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Automatic diagnosis of neuro-degenerative diseases using gait dynamics

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ARTICLE INFO

Article history:

Received 10 November 2011

Received in revised form 27 February 2012

Accepted 21 April 2012

Available online 27 April 2012

Keywords:

Neuro-degenerative diseases

Parkinson

Huntington

Amyotrophic Lateral Sclerosis

Gait dynamics

Support vector machines

Genetic algorithm

ABSTRACT

Here an approach for the diagnosis of neuro-degenerative diseases based on gait dynamics is proposed. The proposed method uses information from a time series of stride intervals, swing intervals, stance intervals and double support intervals of stride-to-stride measures of footfall contact times using force-sensitive resistors. Different features were extracted from these time series and the best of them were selected for the diagnosis. The support vector machines using different kernels were examined for the diagnosis. The radial basis function kernel obtained the best performance for this aim. The results show that features derived from double support intervals are common effective features for the diagnosis of neuro-degenerative diseases using the gait dynamics.

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1. Introduction

Walking is a process that is controlled by the nervous system. If a part of the neural network that controls this process is damaged, this can cause to produce abnormal movement in the person having this failure [1]. So by study the walking process and the gait dynamics in normal subjects and the subjects with neurodegenerative diseases, it is possible to distinguish the type of brain abnormality of the subjects. This can help to produce automatic non-invasive method based on gait dynamics for the diagnosis of neurodegenerative diseases.

In normal subjects stride time or stride interval which is the gait cycle duration has a complex fluctuation from one stride to another one [2,3]. The dynamics of fluctuations for the people with some type of neurological disorders is altered in terms of the magnitude and also its temporal dynamics [4–7].

The gait information has been widely used for the movement studies in healthy subjects and also in subjects

with different types of diseases. Here we review some of these studies that are related to the present manuscript.

Hausdorff et al. [8] studied the stride interval time series of the gait in subjects with Huntington's disease and also the healthy elderly subjects in compared to control subjects. They computed the degree of correlation between one stride interval with previous and subsequent intervals at different time scales. Their results showed that stride interval variations are more random in subjects with Huntington's disease and in elderly subjects in compared to control subjects.

In [9], the magnitude of the stride-to-stride fluctuations and perturbations of the gait rhythm were considered in subjects with Amyotrophic Lateral Sclerosis (ALS) in compared to normal subjects. Also these parameters were studied in subjects with Parkinson's disease and Huntington's disease. They found that patients with ALS has less steady gait in compared to healthy subjects. In general stride-to-stride variability was increase in all three groups of subjects with neurological diseases in compared to healthy control subjects.

Wu and Ng [10] proposed a statistical analysis method for classification of gait cadence in subjects with ALS and normal subjects. In their approach, the probability density

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functions of gait cadence were estimated using Parzen-window method and then the Kullback–Leibler divergence was computed from them. With this method they were able to classify the stride patterns of the ALS and the control subjects with the rate of 82.8%. In another similar study [11], using the swing-interval turns count parameter and the average stride interval could reach to the classification rate of 89.66% for the gaits in subjects with ALS and gaits in healthy control subjects.

The information about the gait dynamics can be measured using different type of systems. The simplest system is to use the footswitches and one type of the footswitches is applying the force sensitive resistor switches placed underneath each foot to measure the footfall contact times. Other types of measurement systems have been proposed for the human motion analysis. A new generation of motion analysis systems is based on inertial and magnetic sensors. An example of these systems has been proposed recently by Cutti and his colleagues [12] for ambulatory measurement of shoulder and elbow kinematics.

Recently Liu et al. [13] presented a wearable sensor system for analyzing the gait information. Their system uses the inertial sensors of gyroscopes and accelerometers. This system is inexpensive in compared to conventional 3D motion analysis systems that use high-speed cameras.

Previous evidences show that it is possible to extract features from the gait dynamics to be used for the diagnosis of neurological disorders. The aim of this paper is to present a new approach for automatic diagnosis of neuro-degenerative diseases in a non-invasive manner.

The rest of this manuscript has been organized in the following form: The next section describes the proposed method. This is including the feature extraction, feature selection and the classification modules. Section 3 presents the experimental results and the conclusions are given in the section 4.

2. Method

The simplest way to measure the gait dynamics and extracting temporal parameters of the gait are the footswitches [18]. Different types of footswitches are available commercially [19] or they can be build-in house [20]. The system here for collecting the gait information is a build-in house system [20] that uses the force sensitive resistor switches from the Noraxon (<http://www.noraxon.com>).

The aim here is to propose an automatic system for the diagnosis of neuro-degenerative diseases using the information from the gait dynamics. The proposed system measures the raw data using force-sensitive resistors which is approximately corresponding to the force under the foot. Several time series data are created from these force measurements for the left and right foot. We then extract some features from each time series as our feature vectors for the diagnosis of neuro-degenerative diseases. Not all of these features are important for the diagnosis, so we use a feature selection strategy to create a subset of features that can be more involved in the diagnosis. The selected features are then fed to a classifier in which can distinguish

the healthy group from the group of subjects with the neuro-degenerative diseases. The outline of the proposed method has been shown in Fig. 1.

2.1. Feature extraction

For each time series explained in the previous section, we extracted some features to create our feature vectors for the diagnosis. Four different features were extracted from each time series data. These are the minimum, maximum, average and the standard deviation of each sequence. These features were extracted for the left and right stride interval, left and right swing interval, left and right stance interval and double support interval creating a feature vector of 28 dimensions for each subject in the database.

2.2. Feature selection

As mentioned before not all features extracted from the previous section contribute in the diagnosis of neuro-degenerative diseases. To reduce the number of features and also discovering those features that have more contribution in the diagnosis, we used a feature selection approach. To this aim, we used a genetic algorithm (GA) [14,15] to select those features that create higher accuracy in the classification. In GA populations of strings that are called chromosomes are created in which each individual chromosome can take a binary value of 0 or 1. The initial populations are created randomly and according to a fitness function they generate new chromosomes that have higher score in terms of this function. In our application, the value of 0 in a population indicates that the feature dimension associate to that should not be selected and the value of 1 means that this feature dimension is important for the task on hand and has to be selected. To create new generations from the old ones (parents), several stochastic approaches are used namely the crossover and the mutation operators. In crossover operation, a pair of parents is selected from the population and they are combined to create a child. The child is evaluated according to the fitness function and if it has a higher score than its parent, it will be added to the population for the next generations. The mutation operator instead takes just one single string of chromosome and it randomly changes one of its bits. The fitness function we used in our application is the accuracy of the diagnosis of a neuro-degenerative disease. This was calculated using a support vector classifier. We explain the support vector classifier in the next section.

2.3. Classification

The support vector machines (SVMs) is a very successful class of classifiers which it has been used extensively in the literature. It was proposed by Vapnik [16] for the first time. In its original form it can classify the data in two classes but there are several approaches which can extend the SVMs to be used for multi-class classification. For two class problem, the SVM tries to maximize the margin between the hyper-plane and the closest points to the hyper-plane which are called the support vectors. This is normally done

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