Review On: GAIT Recognition Technique using SVM and K-MEANS with Gait PAL and PAL Entropy

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Abstract- **Gait recognition is one kind of biometric technology that can be used to monitor people without their cooperation. Controlled environments such as banks, military installations and even airports need to be able to quickly detect threats and provide differing levels of access to different user groups. This paper proposed new method for gait recognition using K-means with Gait PAL and PAL Entropy. In this method, firstly binary silhouette of a walking person is detected from each frame. Secondly, feature from each frame is extracted using image processing operation. Here height, length of hand, length of leg, distance between left hand and right leg and distance between right hand and left leg are talking as key feature. At last SVM is used for training and testing purpose. We have created different model of neural network based on hidden layer, selection of training algorithm and setting the different parameter for training. Here all experiments are done on gait database. Different groups of training and testing dataset give different results.**

Keywords:- Gait Recognition, biometric system, PCA, k-means, Gait PAL and PAL Entropy and SVM

I. INTRODUCTION

Recognition of an individual is an important task to identify people. Identification through biometric is a better way because it associate with individual not with information passing from one place to another. Biometrics is a physiological or behavioral characteristic, which can be used to identify and verify the identity of an individual. There are numerous biometric measures which can be used to help derive an individual identity. They are physiological, like fingerprints, face recognition, iris-scans and hand scans and behavioral, like keystroke-scan and speech patterns. The appearance based method can be also subdivided in two types; state space methods and spatial-temporal methods. Biometric gait recognition refers to verifying or identifying persons using their walking style. Human recognition based on gait is relatively recent compared to other biometric approaches such as fingerprint, iris, facial etc. The wearable sensors and floor sensors systems are also able to identify persons but in different conditions compared to motion vision technique. The wearable sensors technique needs to carry necessary sensors which enable to measure the different walk styles. The sensors can be set on any part of the body according to the sensors characteristics to get gait data to match up with training dataset. The sensors may be set up on hip, legs, arms or other parts of the body [1,3].

The floor sensors are put into the floor or on the floor which enable to detect the required measurement. The most important point is to match up testing dataset with training dataset to identify the subjects. Both systems are useful for access control such as office, airport, mega mall and other restricted places. Motion vision can be used for surveillance, access control, detection and other monitoring purposes. The most important advantage is that person walking image can be captured from long distance and the image is then processed with low resolutions. In this paper, we focus on two different techniques Principle Component Analysis (PCA) only and PCA with radon transform (RT) on machine vision for gait recognition purposes [5,7].

II. GAIT RECOGNITION

Gait recognition is relatively new biometric identification technology which aims to identify people at a distance by the way they walk. It has the advantage of being unobtrusive, difficult to conceal, non invasive and effective from a distance. Human gait recognition as a new biometric aimed to recognize person via the style of people walking, which contain the physiological or behavioral characteristics of human. Gait recognition system can be classified depending on the sensors used into three groups namely; motion vision based, wearable sensor based and floor sensor based. The motion vision can be divided into two groups namely; appearance based methods and model based methods.

We use the term gait recognition to signify the identification of an individual from a video sequence of the subject walking. This does not mean that gait is limited to walking, it can also be applied to running or any means of movement on foot. Gait as a biometric can be seen as advantageous over other forms of biometric identification techniques for the following reasons:

1. Unobtrusive – the gait of a person walking can be extracted without the user knowing they are being analyzed and without any cooperation from the user in the information gathering stage unlike fingerprinting or retina scans.
2. Distance recognition – the gait of an individual can be captured at a distance unlike other biometrics such as fingerprint recognition.
3. Reduced detail – gait recognition does not require images that have been captured to be of a very high quality unlike other biometrics such as face recognition, which can be easily affected by low resolution images.
4. Difficult to conceal – the gait of an individual is difficult to disguise, by trying to do so the individual will probably appear more suspicious. With other biometric techniques such as face recognition, the individuals face can easily be altered or hidden.

