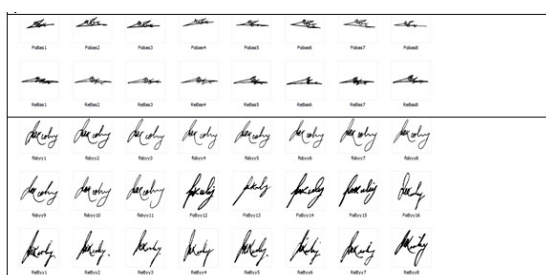


Fig.2 Two complete sets of the signatures of 2 persons. Each set consists of unequal number of genuine and forgery samples

3. Signature verification and feature selection

Signature verification systems usually use the general approach shown in fig.3 below in order to give a decision about the authenticity of a given input signature, whether it is genuine or an attempted forgery.

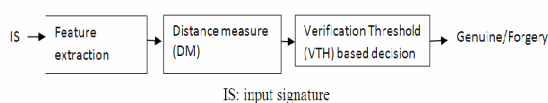


Fig. 3 The general approach for signature verification

3.1 Feature extraction

This stage may follow a preprocessing one[7,8]. Features in off-line systems are essentially two types: (1) shape features like handwriting slants(positive, vertical, negative, and horizontal), relative measures of signature height and width, middle zone width

and signature width, and (2) pseudo-dynamic features like High Pressure Factor. Those features can be extracted globally on the signature as a whole, and locally on the signature divided into specific parts[7,8].

3.2 Distance Measure (DM)

DM measures the similarity between the input signature and the reference ones. The Euclidean distance is used for this purpose. It is computed from the features of the test signature using Eq. (1):

$$DM = (1/n \sum_{i=1}^n (f_i - \mu_i / \sigma_i)^2)^{1/2} \quad (1)$$

Where:

f_i : the i^{th} feature ($1 \leq i \leq n$).

n : number of used features.

μ_i : the mean the i^{th} feature computed on the set of genuine (training) samples of the related person.

σ_i : the standard deviation of the i^{th} feature computed on the same set.

3.3 Verification decision

The verification decision is made as follows:

If $DM > VTH$, the input signature is judged to be "genuine", otherwise, it is judged to be "an attempted forgery". VTH is the Verification Threshold.

The value of the threshold VTH is usually determined based on some evaluation experiments using a reference signature data so that it minimizes the error rate (maximizes the correct decisions).

Selecting the used features is usually done either based on the developer experience (not very accurate, but works), or based on a feature selection technique that selects the best feature set (bfs). bfs is the feature set that gives the highest performance (maximizing the percentage of correct decisions, or

minimizing the error rate). M. Ammar et. al, developed in 1989 a feature selection technique based on the principle of the "Circulant Matrix" (Circulant Matrix-Based Feature Selection Technique CMBFST) to generate n^2 feature sets among the possible $n!$ feature sets of n given features, and found that evaluating the signature data available using these n^2 feature sets will lead to the best one after, at most, one or two shuffling process of the initial order of the features (f_1, f_2, \dots, f_n) [8]. This CMBFST is a very fast one and gives a clear idea of the effectiveness of the individual features, and their contribution to the effectiveness of the different feature sets, if augmented by, to form a new one. Since this CMBFST will be used to develop the MSF technique for ASV in this paper, it will be briefed below with some experimental results.

The CMBFST

For a given primary feature set $\{f_1, f_2, \dots, f_n\}$, the n^2 feature sets are formed as follows:

Step 1:

A matrix of $n \times n$ entries is formed as follows: the first row is made to be the primary feature set. Each following row is formed from the preceding one by shifting its contents one entry to the right (could be to the left) until we reach the initial order after $n-1$ shifts, as shown below for $n=5$ (in actual systems n may reach tens of features but taken here 5 for simplicity of explanation):

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f1  f2  f3  f4  f5
f5  f1  f2  f3  f4
f4  f5  f1  f2  f3
f3  f4  f5  f1  f2
f2  f3  f4  f5  f1
    
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Step2:

from each row, n different feature sets are formed starting from the first row as follows:

$$S_1= \{f_1\}; S_2=\{f_1,f_2\}; S_3=\{f_1,f_2,f_3\}; S_4=\{f_1,f_2,f_3,f_4\}; S_5= \{f_1,f_2,f_3,f_4,f_5\}.$$

In this way, we generate $n \times n$ feature sets, but since the last feature set generated from each row is essentially the same, $n \times n - (n-1)$ different feature sets are actually generated.

