

# Motor Symptoms Detection and Analysis for Parkinson's and Huntington's Disease by Hidden Markov Model based Activity Detection

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## Abstract

In this project we try to detect and analyze the motor symptoms present in the Parkinson's (PD) and Huntington's (HD) disease individuals and segregate them from the normal cohort using Hidden Markov Model (HMM) based activity recognition. PD and HD are neurological disorders that affects physical motor skills and cognitive abilities of the subject. Motion which is either rhythmic or erratic is inherent in both the diseases. To analyze the motion in PD and HD subjects, the use of wearable sensors, especially the accelerometer sensors which measures the acceleration in various axes has increased. Hence, our aim is to perform triaxial accelerometer based motion analysis of PD and HD subjects. The motor symptoms that we are analyzing in HD is gait and in PD is at rest tremor. In the first part we try to come up with features by manually locating the durations of movement (walk) and non-movement (sit). We come up with cross-correlation of leg sensors and auto-correlation of chest sensor as features characterizing the lack of co-ordination and step duration variation in HD. We also came up with spectrum analysis to characterize the tremor in PD. In particular, we use HMM based activity recognition to recognize the durations of movement and non-movement. The movement duration data is used to analyze the gait in HD and non-movement duration data can be used for analyzing tremor in PD. Next, we try to automate the process of activity duration selection by using HMM based activity recognition. Experimental results for preliminary analysis to come up with features are promising and the HMM results on the in-clinic data which has labels for test durations show a good accuracy. However, the extending the same set of features for HMM based activity recognition has not worked well.

## 1 Introduction

Parkinson's disease (PD) is a progressive neurological disorder characterized by tremor, rigidity and freeze of gait episodes [12]. In order to rate the severity of the disease, in-clinic tests are conducted on the PD patient and rated using Unified Parkinson's Disease Rating Scale (UPDRS) [6]. In US, a million people are suffering form PD with debilitation in the quality of life [11]. Huntington's disease (HD), apart from being progressive neurological disorder, is also an inherited disease marked by jerky movements in the body referred as chorea, unsteady gait and cognitive impairments [8]. To rate the severity, as in case of PD, several in-clinic tests are conducted and rated using Unified Huntington's Disease Rating Scale (UHDRS) [3]. Around 30k people in US are suffering from HD with degradation in quality of life much severe when compared to PD [9]. The motor symptoms that we are analyzing, particularly, is gait in HD and at rest tremor in PD. The UPDRS and UHDRS rating scales, which rate the severity of the disease are based on short duration in-clinic assessment and are subjective in nature as rating is given by physician conducting the test on patients. Hence the temporal progression of the disease cannot be captured by the rating scale assessments. Among the alternatives present, utilization of wearable sensors has emerged as attractive alternative as the data obtained is objective and can track longitudinal progression of the disease [7]. Hence in this project, initially, we utilize the accelerometer data to come up with features to differentiate the PD and HD subjects from control by manually picking durations of activity (movement for gait analysis and non-movement for tremor analysis) followed by use of HMM

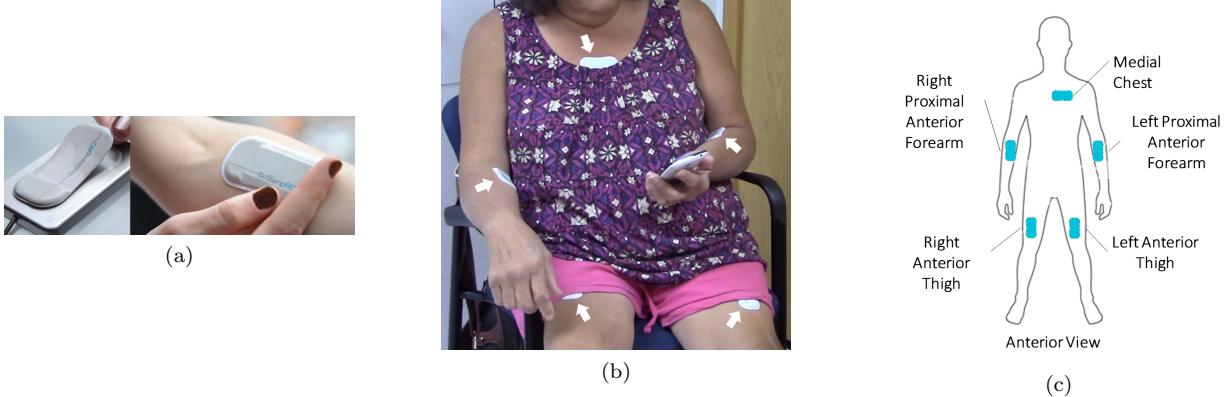


Figure 1: (a) BioStampRC sensor from MC10.Inc (b) Subject wearing the sensors in 5 different locations of body (c) Graphics showing the sensor placement locations on the body

to automatically detect the activity duration and use the features to differentiate between HD and PD subjects from controls.

