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Automated Epileptiform Spike Detection via Affinity Propagation-Based Template Matching

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Abstract

Interictal epileptiform spikes are the key diagnostic biomarkers for epilepsy. The clinical gold standard of spike detection is visual inspection performed by neurologists. This is a tedious, time-consuming, and expert-centered process. The development of automated spike detection systems is necessary in order to provide a faster and more reliable diagnosis of epilepsy. In this paper, we propose an efficient template matching spike detector based on a combination of spike and background waveform templates. We generate a template library by clustering a collection of spikes and background waveforms extracted from a database of 50 patients with epilepsy. We benchmark the performance of five clustering techniques based on the receiver operating characteristic (ROC) curves. In addition, background templates are integrated with existing spike templates to improve the overall performance. The affinity propagation-based template matching system with a combination of spike and background templates is shown to outperform the other four conventional methods with the highest area-under-curve (AUC) of 0.953.

I. INTRODUCTION

Epilepsy refers to a group of chronic brain disorders which are characterized by unpredictable seizures. It is rated as the fourth most common neurological disorder by the Epilepsy Foundation [1]. Approximately 65 million people are affected worldwide [2]. An electroencephalogram (EEG) is a recording of the electrical activity of the brain collected by placing electrodes on the scalp of subjects. Interictal epileptiform discharges (IEDs) that appear in the EEG are distinctive biomarkers of epilepsy. IEDs are further categorized into sharp waves, spikes, spike-wave-complexes, and polyspike-wave-complexes [3]. We primarily focus on spikes in this research. The presence of spikes allows a physician to make a confident diagnosis of epilepsy, predict seizure recurrence, and prescribe an appropriate treatment. In current clinical practice, spikes have to be visually identified by neurologists. This process is tedious and time-consuming. Moreover, there is significant disagreement over EEG interpretation amongst experts [4]. Spike detection is a difficult task as the spikes exhibit a large morphological variety across patients. In addition, a standard definition of spikes is not available [5]. Consequently, the reliability of the diagnosis heavily depends on

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the experience and expertise of experts. There exists a great need for automated spike detection systems. Automated spike detection would be objective, faster, and potentially more accurate [6]. Several methods [7] have been tested to develop reliable automated spike detection systems. Unfortunately, these methods have not been validated on a sizable dataset and consequently are not universally accepted.

Today, fast and efficient template matching systems [8] are available that can solve the problem of processing delays in the diagnostic process. The efficiency of a template matching system primarily depends on the quality of the template library. In order to establish effective spike template libraries, we apply various clustering techniques on the database of spikes extracted from the 50 patients. In this paper, we investigate five different clustering techniques to extract a template library, namely, K-means clustering [9], K-medoids clustering [10], fuzzy C-means clustering [11], agglomerative clustering [12], and affinity propagation [13]. These algorithms have been investigated for grouping epileptiform spikes [14]–[18]. With the libraries, we develop and benchmark five template-based spike detection systems on 50 patients with epilepsy. The ROC curves and the AUC values are computed to evaluate the performance of each system. We also demonstrate an optimization of the system based on a combination of spike templates with a set of background or non-spike templates. The system based on the combined set of templates produced by affinity propagation is proved to be the best template matching system with an AUC value of 0.953.

In Section II, we describe the analyzed patient data and the various methods implemented in this study. In Section III, we illustrate and discuss our results for spike detection systems. In Section IV, we conclude our work and elaborate on the future scope of the study.

II. Methods

A. Scalp EEG

In this study, we analyze 30-minute EEG recordings of 50 patients with epilepsy. The data was acquired at the Massachusetts General Hospital (MGH), Boston, according to the standard 10–20 electrode placement system. The data is down-sampled at 128 Hz and the common average reference (CAR) montage is applied. A notch filter of 60 Hz is applied to remove the power-line interference and a high-pass filter of 1 Hz is applied to remove the baseline drifts. The epileptiform spikes are cross-annotated by two neurologists. A total of 8,929 spikes with a duration of 500 milliseconds (64 samples) each are extracted for the analysis. The remaining EEG portions including the artifacts are considered as background data. The background waveforms are extracted at 500 milliseconds with an overlap of 75%. The spike duplicates in the neighboring channels are removed from the EEG data before extracting background waveforms.

B. Spike clustering

We propose a template matching system for fast and reliable spike detection, as illustrated in Fig. 1. The performance of the template matching systems heavily relies on the quality of templates. We identify spike templates by clustering the MGH spike database. We explore five clustering techniques. Next the template libraries are employed as lookup tables for classifying new waveforms according to a set of decision rules.