Now, in order to find the best feature set, among the $n \times n - (n-1)$ sets, the signature data is verified using all generated feature sets forming 3 result matrices: SR, PCA, and PCR where:

PCA: Percentage of Correct Acceptance (percentage of genuine signatures accepted as genuine samples).

PCR: Percentage of Correct Rejection (percentage of forgeries rejected and classified as attempted forgeries).

$$SR: \text{System Reliability} = (PCA+PCR)/2.$$

Tables 1-3, below show a practical example of the three result matrices of 144 entries each, formed by the CMBFST using the 12 shape features with the following initial order (global area, global positive, vertical, negative, and horizontal slants, x , and y gravity center coordinates, the area measured on the signature divided into three equal length parts, and in its left and right halves) . The way of extracting these features can be found in [7,8].

It is obvious that the last column of each matrix has the same value because the feature set is essentially the same.

Since the best feature set is chosen to maximize SR, it will be that of the entry (7,7) which gives $SR=88.17$ with corresponding $PCA=92.45$ and $PCR=83.89$.

Table 1 SR Matrix of 144 entries

72.8	79.43	82.595	83.685	84.165	83.33	84.105	84.44	84.775	84.045	85.425	86.645
73.975	78.045	82.975	82.595	82.91	84.125	83.16	83.265	83.035	84.73	85.76	86.645
72.755	81.9	81.465	81.315	82.765	83.745	83.435	83.745	84.945	86.265	86.995	86.645
76.68	78.485	78.925	81.695	84.125	83.555	84.275	85.975	87.5	87.485	86.62	86.645
73.685	73.83	79.535	81.02	83.075	83.015	85.235	86.765	88.05	86.265	85.675	86.645
66.715	74.73	77.935	81.295	82.655	85.11	86.98	87.165	86.575	87.125	87.355	86.645
73.895	77.265	80.96	82.425	84.985	87.02	88.17	87.27	87.105	87.63	86.935	86.645
74.06	78.025	82.03	84.21	86.92	87.315	87.27	87.145	87.88	86.43	86.6	86.645
78.8	77.455	82.385	84.715	85.005	86.6	86.81	87.71	86.515	86.31	86.645	86.645
81.19	82.47	82.825	83.6	85.7	86.12	86.915	86.43	85.53	86.575	86.225	86.645
61.62	65.085	71.545	84.38	86.475	87.65	87.185	86.6	86.645	86.98	86.79	86.645
59.61	74.84	82.325	84.775	85.405	85.845	85.11	85.805	85.615	86.12	85.28	86.645

Table 2 PCA Matrix of 144 entries

78.49	76.98	85.66	84.15	89.81	83.77	91.7	91.7	91.7	87.55	91.32	92.08
78.49	88.3	83.4	91.7	88.3	92.08	83.77	88.68	87.55	90.94	91.32	92.08
83.77	82.26	86.42	80.75	82.64	88.3	88.68	88.3	91.7	88.3	89.43	92.08
87.92	84.15	86.04	81.51	92.08	87.92	91.7	92.08	92.45	89.06	91.7	92.08
76.23	69.81	84.91	93.58	91.32	87.17	87.92	88.3	93.21	91.32	83.77	92.08
83.77	83.02	89.43	83.4	83.77	88.68	89.06	92.45	87.92	88.68	92.83	92.08
83.02	92.45	86.42	85.66	89.43	86.79	92.45	88.3	88.3	88.68	88.3	92.08
86.04	81.89	87.55	90.57	84.91	86.04	91.32	92.08	93.21	88.3	88.3	92.08
89.81	86.79	90.94	90.57	89.81	85.28	89.06	93.21	92.83	92.08	92.08	92.08
84.53	86.42	86.79	82.64	84.15	91.7	87.92	88.3	87.17	87.92	87.55	92.08
79.62	69.43	73.96	78.49	89.06	89.06	92.83	88.3	92.08	89.06	91.7	92.08
91.7	78.87	77.74	85.66	87.92	89.81	88.68	92.08	91.7	91.7	91.7	92.08