The sensors we are using called BioStampRC sensors, a product from MC10.Inc [1], are light weight, body affixable sensors which can be worn like a tattoo on our body as shown in Fig. 1a. The sensors consume low power and have long recording abilities. Table 1 [1] shows that the sensors are multi-modal in nature with various modalities such as accelerometer, ECG, EMG, gyroscope and combinations of these. Various modalities also have varied sampling rates, dynamic range and recording times. Since we are analyzing motor symptoms we use accelerometer and hence the data that we obtain is the tri-axial accelerometer data with a sampling rate of 31.25 Hz and 40-45 hours recordings. 16 PD, 10 HD and 15 Controls were recruited for the study. Fig. 1b and Fig. 1c shows the locations of the body where sensors are placed for the study. Hence it is a multi sensor study which is advantageous because we can utilize the sensors individually and jointly which will be seen in the next section.

Mode	Sampling Rate	Dynamic Range	Recording Time (Max)
Accelerometer (Accel.)	31.25, 50, 100, 200 Hz	$\pm 2$ , $\pm 4$ , or $\pm 8$ g	8-35 hours
ECG	125, 250 Hz	$\pm 0.2$ V	17-35 hours
EMG	250 Hz	$\pm 0.2$ V	17 hours
Accel.+ECG	50 Hz(accel) 125, 250 Hz (ECG)	$\pm 2$ , $\pm 4$ , or $\pm 8$ g (accel) $\pm 0.2$ V (ECG)	11-22 hours
Accel.+EMG	50 Hz(accel) 250 Hz(EMG)	$\pm 2$ , $\pm 4$ , or $\pm 8$ g (accel) $\pm 0.2$ V (EMG)	11 hours
Gyro.+Accel	25, 50, 100, 250 Hz	$\pm 2$ , $\pm 4$ , $\pm 8$ , $\pm 16$ g (accel) Off, $\pm 250$ , $\pm 500$ , $\pm 1000$ , $\pm 2000$ /sec (gyro)	2-4 hours

Table 1: Key specifications of the BioStampRC sensor from MC10 Inc.

## 2 Methodology

Here, initially, we detect and analyze the motor symptoms and come with characterizations which help us dissociate the PD/HD subjects from controls by manually picking the activity locations from in-clinic test. In the next part, we come up with an automated process to recognize the activity duration based on HMM.

## 2.1 Motor Symptoms Detection and Analysis for PD and HD

The aim of motor symptoms detection and analysis is to come up with a feature that helps differentiate PD and HD from the controls. We arrive at the features based on the visual cues by observing the subjects. For HD, there was lack of co-ordination between the legs and step duration variation when compared to normal people and in PD, at rest tremor was the visible cue [5].

**Gait Analysis in HD:-** For analysis the gait in HD we manually choose walking activity duration from the in-clinic tests. In order to capture the lack of co-ordination between the sensors we make joint utilization of the sensors by calculating the cross-correlation between the leg sensors. Let  $\mathbf{a}_L(n)$  and  $\mathbf{a}_R(n)$  for  $n = 1, 2, \dots, N$  represent the mean subtracted tri-axial data from sensor in the left leg and right leg, respectively with  $N$  representing total number of samples. The normalized vector cross-correlation  $R_{LR}(m)$  as a function of time lag  $m$  [5] is then given by,

$$R_{LR}(m) = \frac{\sum_{n=1}^{N-m} (\mathbf{a}_L(n)\mathbf{a}_R(n+m))}{\left(\sum_{n=1}^{N-m} \|\mathbf{a}_L(n)\|^2\right)^{1/2} \left(\sum_{n=1}^{N-m} \|\mathbf{a}_R(n+m)\|^2\right)^{1/2}}. \quad (1)$$

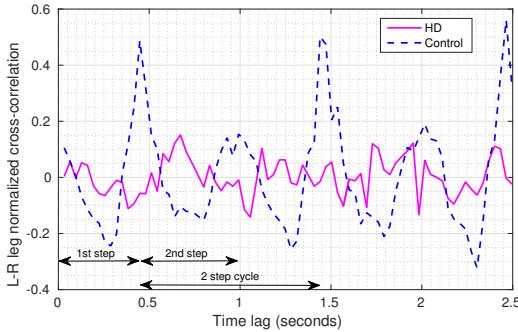


Figure 2: Normalized vector cross-correlation of leg sensors as a function of time lag for a 10 m walk instantiation for HD and Control

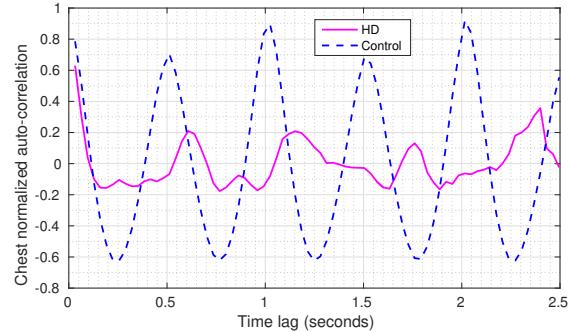


Figure 3: Normalized vector auto-correlation of chest sensor as a function of time lag for a 10 m walk instantiation for HD and Control

