

# $ER^2$ : an Intuitive Similarity Measure for On-line Signature Verification

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## Abstract

$ER^2$  (Extended  $R$ -squared) is proposed as a similarity measure for on-line signature verification. SLR (Simple Linear Regression) defines  $R^2$  as a measure of goodness-of-fit. We observed that  $R^2$  is a good similarity measure for 1-dimensional sequences. However, many kinds of sequences are multidimensional, such as on-line signature sequences, 2D curves, etc. Therefore, we extend  $R^2$  to  $ER^2$  for multidimensional sequence matching. Coupled with optimal alignment,  $ER^2$  outperforms DTW-based curve matching on on-line signature verification.

## 1. Introduction

On-line signature verification field has gained increasing attention in recent times. As one of the biometric authentication methods, signature has been widely accepted in real life, because it is more user-friendly than fingerprint, iris, retina and face. On-line signatures are acquired using digitizing tablet which captures both temporal and spatial information, such as coordinates, pressure, inclinations, etc. On-line personal identification is facing increasing need due to the rapid development of digitizing technology.

Two aspects pose challenges in the field of online signature verification. On one side, intra-personal variation can be large. Some people provide signatures with poor consistency. The speed, pressure and inclinations pertaining to the signatures made by the same person can differ greatly, which makes it quite challenging to extract consistent features. On the other side, we can only expect few samples from one person and no forgeries in practice. This makes it very difficult to determine the consistency of extracted features. Due to limited number of training samples, the determination of threshold that decides rejection or acceptance is also an open problem.

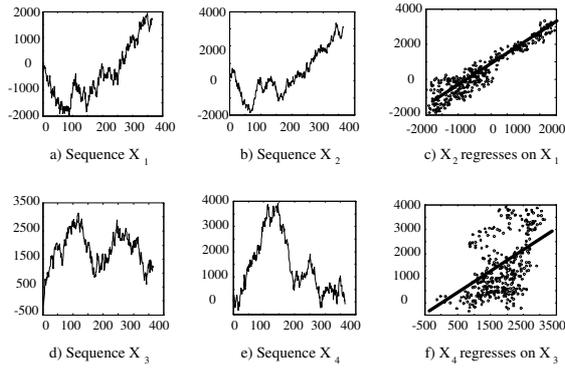
Two sets of features are listed in [6], including 91 features altogether. Different research groups propose different features. Unfortunately, most of them are not consistent [2].

According to our experience, one of the most reliable feature is the *shape* of the signature. The next reliable feature is the *speed* of writing. Due to lack of benchmark databases for on-line signatures, we will not argue the consistency of these features here but propose a novel similarity measure for signature verification.

Given two signatures to compare, it is natural to ask "how similar are they?" or "what is their similarity?". It is intuitive to answer the similarity with a value between 0%-100% and this value should make sense. For example, when we quantize the similarity of two signatures as 90%, they should be very close to each other objectively, even it is subjective to say how similar they are.

No matter what kind of features are extracted, such a similarity measure is unavoidable. Euclidean distance, DTW (Dynamic Time Warping) or other distances are of relative meaning. That is, the distance itself cannot give us any information about similarity without comparing it with other distances. We observed that  $R^2$  is a good similarity measure with intuitive meaning [1]. Given two sequences,  $R^2$  answers the similarity with a value between 0%-100%. This kind of similarity measure is very useful for signature verification, especially noting that only few genuine signatures are available in practice. However,  $R^2$  comes from SLR (Simple Linear Regression) which traditionally measures two 1-dimensional sequences. In this paper, extend  $R^2$  is extended to  $ER^2$  for multidimensional sequence matching. Also, the optimal alignment by DTW (Dynamic Time Warping) is coupled into  $ER^2$  to enhance robustness on signature verification.

The rest of paper is organized as follows. After §1 introduction, we first provide the background of SLR and  $R^2$  in §2. Then, we extend 1-dimensional  $R^2$  to multidimensional  $ER^2$  in §3. In §4, we combine DTW and  $ER^2$  together for signature verification. §5 evaluates the performance of  $ER^2$ . Finally, §6 draws conclusion and states future work.



**Figure 1. Two pairs of sequences.**  $R^2(X_1, X_2) = 0.91(91\%)$  and  $R^2(X_3, X_4) = 0.31(31\%)$ .  $X_1$  and  $X_2$  have high similarity (linearity) because the points in c) are distributed along a line.  $X_3$  and  $X_4$  have low similarity with scattered distribution in f).