Table 3 PCR Matrix of 144 entries

67.11	81.88	79.53	83.22	78.52	82.89	76.51	77.18	77.95	80.54	79.53	81.21
69.46	67.79	82.55	73.49	77.52	76.17	82.55	77.85	78.52	78.52	80.2	81.21
61.74	81.54	76.51	81.88	82.89	79.19	78.19	79.19	78.19	84.23	84.56	81.21
65.44	72.82	71.81	81.88	76.17	79.19	76.85	79.87	82.55	85.91	81.54	81.21
71.14	77.85	74.16	68.46	74.83	78.86	82.55	85.23	82.89	81.21	87.58	81.21
49.66	66.44	66.44	79.19	81.54	81.54	84.9	81.88	85.23	85.57	81.88	81.21
64.77	62.08	75.5	79.19	80.54	87.25	83.89	86.24	85.91	86.58	85.57	81.21
62.08	74.16	76.51	77.85	88.93	88.59	83.22	82.21	82.55	84.56	84.9	81.21
67.79	68.12	73.83	78.86	80.2	87.92	84.56	82.21	80.2	80.54	81.21	81.21
77.85	78.52	78.86	84.56	87.25	80.54	85.91	84.56	83.89	85.23	84.9	81.21
43.62	60.74	69.13	90.27	83.89	86.24	81.54	84.9	81.21	84.9	81.88	81.21
27.52	70.81	86.91	83.89	82.89	81.88	81.54	79.53	79.53	80.54	78.86	81.21

Published works on signature verification usually mention total evaluation results like the curves shown in Fig. 4 or as total performance expressed as percentage of correct decisions or type I and type II error rates. M. Ammar et al. in 1987 displayed the result as (X,O) graph which gives a clear insight into the evaluation process enabling to see what is happening to each sample, and the performance of the verification approach for individual persons. Fig. 4 shows the SR, PCA and PCR curves corresponding to (7,7) entry in the SR matrix (the best feature set that can be formed from the mentioned features), and Fig. 5 shows its corresponding (X,O) graph. In Fig. 5, persons included in the signature database are displayed on the horizontal axis, and the distance measure of each sample is displayed on the vertical axis. Forgery

samples are represented by "X", and genuine samples are represented by "O". Each X above the verification threshold VTH is a correct decision, and each "O" below VTH is a correct decision. The clear view provided by the (X,O) graph, and the result of the 3 persons marked by ellipses will be used to explain the motivation for the MSF technique.

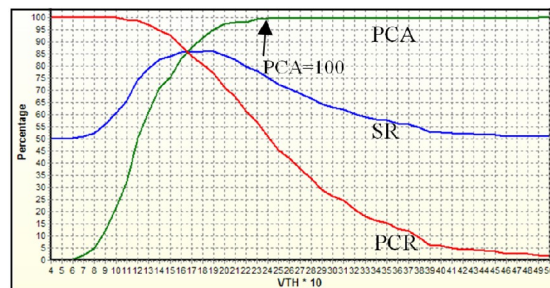


Fig. 4 SR, PCA and PCR curves of the entry (7,7) of the SR result matrix in Table 1.