Peak in cross correlation occurs when left foot crosses the right foot. In other words, the figure tells us how well the left foot comes into same position as that of right foot or how well the left foot characterizes the right foot after some time lag. As we can observe in Fig.2, for a control the peak occurs at around 0.5 and 1.5 second time lag with a higher amplitude when compared to HD. Apart from the amplitude variation we can also observe that the time lag at which the peak occurs varies for HD and control. This results in consideration of step duration variation as another feature which helps us separate HD from control. However, the precision is less in cross-correlation and hence we look into data of such a sensor which captures the movement of both the legs. So we do the auto-correlation of the chest sensor to characterize the step duration variability [5]. Let  $\mathbf{a}_C(n)$  for  $n = 1, 2, \dots, N$  represent mean subtracted tri-axial data from sensor in the chest with  $N$  representing total number of samples. The normalized vector auto-correlation is given by,

$$R_{CC}(m) = \frac{\sum_{n=1}^{N-m} (\mathbf{a}_C(n)\mathbf{a}_C(n+m))}{\left(\sum_{n=1}^{N-m} \|\mathbf{a}_C(n)\|^2\right)^{1/2} \left(\sum_{n=1}^{N-m} \|\mathbf{a}_C(n+m)\|^2\right)^{1/2}}, \quad (2)$$

Peak in the auto-correlation occurs when chest comes into same position after some time lag. In Fig.3 we can see that for the control the peak occurs around multiples of 0.5 second lag whereas it varies for HD. Hence cross-correlation of the legs sensors and auto-correlation of the chest sensor gives us a good feature for characterizing lack of co-ordination between the legs and step duration variability.

**Tremor analysis in PD:-** At rest tremor in PD has a specific frequency band of 4-7 Hz, hence, we do frequency spectrum analysis to segregate PD from control [5]. Here we manually choose the duration of rest tremor and postural tremor test from in-clinic data to the analysis. Since we have tri-axial accelerometer data, instead of using each axis, we obtain the dominant acceleration component through principal component analysis (PCA) [10] for frequency analysis. Let  $a_S^{pc}(n)$ , a vector of length  $N$ , represent dominant acceleration component which is segmented using a window  $w(n)$  of length  $M$  and

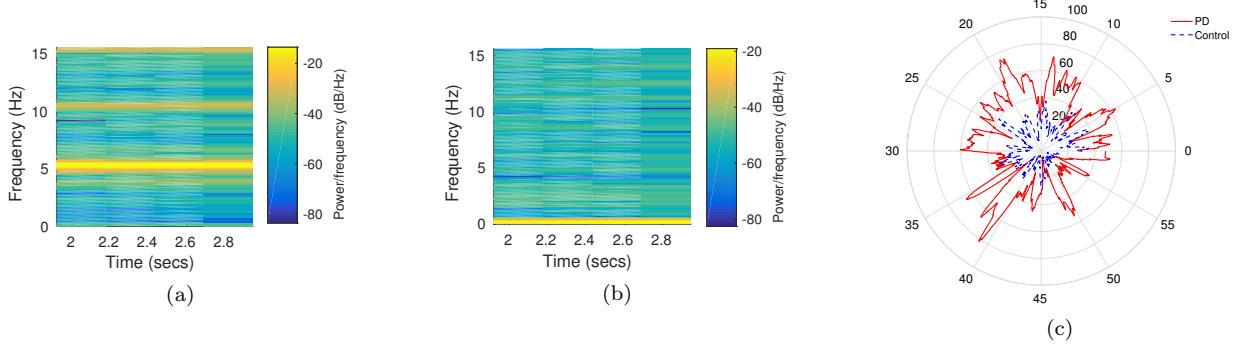


Figure 4: (a) Spectrogram showing energy distribution for PD (b) Spectrogram showing energy distribution for Control (c) Polar plot showing fraction of total power in [4 7]Hz band for a PD and Control for an hour duration

overlap of  $k$ , with  $a_{Sl}^{pc}(n)$  representing the  $l^{th}$  segment. The short time Fourier transform (STFT) is given by,

$$A_{Sl}(k, \omega) = \sum_{n=-\infty}^{\infty} a_{Sl}^{pc}(n)w(n-k)e^{-j\omega n}, \quad (3)$$

Discretization of frequency results in,

$$A_{Sl}(k, p) = A_{Sl}(k, \omega) , \text{ at } \omega = \frac{2\pi}{M}p, \quad (4)$$

Spectrogram is represented as,

$$S(k, p) = |A_{Sl}(k, p)|^2. \quad (5)$$

Fig. 4a and Fig. 4b represents the spectrograms of one of the segments of dominant acceleration component of PD and control respectively. Energy distribution in the [4 7]Hz band and its harmonics is clearly visible for the PD where as for the control we do not see it. Choosing fraction of total power as one the feature, utilizing one hour duration of data, we obtain polar plot shown in Fig. 4c. We can clearly see the energy distribution variation for a PD subject when compared to the control.

## 2.2 Hidden Markov Model Based Activity Detection

The data we have is a time-series data and it has inherent dependencies that can be modeled as being Markovian. This combined with the fact that the accelerometer data is the visible observation but we do not know the states corresponding to each data point, thus making the states hidden. So, we decided to model our approach as HMM [13]. We are hoping to train a model that can viably predict the states for data that is not labeled or logged. In order to get a separate movement and non-movement data points for all the patients we decided to use two hidden states for HMM, namely movement and non-movement. **Model Specifications and Baum-Welch Parameter Estimation:-** The next step was to model the data using HMM in order to detect the activities. Since for the PD patients it is the at rest tremor that is needed to be analyzed we decided to use the data corresponding to non-movement states for a PD vs control tremor analysis. Also, since the gait analysis is best able to differentiate between a normal person and a HD patient, the data from the movement states will be used for HD vs control analysis. Thus for further analysis we planned to use the data points corresponding to the two states separately.