## 2. Simple Linear Regression Background

Given two sequences  $X = (x_1, x_2, \dots, x_n)$ ,  $Y = (y_1, y_2, \dots, y_n)$ , linear regression statistically analyses the distribution of points  $(x_1, y_1), (x_2, y_2), \dots, (x_n, y_n)$  in the  $X$ - $Y$  space. If  $X$  and  $Y$  has strong linear relation, i.e.,  $Y \approx \beta_0 + \beta_1 X$ , we can expect the distribution of these points is along a line, called the *regression line*. Fig. 1 shows examples.

To regress sequence  $Y$  on  $X$ , we first establish a *model*:  $Y = \beta_0 + \beta_1 X + u$ , where  $u$  is the *error term*. Note that  $u = (u_1, u_2, \dots, u_n)$ . Then we estimate the parameter  $\beta_0$  and  $\beta_1$  in the sense of minimum-sum-of squared-error, i.e.,  $\sum_{i=1}^n u_i^2 = \sum_{i=1}^n (y_i - (\beta_0 + \beta_1 x_i))^2$  is minimized. From a geometric point of view, we estimate the regression line which is determined by  $\beta_0$  and  $\beta_1$  so that the line fits the points in the  $X$ - $Y$  space as close as possible. Let  $Q(\beta_0, \beta_1) = \sum_{i=1}^n u_i^2$ . Note that  $Q$  is a function of  $\beta_0$  and  $\beta_1$ . To minimize  $Q(\beta_0, \beta_1)$ , we have  $\frac{\partial Q}{\partial \beta_0} = 0$  and  $\frac{\partial Q}{\partial \beta_1} = 0$ . Starting from this, we can obtain the following results [8]:

$$\beta_0 = \bar{Y} - \beta_1 \bar{X} \quad (1)$$

and

$$\beta_1 = \frac{\sum_{i=1}^n (x_i - \bar{X})(y_i - \bar{Y})}{\sum_{i=1}^n (x_i - \bar{X})^2} \quad (2)$$

where  $\bar{X} = \frac{1}{n} \sum_{i=1}^n (x_i)$ ,  $\bar{Y} = \frac{1}{n} \sum_{i=1}^n (y_i)$ .

With  $\beta_0$  and  $\beta_1$  as above, the regression line is determined. There remains a question: how well the regression line fits the points in the  $X$ - $Y$  space? As a measure of the

goodness-of-fit, *R-squared* is defined as:

$$R^2 = 1 - \frac{\sum_{i=1}^n u_i^2}{\sum_{i=1}^n (y_i - \bar{Y})^2} \quad (3)$$

*R-squared* is also called the *coefficient of determination*. It can be interpreted as the *fraction of the variation in  $Y$  that is explained by  $X$* . *R-squared* can be further derived as:

$$R^2 = \frac{[\sum_{i=1}^n (x_i - \bar{X})(y_i - \bar{Y})]^2}{\sum_{i=1}^n (x_i - \bar{X})^2 \sum_{i=1}^n (y_i - \bar{Y})^2} \quad (4)$$

$R^2$  has following properties:

- **Reflexivity**, i.e.,  $R^2(X, X) = 1$ .
- **Symmetry**, i.e.,  $R^2(X, Y) = R^2(Y, X)$ . According to equation (4), no matter  $Y$  regresses on  $X$  or  $X$  regresses on  $Y$ ,  $R^2$  is the same.
- $R^2 \in [0, 1]$ . The closer the value to 1, the more the points tend to fall along the regression line, thus, the stronger linear relation the two sequences have.  $R^2 = 1$  means the two sequences have perfect linear relation, while  $R^2 = 0$  means they have no linear relation at all.

Based on the properties of  $R^2$  as above,  $R^2$  is defined as the *confidence* of the linear relationship. Also,  $R^2$  is a good measure for similarity. Fig. 1 show examples that high (low)  $R^2$  value means high (low) similarity. Threshold based on  $R^2$  is much more intuitive than some distance tolerance  $\epsilon$ , such as Euclidean distance or DTW distance. Given two sequences,  $R^2$  directly tells their similarity.