C. Clustering techniques

We investigate five different clustering algorithms: K-means clustering [9], K-medoids clustering [10], fuzzy C-means clustering [11], agglomerative clustering [12], and affinity propagation [13].

K-means clustering is a traditional clustering algorithm in which the data points are grouped into a specified number of clusters by minimizing the inertia or the sum of squares within clusters [9]. The objective function is given by:

$$J=\sum_{i=1}^{N}\sum_{j=1}^{K}\|x_j-c_i\|^2, \quad (1)$$

where K is the number of clusters, N is the number of data points, c_i is the cluster center, and $\|x_j - c_i\|^2$ is the distance between the data point x_j and c_i. Initially, the set of cluster centers is chosen randomly. This set is updated repeatedly till the squared error is below a specified threshold. The cluster center c_i is determined as the mean of the data points in that particular cluster. The main drawback of the algorithm is the need to declare the number of clusters K, which is unknown in many applications, a priori. Moreover, random initialization can lead to distinct outcomes. The K-medoids clustering algorithm is similar to K-means algorithm, where the real data points are chosen as the cluster centers.

Fuzzy C-means (FCM) is a clustering algorithm which groups the observations or data points into multiple clusters with varying degrees of membership specified by an objective function [11]:

$$J_m=\sum_{i=1}^{N}\sum_{j=1}^{K}\mu_{ij}^{m}\|x_i-c_j\|^2, \quad (2)$$

where N is the number of data points, K is the number of clusters, m is the fuzzy partition matrix exponent for controlling degree of fuzzy overlap (with m>1), x_i is the i^{th} data point, c_j is the center of the j^{th} cluster, and μ_{ij} is the degree of membership of x_i in the j^{th} cluster. For a given data point x_i, the sum of membership values for all clusters is one. In our implementation, the value of m is set to 2, the maximum number of iterations is set to 100, and the minimum improvement in J_m between two consecutive iterations is set as 10^{-5}. At convergence, each data point is assigned to the cluster having the highest membership value. Any remaining empty cluster is discarded.

Agglomerative clustering is a bottom-up hierarchical clustering approach. Each data point starts as an individual cluster. Next the closest clusters are merged together until the pre-specified number of clusters is achieved. We apply Ward's linkage criterion [19]. The cluster center is chosen as the mean.

Affinity propagation is a clustering method based on an exchange of real-valued messages between the data points [13]. The inputs to the algorithm are the pairwise similarities between the data points and the initial priorities. Unlike the traditional algorithms, affinity propagation algorithm estimates the number of clusters based on the input similarity and priority values. There are two types of messages exchanged between the data points: responsibility and availability [13]. Let $s(i, j)$ be the similarity value between data points i and j. Then the responsibilities are updated as:

$$r(i,k) \leftarrow s(i,k) - \max_{k' s.t. k' \neq k} \{a(i,k') + s(i,k')\}. \quad (3)$$

The availabilities are updated as:

$$a(i,k) \leftarrow \min \left\{ 0, r(k,k) + \sum_{i' s.t. i' \notin \{i,k\}} \max\{0, r(i',k)\} \right\}. \quad (4)$$

The algorithm iteratively updates the messages until the convergence criterion is satisfied or until it exceeds a specified number of iterations. At any iteration, for a point i, the value of k which maximizes the sum of responsibility and availability, $a(i,k) + r(i,k)$, is chosen as the cluster center for i. In addition, a damping factor λ is introduced to prevent oscillations. The initial priorities are set to the median of the similarity values and λ is set as 0.9.

D. Approach

After data extraction from the original EEG, each spike waveform is z-normalized by subtracting the mean and dividing by its standard deviation [20]. Affinity propagation is applied on the spike database with the negative of Euclidean distance as the similarity measure. Next we evaluate the other four clustering algorithms with the same number of clusters, K, as identified by affinity propagation. The entire flow chart of proposed steps is illustrated in Fig. 2. In traditional template matching systems, only the templates of the patterns of interest are employed. In other words, only spike templates are employed in conventional template-based spike detectors. Here, we apply a combination of spike and background templates, as illustrated in Fig. 3.

We apply the same clustering system on a subset of background waveforms to generate the templates. We maintain the spike to background ratio as 1:1 for training and 1:5 for testing. The final decision is based on similarity with the combined set of templates according to certain decision-making rules: Consider a waveform x to be classified. Let S_t and B_t be the spike and background template sets, respectively. The decision rules for each system is described in Table I.