We model the observed tri-axial accelerometer data as multivariate gaussian,  $\mathcal{N}(\mu_1, \Sigma_1)$  and  $\mathcal{N}(\mu_2, \Sigma_2)$ , and the tri-axial observational data from the accelerometer readings will be referred to as X in this and the following subsection. The HMM was initialized with two hidden states,  $Z = [M, NM]$ , a randomly chosen initial stationary distribution  $\pi = [\pi_0 \ \pi_1]$  and transition matrix,  $T = \begin{bmatrix} 1-\alpha & \alpha \\ \beta & 1-\beta \end{bmatrix}$ . The observations were initialized with their own  $(\mu, \Sigma)$  combination which was calculated using the accelerometer data. Thus giving us parameters list,  $\theta = [\pi, T, (\mu_1, \Sigma_1), (\mu_2, \Sigma_2)]$ .

We used Baum-Welch algorithm [13] for our parameter estimation. Every iteration of Baum-Welch algorithm consists of two steps. The first step is where the algorithm estimates the current states and

in the next step it updates the parameter list using the new state assumptions. This goes on until the difference between two consecutive log likelihoods goes below a certain threshold. In our case the threshold =  $10^{-5}$ . So the Baum-Welch iteration stops the moment the difference between two consecutive log likelihoods becomes less than the threshold and the current parameter list is given out as the output. This process can be shown as:

Step1: Obtain MAP estimate of the state sequence

$$\hat{Z} = \arg \max_{Z} p(X, Z | \theta^t) \quad (6)$$

Step 2: Update the parameter

$$\theta^{t+1} = \arg \max_{\theta} p(X, \hat{Z} | \theta) \quad (7)$$

The complementary state path sequence was calculated using Viterbi algorithm [13] with the final transition matrix and final stationary distribution , given by Baum-Welch algorithm, as its parameters.

**Activity Predictor:-** Now, as all the patients are independent we couldn't have used one patient's outputs to predict the states for any different data. So, we took the  $(\mu, \Sigma)$  for all the individual patients and averaged it out to get a general  $(\mu, \Sigma)$  combination to be used for future classification. The  $\mu$  was obtained by applying the K-Means algorithm on all the individual  $\mu$  and then using the centroids thus obtained for both he states. Whereas the  $\Sigma$  was obtained by a normal arithmetic mean on all the  $\Sigma$  for the various patients.

The  $(\mu, \Sigma)$  combinations were obtained separately for PD patients, HD patients and the Controls using the same procedure as above but using the respective patients' observational data only. The classification was done by calculating the distance between the Gaussian, that the new averaged out  $(\mu, \Sigma)$  refers to, and each point of the unclassified data. Any point is classified as the state it is closest to. We have used Mahalanobis distance [4] as metric given by,

$$D_M(\vec{x}) = \sqrt{(\vec{x} - \vec{\mu})^T \Sigma^{-1} (\vec{x} - \vec{\mu})}. \quad (8)$$

Using the method mentioned in this section we speed up our classification procedure as we need not model every data point as an HMM but just use the Mahalanobis distance metric and get the corresponding states. We call this model as Activity Predictor.

### 3 Experimental Results

#### 3.1 HMM Results

The Hidden Markov Model is a widely used algorithm to analyze time series data and has many programmatic implementations in a range of programming languages. We use the "Kevin Murphy HMM Toolbox" [2] for MATLAB to estimate parameters and obtain the best state sequence to explain the observed data. Our aim is to detect the movement/non-movement states of the underlying Markovian process. Our intuition was to use either of the leg sensor data for the analysis as it best captures these states. To be sure however, we ran the simulations on chest sensor's data and found that it was not as accurate as using the leg sensor's data. For our analysis, we use the in-clinic duration of data. The initial HMM path sequence provided a fairly good estimate of the state duration but included a high number of erratic jumps from one state to the other as shown in Fig. 5. We required long sequences of data where the system stayed in either of the states for the motor symptom analysis. These erratic jumps required some kind of smoothing to aid our analysis. From the figure below, we can see that from 9:39:16 to almost 9:48:19, the system is almost always in State 2. But this duration includes several unnecessary jumps to State 1 and back

The fundamental assumption we make in the smoothing process is that the system will lie in one state for at least one second. The tests that each participant undergoes do not allow for erratic jumps from the movement state to the non-movement state making our assumption a fair one. We implemented our own algorithm to smooth the state sequence estimate as shown in algorithm 1 . The idea was to look for the instants when there was a state transition and then look into the next second of data to ensure that the system stayed there for the duration. We note down all transition times where the system stays in