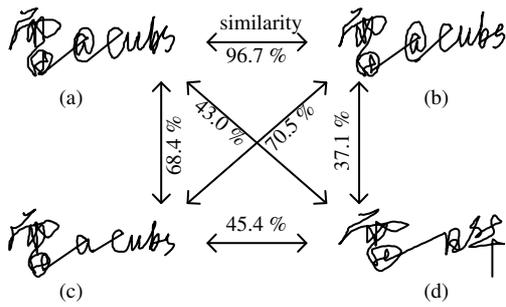
## 3. Extending $R^2$ to $ER^2$

Traditionally, SLR is only applied to 1-dimensional sequence. However, many kinds of sequences are multidimensional. For an instance, the on-line handwritten signature sequence is multidimensional, including coordinates ( $x$  and  $y$ ), pressure, inclination, etc. To match  $M$ -dimensional sequence, we define  $ER^2$  (Extended R-squared) as:

$$ER^2 = \frac{[\sum_{j=1}^M (\sum_{i=1}^n (x_{ji} - \bar{X}_j)(y_{ji} - \bar{Y}_j))]^2}{\sum_{j=1}^M \sum_{i=1}^n (x_{ji} - \bar{X}_j)^2 \sum_{j=1}^M \sum_{i=1}^n (y_{ji} - \bar{Y}_j)^2} \quad (5)$$

where  $\bar{X}_j$  ( $\bar{Y}_j$ ) is the average of the  $j$ -th dimension of sequence  $X$  ( $Y$ ).

$ER^2$  has similar properties as  $R^2$ , i.e., *reflexivity*, *symmetry* and  $ER^2 \in [0, 1]$ . The only difference is that  $ER^2$  can measure multidimensional sequences. Just like  $R^2$ ,  $ER^2$  directly tells how similar they are. In contrast, DTW or Euclidean norms can only give a distance with relative meaning.



**Figure 2. Four signatures and their similarities with each other defined by  $ER^2$ . We can see that similarity measure by  $ER^2$  is much more intuitive than the "distance", such as DTW or Euclidean distance.**

Fig. 2 shows examples that  $ER^2$  makes sense. Signature (a) and (b) are genuine signatures. Signature (c) and (d) are forgeries, although they are made by the same person. We can see that signature (a) has high similarity with signature (b). The  $ER^2$  between them is as high as 96.7%. The major difference in signature (c) is that the character "@" is replaced by "a". So, the similarity between (c) and the genuine ones drops to 68.4% or 70.5%. Signature (d) is made up of two Chinese characters. The first character is the same as other signatures while the second one is totally different from "@cubs". Therefore, its similarities with other signatures are all below 50%.

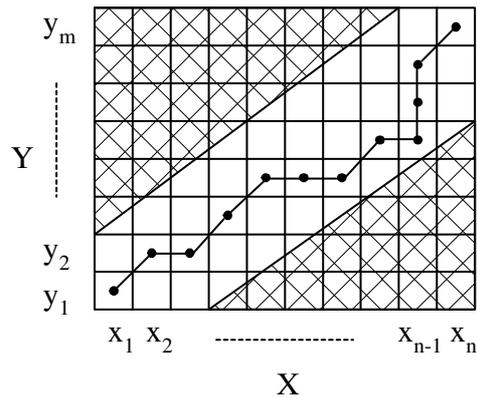
The signatures here are made up of Chinese character, English character and special symbol as "@". The examples also demonstrates that  $ER^2$  is a language-independent measure.

#### 4. Combining DTW and $ER^2$

$ER^2$  has its drawback. It only allows one-one matching between two sequences, just like the Euclidean norm. If two sequences are not aligned very well or they have different lengths,  $ER^2$  cannot be applied directly. Usually, signature sequences are neither of the same length nor aligned well, even by the same person. It is well known that DTW is able to determine the optimal alignment between two sequences with different lengths. Therefore, DTW is combined with  $ER^2$  to unify their advantages.