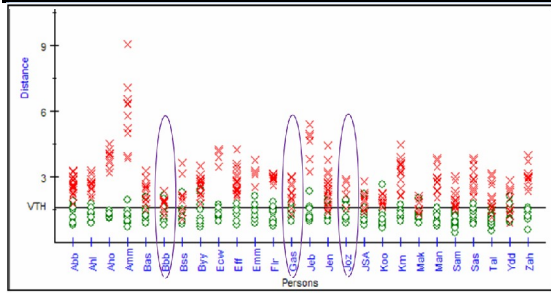


Fig. 5 The (X,O) graph belonging to SR_{max} of fig. 4.

4. The motivation for the MSF technique

If we examine the result of the persons Bbb, Gas, and Joz in Fig. 5 obtained from the bfs (marked by ellipses) and compare it with the result of the same persons in Fig.6 obtained from the feature set of the entry (11,6) in Table 1 which gave $SR=87.65$, we find that the result in Fig. 6 is better for those persons, where more forgery samples have been correctly verified (X is above VTH). Since the performance of the feature set which gave the result in Fig. 6 is less than that of the feature set that gave SR_{max} with (X,O) graph in Fig. 5, we lose some effectiveness in detecting forgeries for those persons if we use the best feature set (gives SR_{max}) for verification. In fact, the result may become little bit worse for some other persons with the feature set of Fig. 6, but as a general observation, we lose some ability of further correct forgery detection when we use only the best feature set. MSF, if used properly, will improve the overall performance, as explained in the following section. Hence, the improvement idea is to find some way to collect the effectiveness lost in the excluded Effective Feature Sets (EFS) (close in performance to the bfs) when we use, as usual, a single feature set for verification.

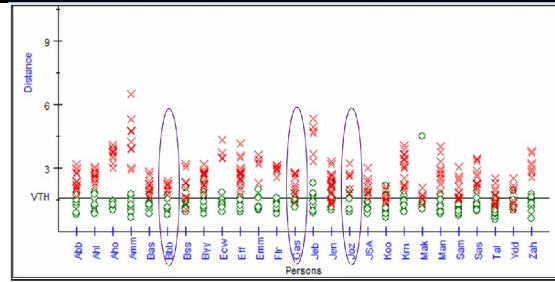


Fig. 6 The (X,O) graph of the entry (11,6); $SR=87.65$.

Fig. 7 illustrates how theoretically the MSF is expected to improve the forgery detection, where:

cvf_i : correctly verified forgery samples by using the feature set number i.

$cvfbfs$: correctly verified forgery samples by using the bfs.

$cvfmfs$: correctly verified forgery

$$\text{samples by using MSF} = \bigcup_{i=1}^n cvf_i ;$$

n: number of feature sets.

The expected result, which will be confirmed experimentally, is $cvfmfs > cvfbfs$. In other words, the MSF technique is a process of collecting the sparse effectiveness that can be provided by the EFS but can not be captured by the bfs.

5. Effect of using MSF on PCR and PCA

In the reality, there is no error free ASV algorithm or system. As the standard form of the SR, PCA, and PCR curves shown in Fig. 4 suggests, increasing PCR by changing VTH value will lead to decreasing PCA, and vice versa. So, this fact must be kept in mind when trying to improve PCR or PCA by changing VTH value.

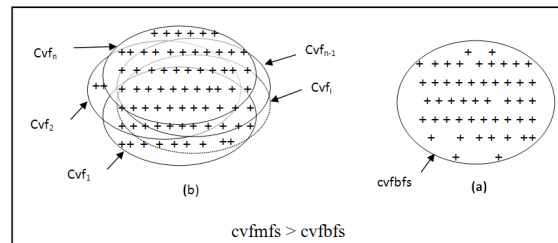


Fig 7 illustration of how the MSF may improve detection of forgeries.