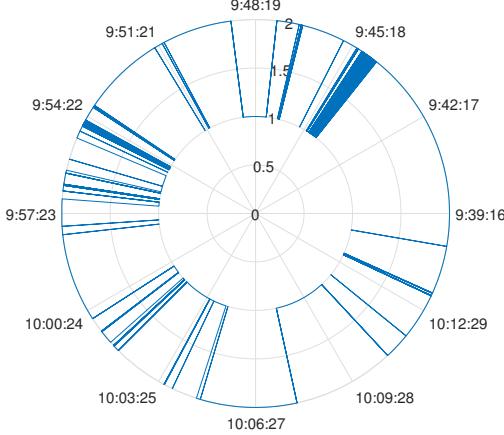


Figure 5: Polar plot showing two states along the radial axis and time along circumference for a participant

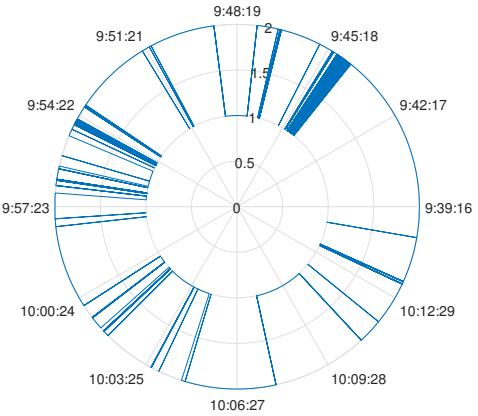


Figure 6: Activity estimation using HMM before smoothing

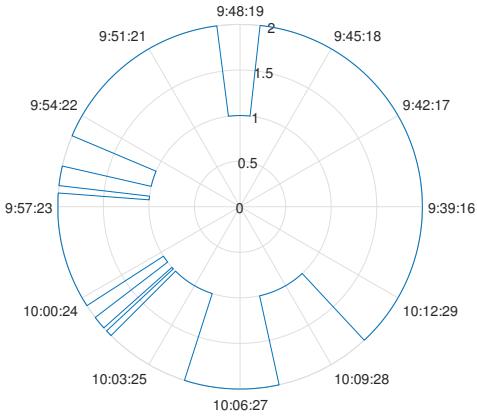


Figure 7: Activity estimation using HMM after smoothing

the new state for at least one second and also the new state that the system is in. The valid transition times are stored in the vector "index" and the corresponding state to which the system transitioned into is stored in the vector "state". We now use these two vectors to generate the smoothed state sequence.

As we can see from the Fig. 7 below, the duration from 9:39 to 9:48 has been smoothed out to state 2 as we require when compared to Fig. 6. Similarly, all other durations have been smoothed out.

The main purpose of using the in-clinic duration of data is the availability of the activity log. Using the activity log we can validate the results of the HMM smoothed state sequence. We validated the state sequence for the control, PD as well as the HD participants. Figs. 8, 9 and 10 shows the pre/post smoothing effect with validation for a control, HD and PD subject respectively.

### 3.2 Activity Predictor Results

The idea behind creating an activity predictor was to combine the parameter estimates from the HMM for every participant and use the aggregated  $\mu$  and  $\Sigma$  for the multivariate Gaussian emission distribution to classify each observation into states. Another reason for the creating the activity predictor was to eliminate state naming ambiguity generated by HMM. The HMM identifies two states but can interchange the labels causing some confusion in the inferencing process. This activity predictor takes care of this problem.

We ran a simple k-means algorithm to cluster the  $\mu$  estimates to clearly label the states and because of the independence property of each participant, the aggregate covariance matrices was calculated as the mean of the individual. The Figs. 11a, 11b and 11c show the clustering of the means for control, HD and PD participants. Finally, in Fig. 11d we see a clear distinction in the aggregated means for each

### Algorithm 1: Smoothing

```

input : State sequence estimate or path, windowSize
output: smoothpath, index, state

1 while not at end of path do
2   |   if transition occurs at index i then
3     |     t=path(i:i+windowSize)
4     |     if no transition in t then
5       |       add i to index
6       |       add path(i) to state
7     |     end
8   |   end
9 end
10 for each i in index do
11   |   smoothpath(i:index(i+1))=state(i)
12 end