##### 4.1. DTW background

Given two sequences  $X = (x_1, x_2, \dots, x_n)$  and  $Y = (y_1, y_2, \dots, y_m)$ , the distance  $DTW(X, Y)$  is similar to edit distance. To calculate the DTW distance  $D(X, Y)$ , we can first construct an  $n$ -by- $m$  matrix, as shown in fig. 3. Then,



**Figure 3. The path determined by DTW in the  $n$ -by- $m$  matrix has the minimum average cumulative cost. The marked area is the constraint that path cannot go. The path indicates the optimal alignment:  $(x_1, y_1), (x_2, y_2), (x_3, y_2), \dots, (x_{n-1}, y_{m-3}), (x_{n-1}, y_{m-2}), (x_{n-1}, y_{m-1}), (x_n, y_m)$ .**

we find a *path* in the matrix which starts from cell  $(1, 1)$  to cell  $(n, m)$  so that the average cumulative cost along the path is minimized. If the path passes cell  $(i, j)$ , then the cell  $(i, j)$  contributes  $cost(x_i, y_j)$  to the cumulative cost. The *cost* function can be defined flexibly depending on the application, for example,  $cost(x_i, y_j) = |x_i - y_j|^2$ . This path can be determined using dynamic programming, because the recursive equation holds:  $D(i, j) = cost(x_i, y_j) + \min\{D(i-1, j), D(i-1, j-1), D(i, j-1)\}$ .

The path may goes several cells horizontally along  $X$  or vertically along  $Y$ , which makes the matching between the two sequences not strictly one-one but one-many and many-one. This is the robustness that DTW provides to align sequences.

##### 4.2. $ER^2$ coupled with optimal alignment

We first use DTW to determine the optimal alignment between two sequences. Then, we stretch the two sequences to have the same length. It is done like this: if point  $x_i$  in sequence  $X$  is aligned to  $k$  ( $k > 1$ ) points in sequence  $Y$ , we stretch  $X$  by duplicating  $x_i$   $k - 1$  times. For sequence  $Y$ , we stretch it in the same way. For example, in fig. 3, we stretch  $X$  to be  $(x_1, x_2, \dots, x_{n-1}, x_{n-1}, x_{n-1}, x_n)$  and  $Y$  to be  $(y_1, y_2, y_2, \dots, y_{n-2}, y_{n-1}, y_n)$ .

After stretching, the two sequences have the same length. Then, we can feel free to apply equation (5) to calculate similarity.

## 5. Experiments on on-line signature verification

Our experiments focus on this concern: *will  $ER^2$  coupled with optimal alignment improve the performance of DTW on signature verification?* Signature verification based on curve matching [4, 5] is a promising direction, because curve matching is language-independent. Segmentation-based methods [7] are dependent on languages to a large degree, since the words of some languages are complex with a lot of possible segments and the segments may be not consistent.

We assume signature verifications have two basic requirements: 1) At most 6 genuine signatures are provided and no forgeries are available for training. 2) Given signature to be verified, the output is a similarity between 0% and 100%, not just "yes/no". The decision of rejection/acceptance is left to the system operator [3]. In real applications, the requirements are reasonable. Since only few genuine signatures for enrollment, it is appropriate to use all of them as reference prototype rather than statistically generate a single prototype. When a signature is input for verification, we compare it with each of these prototypes and return the highest similarity.  $ER^2$  is a qualified similarity measure with a confidence value between 0% and 100%. Curve matching based on DTW returns a relative distance. We need to translate it to a similarity score. We briefly describe two signature verification algorithms here: 1)  $ER^2$  coupled with optimal alignment; 2) DTW-based Curve matching.

### 1). $ER^2$ coupled with optimal alignment

**Enrollment.** Given  $K$  ( $K \leq 6$ ) genuine signatures,  $Sig_i = [X_i, Y_i]$ , ( $i = 1, \dots, K$ ), we first preprocess each of them and save all of them in a template. Each signature here is a 2-dimensional sequence of  $X - Y$  coordinates. Preprocessing includes: 1) Smooth the raw sequence by Gaussian filter [3]. 2) Rotate if necessary [4]. 3) Normalize each signature  $Sig_i$  by:  $X_i = \frac{X_i - \min(X_i)}{\max(X_i) - \min(X_i)}$ , and  $Y_i = \frac{Y_i - \min(Y_i)}{\max(Y_i) - \min(Y_i)}$ .

**Matching.** Given a signature  $S = [X_s, Y_s]$ , we preprocess it in the same way as in enrollment and match it against each of the preprocessed signatures in the template. The highest similarity score is returned. Matching  $S$  with  $Sig_i$  is done as follows. First, we use a function, namely  $[dist, path] = DTW(S, Sig_i)$  to obtain the  $path$ . Note that we do not need the  $dist$  here. Second, we stretch both  $S$  and  $Sig_i$  to have the same length according to the optimal alignment

indicated by the  $path$ . Then, we calculate  $ER^2$  by equation (5).