Decision rule 1 is the traditional template matching rule, based purely on the spike templates. In decision rules 2 and 3, we incorporate the background templates. In rule 2, the distance from the background templates is integrated as an additive term, whereas in rule 3, the distance is integrated as a decremental term. In both cases, integration of the background templates is intended to improve the classification performance. Here α and β are the weight parameters and $d(x,S_t)$ is the Euclidean distances between the given waveform and the spike templates. We set α to 1 and β to 0.5 in our analysis. We develop three different systems based on the decision rules. Each of the clustering techniques is tested with the different systems. The different systems are evaluated based on their AUC values. A five-fold cross-validation is performed with 40 patients for extracting the templates and 10 patients for testing the template matching system. The performance values are averaged over the different folds.

III. Results

The template libraries were developed using five different clustering algorithms. For fairness, the number of clusters, K, was set to a common value determined by affinity propagation. Each clustering algorithm was evaluated with three decision-making systems utilizing both spike and background templates. Their performance was evaluated based on the AUC values as detailed in Table II. Affinity propagation exhibits superior AUC values in all three decision-making systems. This corroborates with [18], where affinity propagation is proved to be effective in clustering spikes based on mean squared error values. Moreover, affinity propagation has an added advantage that the number of clusters is estimated by the algorithm according to the density of the data.

The AUC shows better values for system 2 and system 3 in comparison with system 1 for all the techniques, except fuzzy C-means clustering. This is mainly attributed to the empty clusters being discarded while assigning each data point to the clusters with the highest membership value. This proves the effectiveness of integrating background templates in the template matching system. Moreover, the AUC values of system 3 are superior to the other two systems. The corresponding ROC curves are illustrated in Fig. 4. In addition, the different performance indices, namely, specificity, balanced accuracy (BAC), precision, and F1-score are evaluated for the three different systems based on affinity propagation templates by keeping the sensitivity threshold at 90% (see Fig. 5). From this figure, we conclude that the system based on decision rule 3 is superior to the other two. The affinity propagation-based system with decision rule 3 is shown to be the better spike detector system. In the current system, the decision rule is based on the minimum distance considering all the templates. This might deteriorate the system performance in the presence of a low-quality template. Also, the precision is in the acceptable range (.668), which is mainly attributed to the unbalanced dataset. Similar studies have been presented in [17], [21]. Lodder et al. implemented a spike detector based on a set of smart spike templates [21]. Here the system is only validated on a set of 241 IEDs, even though it is reported to perform with a sensitivity of 92%. Nonclercq et al. presented an adapted spike detection system based on temporal clustering [17]. This study is validated only with 3 patients with a spike count of 2,500. In our study, we have presented a system based on the combination of spike and background templates. Moreover, the system is validated on a sizable database with a spike count of 8,929. Our system is shown to have comparable performance with recent deep leaning-based spike detector (AUC=0.947) [22].

IV. CONCLUSIONS

In this study, we have demonstrated the importance of background templates in spike detection systems based on template matching. We have also evaluated the performance of various clustering techniques for sorting interictal epileptiform events. Affinity propagation has been proved to outperform the other four conventional clustering methods. The combination of affinity propagation with decision rule three is shown to be the best template-based spike detection system.

In our future work, we intend to incorporate template ranking schemes in order to solve the low-quality template problem. The clustering system will be optimized by adjusting the affinity propagation algorithm parameters and the weight parameters (α and β) of the decision rules. Also, in order to improve the precision, we plan to incorporate a simple background rejection module prior to the template matching system.

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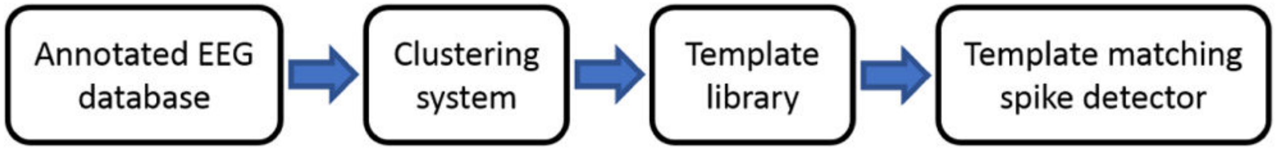

Fig. 1.

The block diagram of the proposed spike detection system implementation.