```

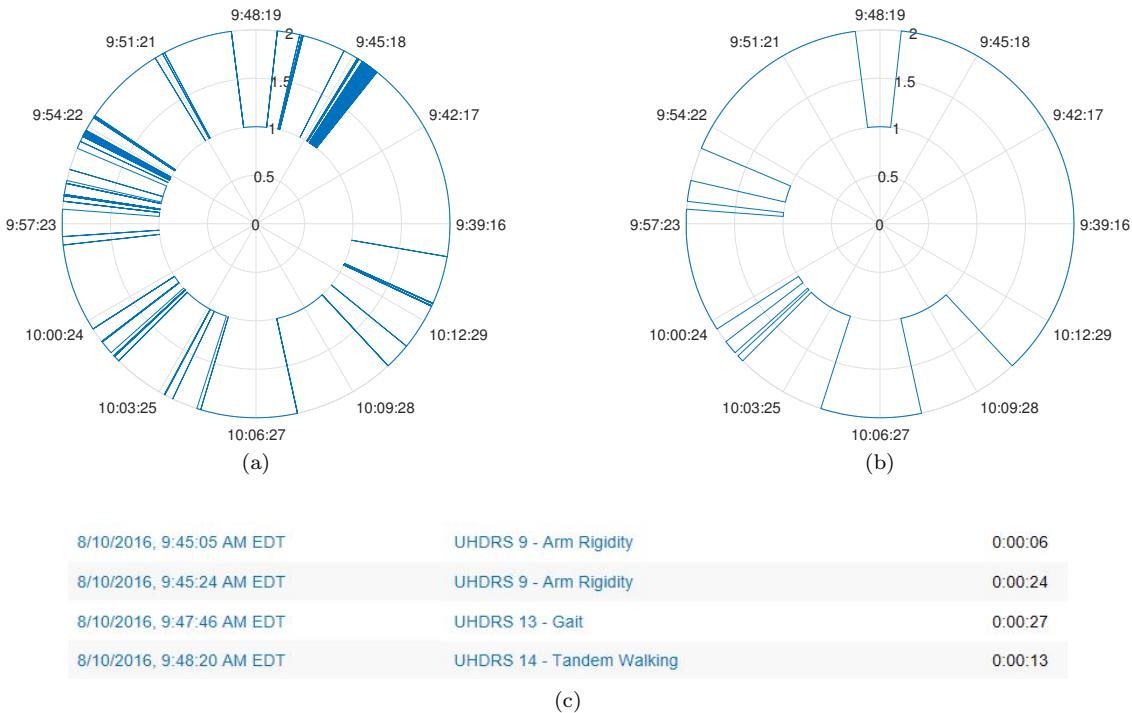


Figure 8: (a) Activity estimation using HMM before smoothing for Control (b) Activity estimation using HMM after smoothing for Control (c) A snap shot of log to validate the estimated states

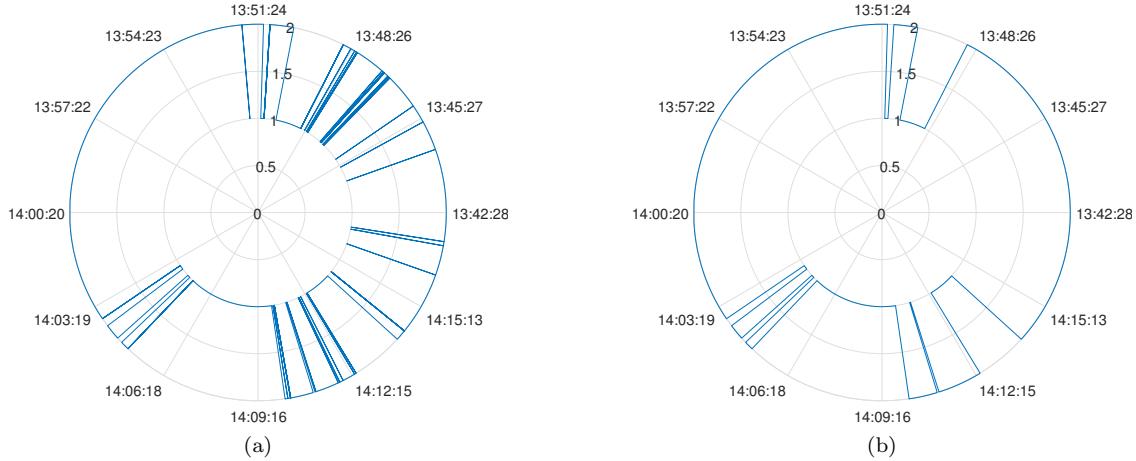


Figure 9: (a) Activity estimation using HMM before smoothing for HD (b) Activity estimation using HMM after smoothing for HD (c) A snap shot of log to validate the estimated states