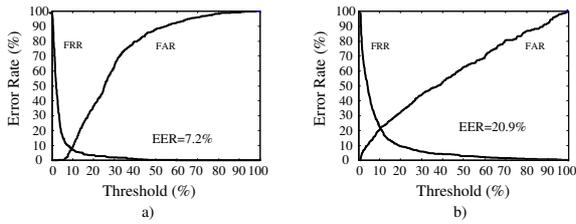
### 2). DTW-based Curve matching

**Enrollment.** Given  $K$  ( $K \leq 6$ ) genuine signatures,  $Sig_i = [X_i, Y_i]$ , ( $i = 1, \dots, K$ ), we first preprocess each of them and save all of them in a template. Preprocessing is the same as above. The additional thing we should do is to find the maximum distance between these preprocessed signatures. We need it to calculate the similarity score. We can obtain this by calculating the pairwise DTW distances within the given samples and save the maximum one (denoted as  $M_d$ ) to the template.

**Matching.** Given a signature  $S = [X_s, Y_s]$ , we preprocess it in the same way as in enrollment and match it against each of the preprocessed signatures in the template. The highest similarity score is returned. Matching  $S$  with  $Sig_i$  is done as follows. First, we use function  $[dist, path] = DTW(S, Sig_i)$  to obtain the  $dist$  (Here, we do not need the  $path$ ). Then, we translate  $dist$  to similarity score by  $exp(\frac{-dist}{2 * M_d})$ .

We can see that the only difference between above two algorithms is the similarity score mechanism. We agree that DTW is the best for curve matching with optimal alignment. Alignment is absolutely necessary, because no user writes his/her signatures exactly the same each time. There always exists some difference in the total length and overall shape. Through the experiments on signature verification, we will compare the accuracy brought by  $ER^2$  and the similarity score by the Gaussian formula as  $exp(\frac{-dist}{2 * M_d})$ . The reason we choose the Gaussian formula is that there is no better choice to directly translate DTW distance to score without statistic (recall that only few genuine samples available). In addition, we have to mention that alternative curve matching based on DTW [4] is done by  $dist = DTW(speed(S), speed(Sig_i))$ , where  $speed(S)$  transforms signature sequence  $S$  to speed sequence by  $S_i = S_{i+1} - S_i$ ,  $i = 1, \dots, length(S) - 1$ . Actually, we tried this and found the results were worse by doing so.

The experimental database we used was kindly provided by Munich etc. [4]. Each signature is a 2-dimensional sequence. Totally, 106 subjects are available. For each subject, there are 24 genuine signatures and 10 skilled forgeries. We used the first 5 signatures for enrollment and the remaining 29 signatures were used in the test with skilled forgeries. Signatures from different subjects including genuine or skilled ones were considered as random forgeries.



**Figure 4. a) FRR and FAR curves by  $ER^2$ . b) FRR and FAR curves by DTW.**

**Table 1. EERs with universal/user-dependent threshold.**

|         | Skilled Forgery |             | Random Forgery |             |
|---------|-----------------|-------------|----------------|-------------|
|         | DTW             | $ER^2$      | DTW            | $ER^2$      |
| Univ. T | 20.9%           | <b>7.2%</b> | 5.7%           | <b>0.9%</b> |
| User. T | 10.8%           | <b>4.9%</b> | 1.3%           | <b>0.2%</b> |

Fig. 4 a) shows the curves of FAR (False Acceptance Rate) and FRR (False Rejection Rate) by  $ER^2$  with universal threshold varying from 0% to 100%. The EER (Equal Error Rate) is 7.2%. Fig. 4 b) shows the results by DTW also with universal threshold. The EER is 20.9%, much higher than that of  $ER^2$ .

We also tested the random forgeries. The results are summarized in table 1. No matter by universal threshold or user-dependent threshold,  $ER^2$  coupled with optimal alignment noticeably outperforms DTW-based curve matching. Please note that if dynamic features such as speed, pressure and inclinations are used to prune forgeries here, the EER is expected to decrease. In future work, we will try to incorporate dynamic features to improve performance further.

## 6. Conclusion and future work

We propose  $ER^2$  as a similarity measure for multidimensional sequence matching. Signature verification system can use  $ER^2$  coupled with optimal alignment for intuitive similarity output and higher performance as well. The experimental results are encouraging, although we have to notice that further evaluation on large and real databases is necessary.

Our future work will explore the feasibility of  $ER^2$  on dynamic features like pressure, speed, etc.

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