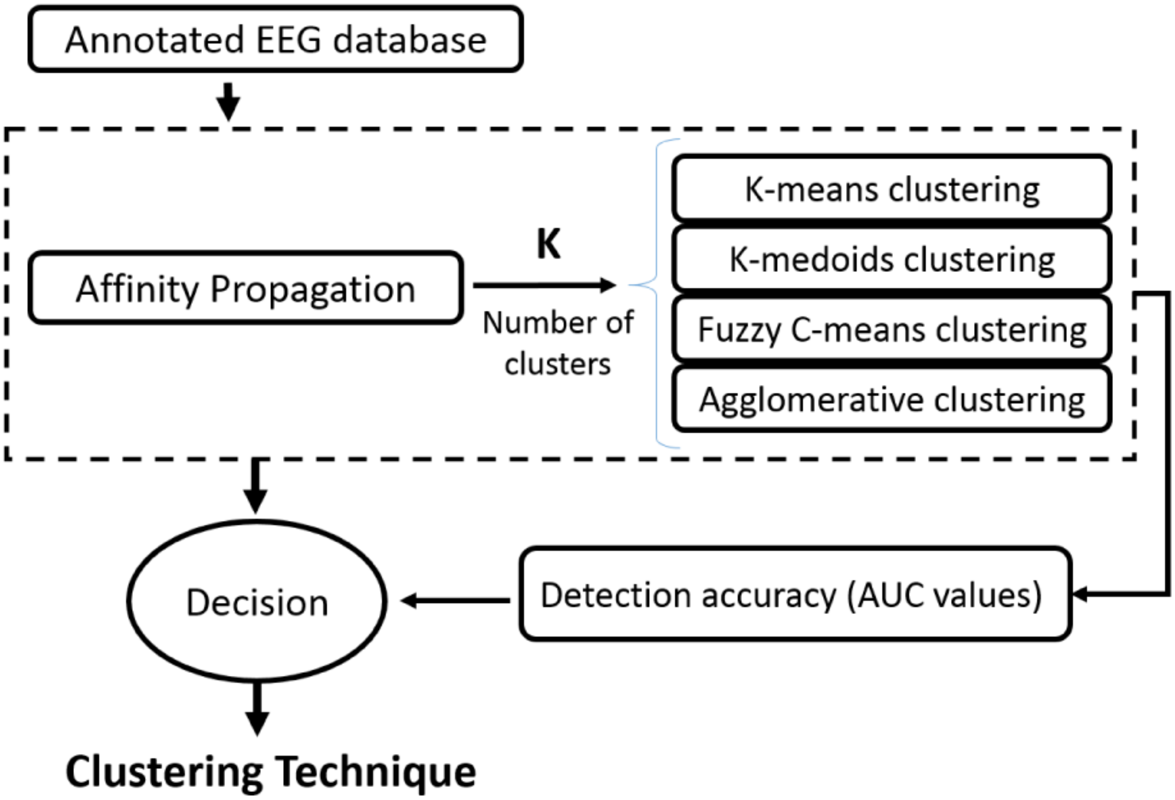

Fig. 2.
The steps for the selection of the appropriate clustering technique.