The principal idea of the MSF verification depends on verification using

several feature sets and gathering the detected forgeries. This process will lead to introducing some error with every feature set used if the VTH goes down below PCA=100 limit: (VTH = 2.4) in Fig. 4, for example. When VTH goes lower than that limit, we will loose in PCA, but will gain in PCR so that the total effect will be positive and in favor of PCR until some VTH value. The effect of using MSF on the overall performance will be discovered experimentally using **compute-multisets-curves** procedure explained below, as follows:

- 1 – Using the selection procedure explained in section 3, the EFS will be found.
- 2 - The MSF-based verification procedure illustrated in Fig. 8 will be applied to the whole signature data for all VTH values (0.4-5.0) in 0.1 steps, and for all feature sets obtained in 1.
- 3- At each VTH value, PCA, PCR, and SR are computed to draw the MSF curves.
- 4 - displaying the curves.

In Fig. 8: f: feature; S1,...,Sm: EFS; ThBD: Threshold-Based Decision; F: Forgery; G: Genuine.

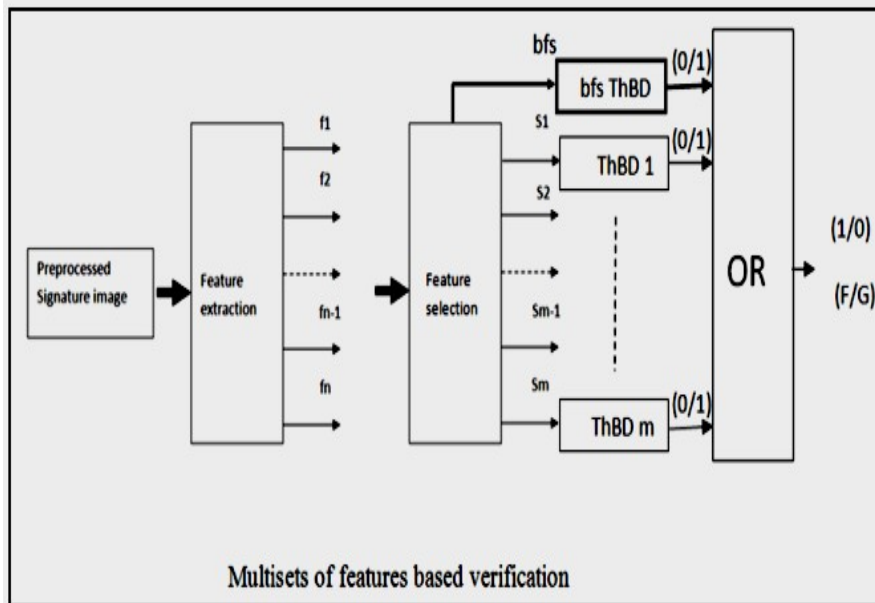


Fig. 8 MSF-based ASV.

Procedure compute-multisets-curves

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For every VTH value in the range (0.4-5.0) with 0.1 steps
For all EFS
For all signature data(genuine and forgeries)
if the distance measure of the signature sample > VTH
classify it as forgery
otherwise
classify it as genuine
end // all signature data.
end // all EFSs.
    