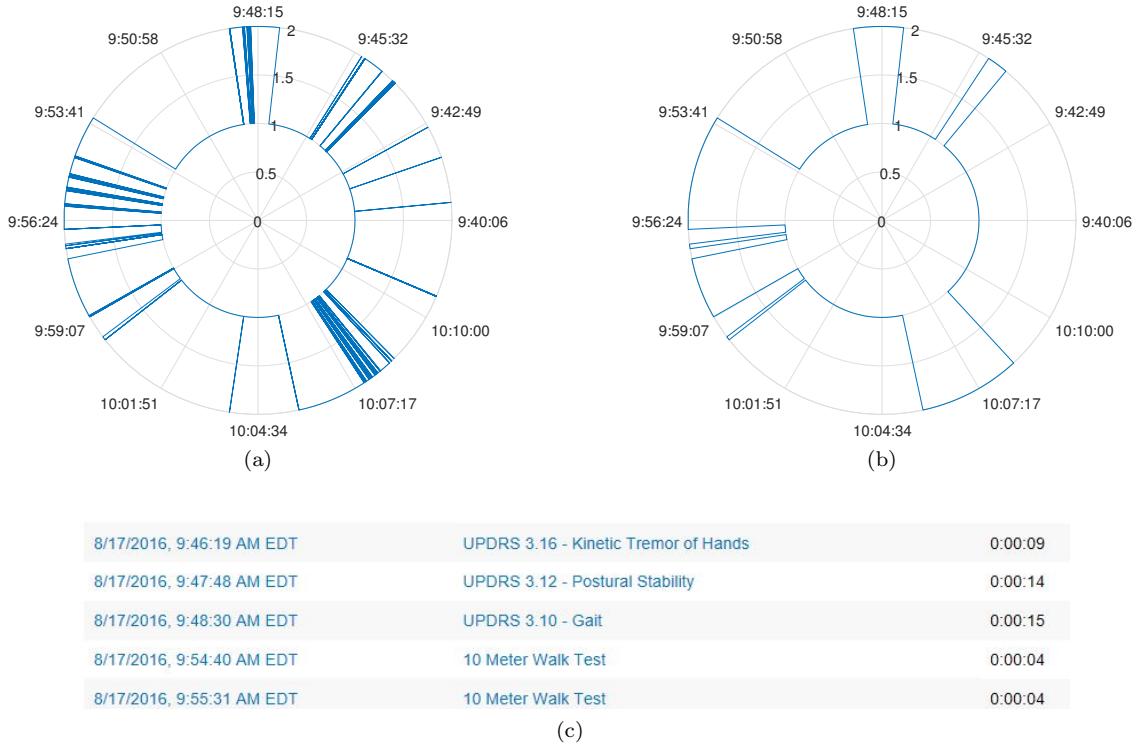


Figure 10: (a) Activity estimation using HMM before smoothing for PD (b) Activity estimation using HMM after smoothing for PD (c) A snap shot of log to validate the estimated states

Patient Type	HMM Runtime	AP Runtime	AP Accuracy
Control	3.33 sec	<b>0.79 sec</b>	99.67%
Control	4.08 sec	<b>1.07sec</b>	99.49%
HD	3.5 sec	<b>1.1 sec</b>	98.34%
HD	3.57 sec	<b>0.94 sec</b>	99.81%
PD	26.8 sec	<b>3.5 sec</b>	99.89%
PD	7.66 sec	<b>3.8 sec</b>	99.45%

Table 2: Comparison of HMM and AP Performance

kind of participant.

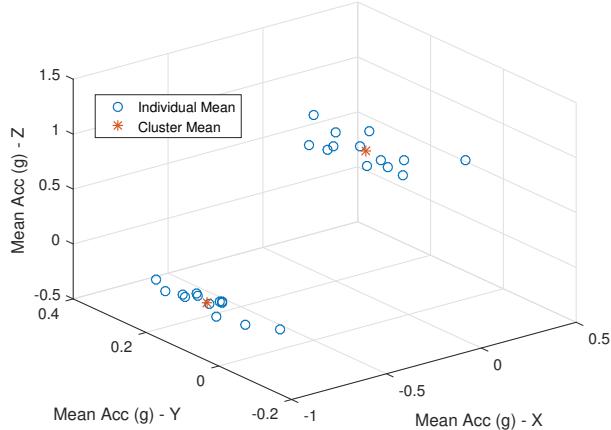
Using the new aggregated emission probability distribution and the Mahalanobis distance measure we can estimate the path sequence as we did with HMM. As we expected, the path sequence generated by the activity predictor is almost exactly same as that generated by the HMM. In addition to this, the runtime is halved. The Figs. 12a, 12c show the comparison of the path sequence generated by HMM with AP shown in Figs. 12b, 12d . The table shows the performance metrics for each method.

## 4 Conclusion

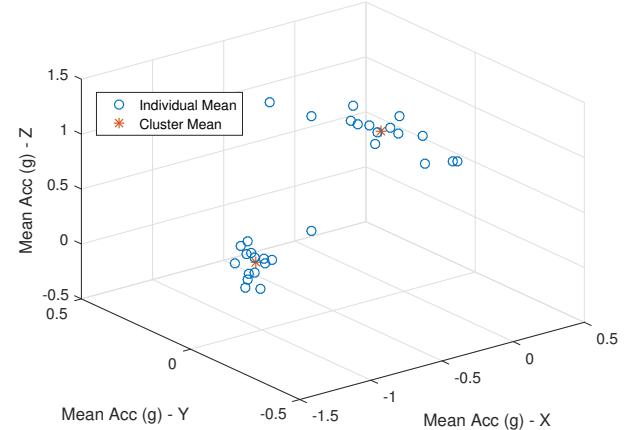
Application of wearable sensors for analysis of PD/HD is advantageous as the sensors we are utilizing are light weight, unobtrusive and high power and recording capabilities. Preliminary analysis to extract the feature by picking up activities from in-clinic tests helped us come up with cross-correlation and auto-correlation characterizations for HD and spectrogram characterization for PD. The process of automating the intake of activity durations using HMM yielded results with highly accurate activity estimation. We also came up with a smoothing algorithm that increases the accuracy of estimated states. We came up with activity predictor which work on par with HMM with better runtime.