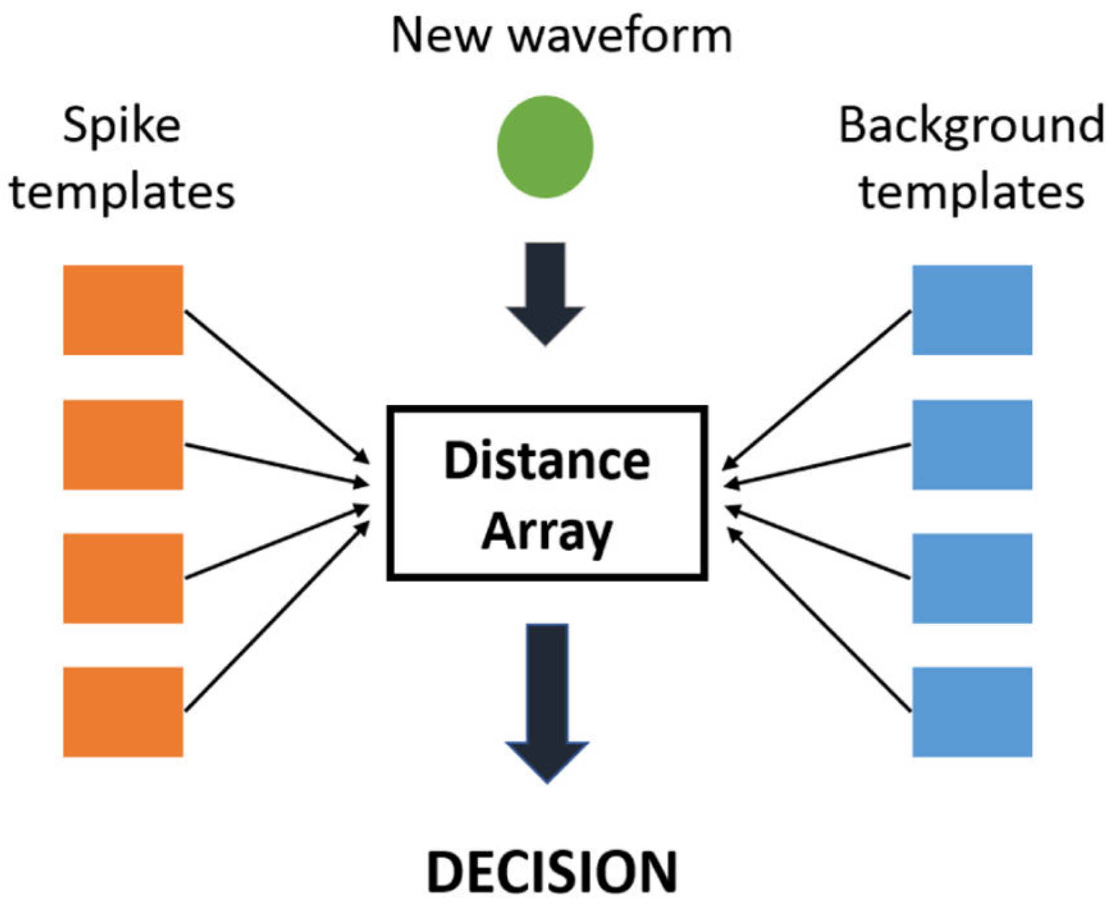

Fig. 3.
The basic structure of the proposed template matching system. Background templates are integrated to improve the detection accuracy.