```

PCR=100X (No. correctly classified forgeries/No. all forgeries).

PCA=100X(No. correctly classified genuine samples/No. all genuine samples)

$$SR = (PCA + PCR) / 2$$

end // every VTH value.

After computing the curves of PCA, PCR, SR using all EFS, those curves are displayed along with the those obtained by the bfs for comparison and estimation of the benefits obtained by the introduced MSF.

6. Results and discussion

Fig. 9 shows the SR, PCA and PCR curves of the MSF-based verification using 18 EFS formed from the primary feature set, used to produce Tables 1-3, with SR over 87.0, as

appears in the screen shot in Fig.9. Fig. 10 shows the curves of both bfs and MSF. In this figure, the merit of MSF over the bfs appears clearly, where the thick curves are those of the MSF, and the thin ones are those of the bfs. Examining these curves shows that:



Fig. 9 SR, PCA, and PCR curves of the MSF using 18 EFS of SR>87.0.

- 1 – There is a considerable gain in PCR between $VTH=1.9$ and $VTH=4.0$ ranging from 10% to 15%. This improvement is the effectiveness that can be provided by the EFS, but can not be captured by the bfs. **This gain has been provided by the new MSF approach.** It is also a real reflection of the fact that every feature can detect some aspects of the variability of the signature that can not be completely compensated by other features.
- 2 – The gain explained above is pure for $VTH>2.9$, since there is no loss in PCA.
- 3 – From $VTH = 2.9$ down, the loss in PCA starts to appear gradually, but remains less than the improvement in PCR so that the total change remains positive until $VTH=1.85$. Below this value, the loss in PCA becomes larger than the gain in PCR, and consequently, we get a loss in SR, as the curves show. In fact, this result is natural because this region below $VTH 1.85$ in the (X,O) graph is the genuine samples zone. *VTH may not be used in this zone at all.*
- 4 – The highest SR (S_{Rmax}) obtained by the MSF is little bit higher than that of the bfs (88.26 in comparison with 88.17), as Fig. 11 shows.
- 5 – In general, by using the MSF we can get at the same SR a PCR higher than that obtainable by bfs.
- 6- The importance of the improvement in performance gained by the MSF technique is that *it can not be obtained by usually used approach. It is usually lost.*

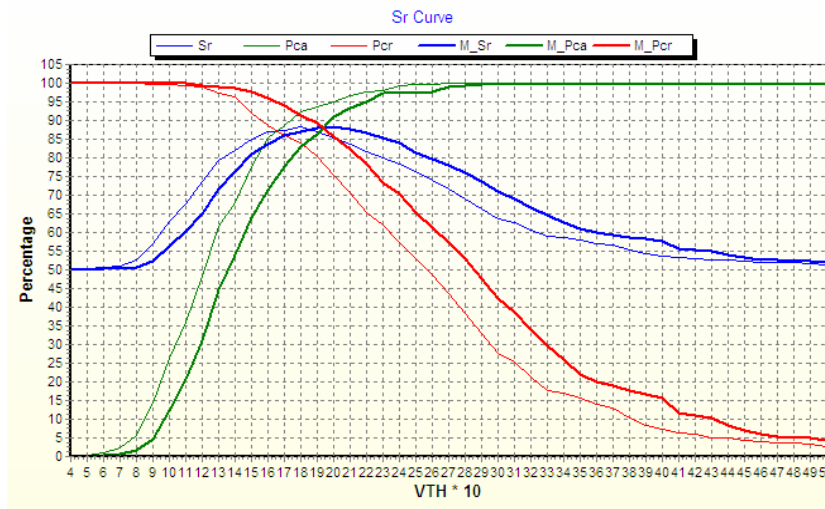


Fig. 10 SR, PCA, and PCR curves of the bfs and MSF.

Sr Curve	Sr Values	Xo Map	VTCH							
Distance	1.4	1.5	1.6	1.7	1.8	1.9	2	2.1	2.2	2.3
707 SR	82.12	84.85	86.94	87.3	88.17	86.89	85.3	83.71	81.59	80.1
707 Pca	67.92	77.74	85.28	88.68	92.45	93.58	95.09	96.6	97.74	98.1
707 PCR	96.31	91.95	88.59	85.91	83.89	80.2	75.5	70.81	65.44	62.08
Multi SR	76.31	80.9	83.65	85.85	87.15	87.84	88.26	87.71	86.64	85.4
Multi Pca	53.96	64.15	71.32	77.74	83.02	86.42	90.94	93.21	95.09	97.36
Multi Pcr	98.66	97.65	95.97	93.96	91.28	89.26	85.57	82.21	78.19	73.48

Fig. 11 SR, PCA, and PCR values for bfs and MSF around the peak.

7. Conclusion

This paper has introduced a new novel MSF-based ASV technique that gives better forgery detection than that obtainable by the best feature set. With MSF, the forgery detection power lost in the excluded effective feature sets and can not be captured by the best feature set, could be recovered.

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