In gait recognition, silhouette is defined as a region of pixels of the walking person. Silhouette extraction mainly focuses on segmenting the human body. The silhouette extraction process is shown in "Figure".
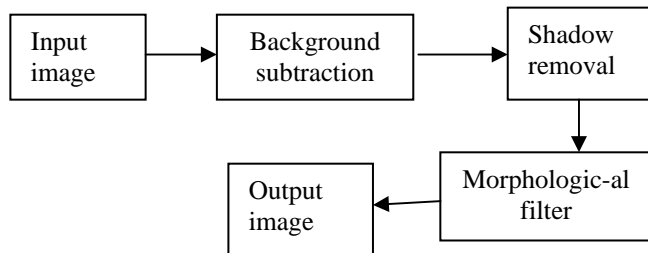

Figure 1: Silhouette extraction

Each of the frames in the image sequence is subtracted from a background model of the respective image sequence. If the pixel value of each frame is not the same with the pixel value of the background, the pixel is marked as region of silhouette [3].

To remove shadow from the difference image, a threshold value is applied to the difference images. The difference image map is first analyzed by generating the intensity histogram of the image so that the pixels distribution along the image can be represented clearly and in an effective way according to an applied threshold value. The threshold must be suitable so that the foreground image is neither under segmented nor over-segmented. Under-segmentation and over-segmentation purpose is to produce first and second reliable silhouette respectively. To remove noises produced during segmentation of silhouette, morphological filters are used. The main components of morphological filters that are used in the system are morphological opening, morphological closing and area thresholding through connected component labelling [4,5].

Model-based approaches employ models whose parameters are determined by processing of gait sequences (binary silhouettes). These methods are scale, view invariant and require good quality video sequences. In these methods, parameters used as features are the height, the distance between head and pelvis, the maximum distance between pelvis and feet and the distance between feet. In, the silhouette of a walking person is divided in to some regions (generally seven regions). Subsequently, ellipses or rectangles are fit to each region and region feature vectors are determined. This includes averages of the centroid and the aspect ratio. Holistic methods operate directly on binary silhouettes without assuming any specific model for the walking human. The contour of the silhouette is the most reasonable feature in this method. For high quality binary silhouettes, width of outer contour of the silhouette was proposed as a suitable feature. For low quality binary silhouettes, the binary silhouette may be is used as a feature.

III. SUPPORT VECTOR MACHINE

The Support Vector Machine (SVM) is a state-of-the-art classification method introduced in 1992 by Boser, Guyon, and Vapnik . The SVM classifier is widely used in bioinformatics (and other disciplines) due to its highly accurate, able to calculate and process the high-dimensional data such as gene expression and exibility in modeling diverse sources of data .SVMs belong to the general category of kernel methods. A kernel method is an algorithm that depends on the data only through dot-products. When this is the case, the dot product can be replaced by a kernel function which computes a dot product in some possibly high dimensional feature space. This has two advantages: First, the ability to generate non-linear decision boundaries using methods designed for linear classifiers. Second, the use of kernel functions allows the user to apply a classifier to data that have no obvious fixed-dimensional vector space representation. The prime example of such data in bioinformatics are sequence, either DNA or protein, and protein structure. Using SVMs effectively requires an understanding of how they work. When training an SVM the practitioner needs to make a number of decisions: how to preprocess the data, what kernel to use, and finally, setting the parameters of the SVM and the kernel [1]. Uninformed choices may result in severely reduced performance. We aim to provide the user with an intuitive understanding of these choices and provide general usage guidelines. All the examples shown were generated using the PyML machine learning environment, which focuses on kernel methods and SVMs.

A. *PRELIMINARIES: LINEAR CLASSIFIERS*

Support vector machines are an example of a linear two-class classifier. This section explains what that means. The data for a two class learning problem consists of objects labeled with one of two labels corresponding to the two classes; for convenience we assume the labels are +1 or -1. In what follows boldface x denotes a vector with components x_i. The notation x_i will denote the ith vector in a dataset, $f(x_i; y_i)g_{i=1}^n$, where y_i is the label associated with x_i. The objects x_i are called patterns or examples. We assume the examples belong to some set X. Initially we assume the examples are vectors, but once we introduce kernels this assumption will be relaxed, at which point they could be any continuous/discrete object (e.g.a protein/DNA sequence or protein structure).A key concept required for defining a linear classifier is the dot product between two vectors, also referred to as an inner product or scalar product. The vector w is known as the weight vector, and b is called the bias. Consider the case b = 0first. The set of points x such that $w^T x = 0$ are all points that are perpendicular to w and go through the origin | a line in two dimensions, a plane in three dimensions, and more generally, a hyper plane [2]. The bias b translates the hyper plane away from the origin. The hyper plane fx : $f(x) = w^T x + b = 0$divides the space into two: the sign of the discriminant function f(x) denotes the side of the hyper plane a point is on. The boundary between regions classified as positive and negative is called the decision boundary of the classifier.