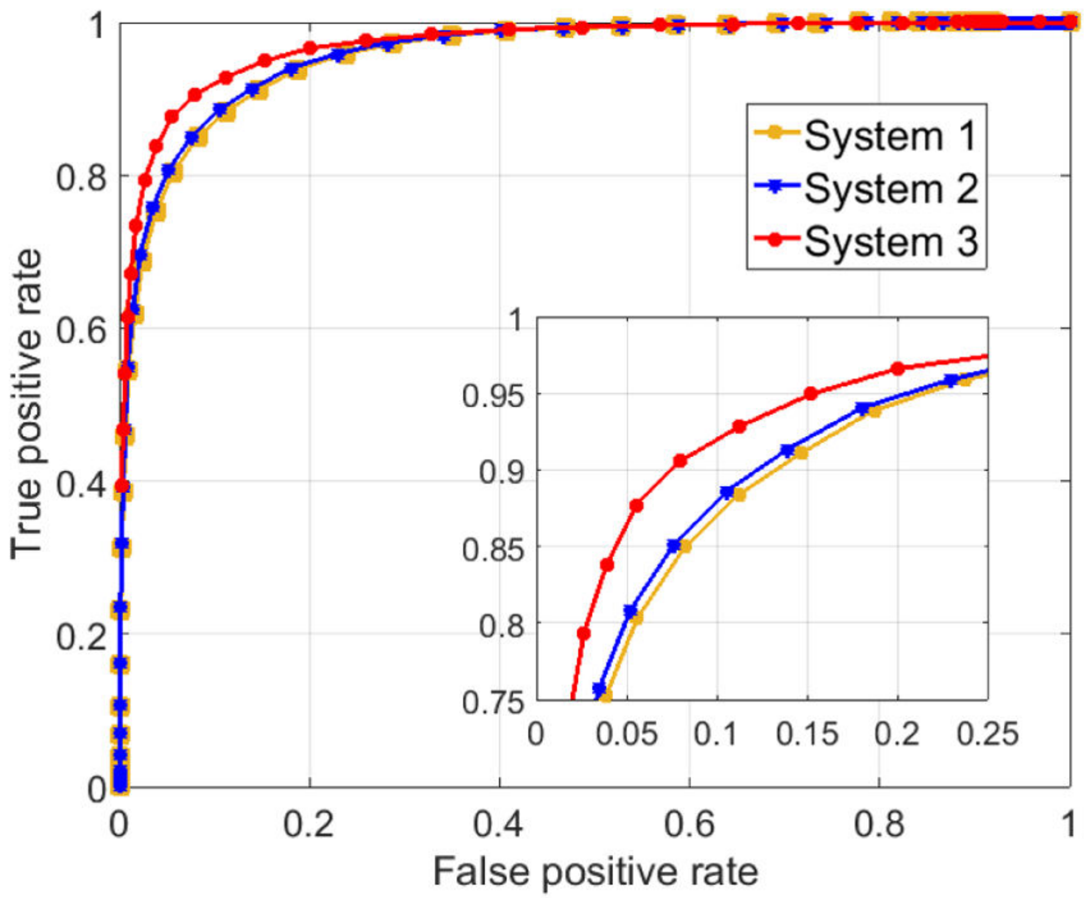

Fig. 4.

The ROC curves for the three different systems with the template library based on affinity propagation.

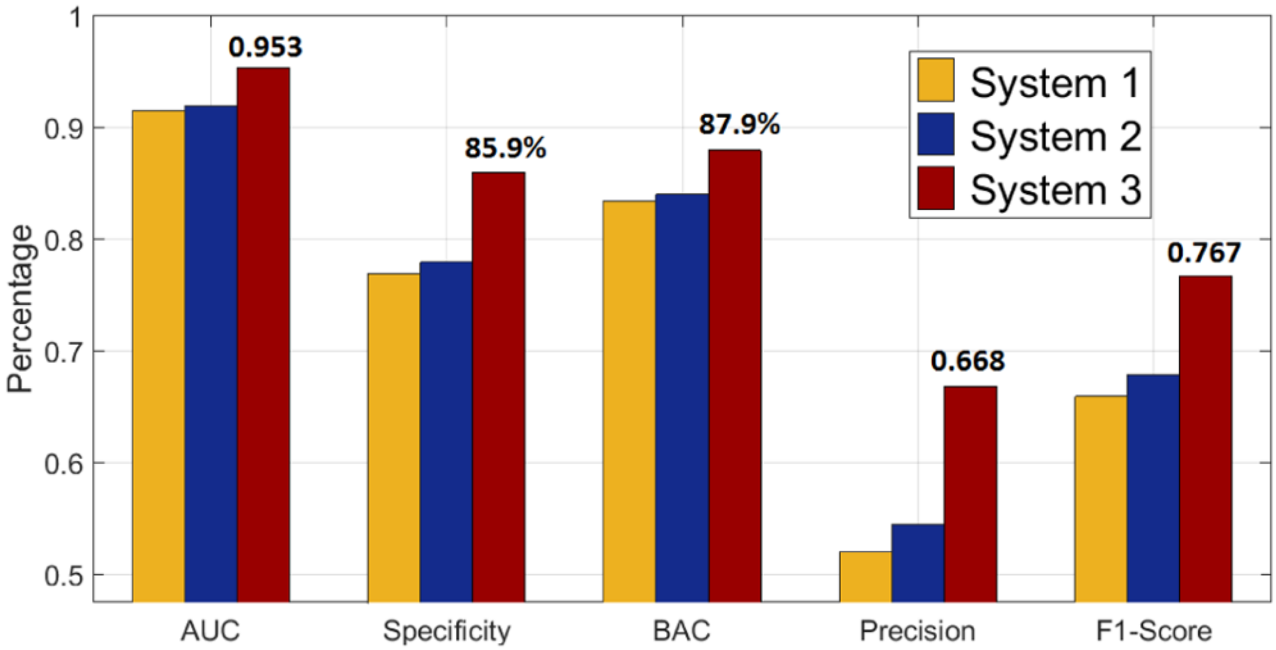

Fig. 5.

The traditional performance indices for the three different systems with affinity propagation-based template library. The specificity, balanced accuracy (BAC), precision, and F1-score are evaluated for the sensitivity threshold of 90%.

TABLE I

Decision rules for the different template matching systems

Decision rule 1	$\min\{d(x,S_t)\}$
Decision rule 2	$\min\{d(x,S_t)\}+\frac{\alpha}{\min\{d(x,B_t)\}}$
Decision rule 3	$\min\{d(x,S_t)\} - \beta \times \min\{d(x, B_t)\}$

TABLE II

5-fold cross-validation testing results for different systems with the three decision rules

Clustering technique	Mean AUC values		
	System 1	System 2	System 3
K-mean clustering	0.908	0.912	0.943
K-medoids clustering	0.912	0.916	0.947
Agglomerative clustering	0.912	0.915	0.947
Fuzzy C-means clustering	0.892	0.893	0.887
Affinity propagation	0.914	0.919	0.953