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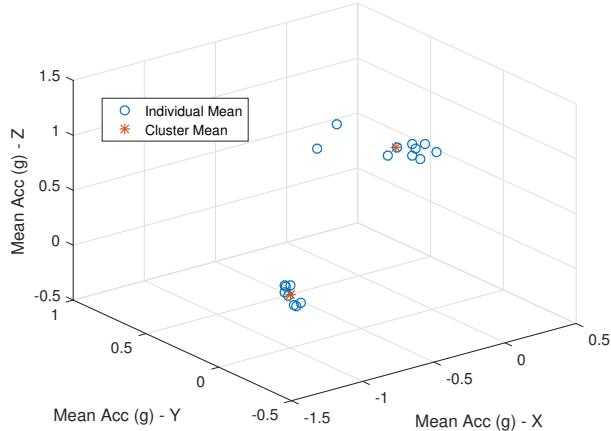
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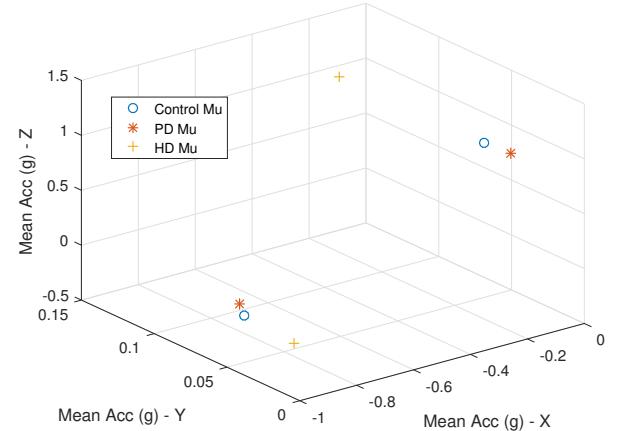
(a)



(b)



(c)



(d)

Figure 11: (a) Scatter plot showing the clustering of mean of the parameter estimates for all controls (b) Scatter plot showing the clustering of mean of the parameter estimates for all PD subjects (c) Scatter plot showing the clustering of mean of the parameter estimates for all HD subjects (d) Plot showing final representative parameter estimate for Control, PD and HD

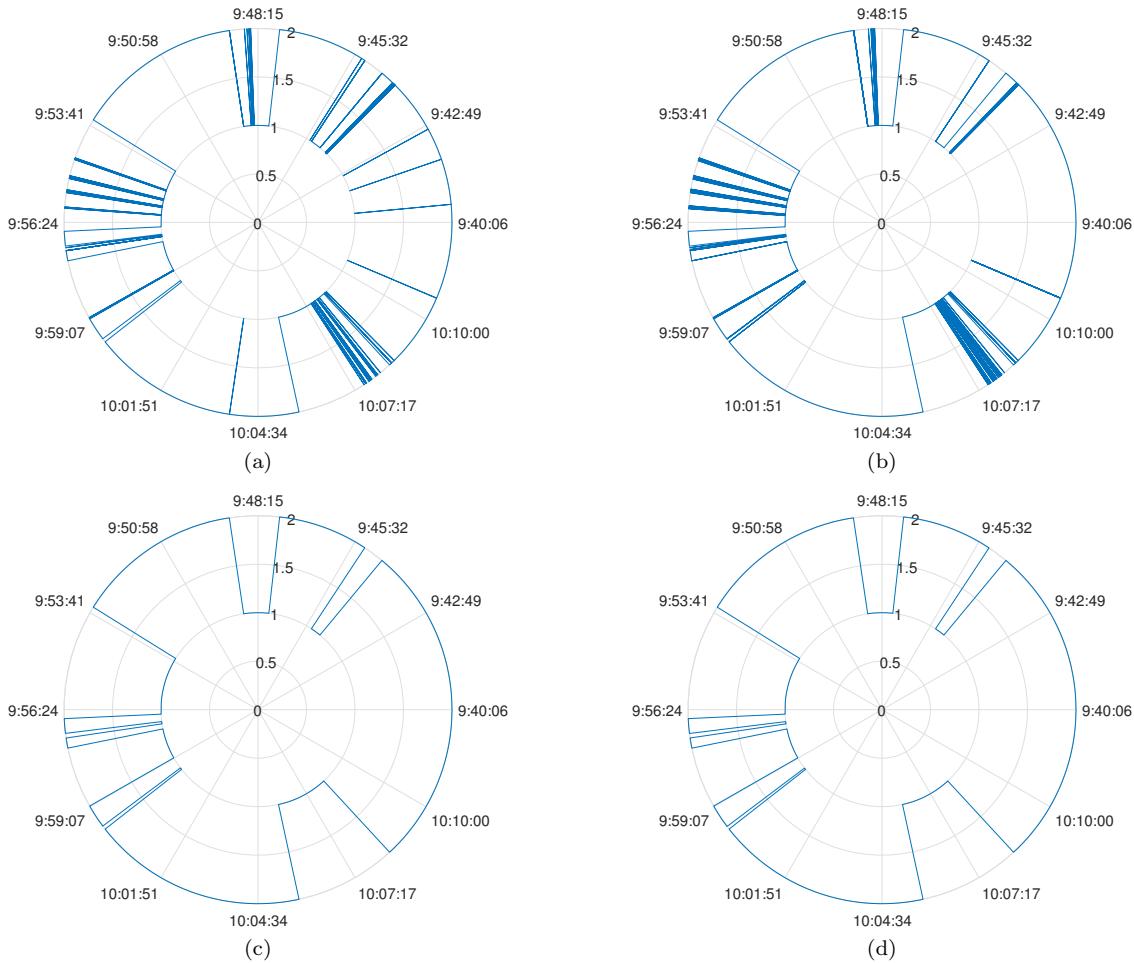


Figure 12: (a) Activity estimation using HMM pre-smoothing (b) Activity prediction using Mahalanobis distance pre-smoothing (c) Activity estimation using HMM post-smoothing (d) Activity prediction using Mahalanobis distance post-smoothing