B. *KERNELS: FROM LINEAR TO NON-LINEAR CLASSIFIERS*
In many applications a non-linear classifier provides better accuracy. And yet, linear classifiers have advantages, one of them being that they often have simple training algorithms

that scale well with the number of examples [9, 10]. This begs the question: Can the machinery of linear classifiers be extended to generate non-linear decision boundaries? Furthermore, can we handle domains such as protein sequences or structures where a representation in a fixed dimensional vector space is not available? The naive way of making a non-linear classifier out of a linear classifier is to map our data from the input space X to a feature space F using a non-linear function.

The approach of explicitly computing non-linear features does not scale well with the number of input features: when applying the mapping from the above example the dimensionality of the feature space F is quadratic in the dimensionality of the original space. This result in a quadratic increase in memory usage for storing the features and a quadratic increase in the time required to compute the discriminant function of the classifier. This quadratic complexity is feasible for low dimensional data; but when handling gene expression data that can have thousands of dimensions, quadratic complexity in the number of dimensions is not acceptable. Kernel methods solve this issue by avoiding the step of explicitly mapping the data to a high dimensional feature-space [8].

Gaussian kernel is define as

$$K(\mathbf{x_i}, \mathbf{x_j}) = \exp(-\frac{\left\|\mathbf{x_i} - \mathbf{x_j}\right\|^2}{2\sigma^2}) \qquad (1)$$

Where k > 0 is a parameter that controls the width of Gaussian. It plays a similar role as the degree of the polynomial kernel in controlling the exibility of the resulting classifier. We saw that a linear decision boundary can be kernelized i.e. its dependence on the data is only through dot products. In order for this to be useful, the training algorithms need to be kernel able as well [6]. It turns out that a large number of machine learning algorithms can be expressed using kernels including ridge regression, the perceptron algorithm, and SVMs.

In general, the RBF kernel is a reasonable first choice. This kernel nonlinearly maps samples into a higher dimensional space so it, unlike the linear kernel, can handle the case when the relation between class labels and attributes is nonlinear. Furthermore, the linear kernel is a special case of RBF since the linear kernel with a penalty parameter ~ C has the same performance as the RBF kernel with some parameters (C;). In addition, the sigmoid kernel behaves like RBF for certain parameters. The second reason is the number of hyper parameters which influences the complexity of model selection. The polynomial kernel has more hyper parameters than the RBF kernel. There are some situations where the RBF kernel is not suitable. In particular, when the number of features is very large, one may just use the linear kernel.

C. SVM FOR UNBALANCED DATA

Many datasets encountered in bioinformatics and other areas of application are unbalanced, i.e. one class contains a lot more examples than the other. Unbalanced datasets can present a challenge when training a classifier and SVMs are no exception see [13] for a general overview of the issue. A good strategy for producing a high-accuracy classifier on imbalanced data is to classify any example as belonging to the majority class; this is called the majority-class classifier. While highly accurate under the standard measure of accuracy such a classifier is not very useful [10]. When presented with an unbalanced dataset that is not linearly separable, an SVM that follows the formulation will often produce a classifier that behaves similarly to the majority-class classifier. The crux of the problem is that the standard notion of accuracy (the success rate, or fraction of correctly classified examples) is not a good way to measure the success of a classifier applied to unbalanced data, as is evident by the fact that the majority-class classifier performs well under it.

The problem with the success rate is that it assigns equal importance to errors made on examples belonging the majority class and errors made on examples belonging to the minority class. To correct for the imbalance in the data we need to assign different costs for misclassification to each class.

CONCLUSION

Human Identification Using Gait Recognition has been proposed previously but there have been always need for better Gait Recognition Technique. The existing Human Identification Using Gait Recognition doesn't consider some important parameters like distance between hands and thus it is poor in quality. The existing Human Identification Using Gait Recognition uses BPNN or only SVM which is less accurate and more time consuming. The existing Human Identification Using Gait Recognition algorithm is costlier. Therefore propose an enhanced Human Identification Using Gait Recognition algorithm which is based on SVM (Support Vector Machine) and k-means algorithm.

And enhanced human identification using gait recognition algorithm is low cost and more accurate. Enhanced human identification using gait recognition algorithm will assures quality of result. My enhanced human identification using gait recognition algorithm is distributed and is range independent for different video images.

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