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## Developing a Hidden Markov Model - Gaussian Mixture Model Framework to Classify Gait Patterns in Huntington's Disease

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### Introduction

Gait abnormality is a potential diagnostic sign which can occur even in the early, pre-manifest stages of neuro-degenerative diseases such as Huntington's disease. Gait patterns in such patients are characterized by irregular, shortened stride lengths and jerky movements. Hidden Markov Models (HMMs) offer a straightforward and effective framework for disease progression prediction and pattern recognition. We propose a two-class Hidden Markov Model (HMM) where a stride model and a transition model were trained individually to identify distinct patterns and abnormalities during the gait-phase transition to distinguish between HD patients with moderate to severe motor dysfunctions and healthy controls. Our HMM-GMM approach was applied on the "Gait in Neurodegenerative Diseases" on physio.net.

### Methodology

#### Feature Processing and Extraction

- computed the inter-stride times for an HD patient with a total functional capacity measure score of 12 (record Hunt14) and a healthy control based on the first 30 seconds of the gait signal data
- aligned the signal on both feet. The location of each crossing for the right foot of a HD patient and a healthy control was determined using the midcross function.
- use midcross to compute the inter-stride times for a group of 5 HD patients with a total functional capacity measure score ranging from 2-12 and 5 healthy controls. First 8 and last 8 crossings of each record were excluded to remove transients from the starting and ending phases of a gait cycle.
- apply dynamic time warping(DTW) to align the two segments and compute the minimum Euclidean distance between the time series of each gait segment

#### Stride Model

As a stride follows a repetitive bio-mechanical order, each hidden state was connected to a sub-phase of a stride. The sub-phases were given by transitioning from the state  $s_0$  to a higher state  $s_n$ . The initial transition probabilities  $p_{n,n}$  were set to correspond to the adjacent state  $p_{n,n+1}$ . Since each gait signal consisted of two time dimensions- the stride length and the step length- a 2-dimensional GMM was applied to train a model of the two components.

- Two separate Gaussian distributions were generated for each signal. To estimate the parameters of the GMMS, the hidden states were initialized by simply dividing the strides into 2 equal sections.
- Existing edges within the transition matrix were initialized uniformly.
- Parameters were subsequently optimized iteratively with a maximum of 20 iterations using the Baum Welch algorithm. The threshold of convergence was set to default of  $1 \times 10^{-4}$ .

#### Transition Model

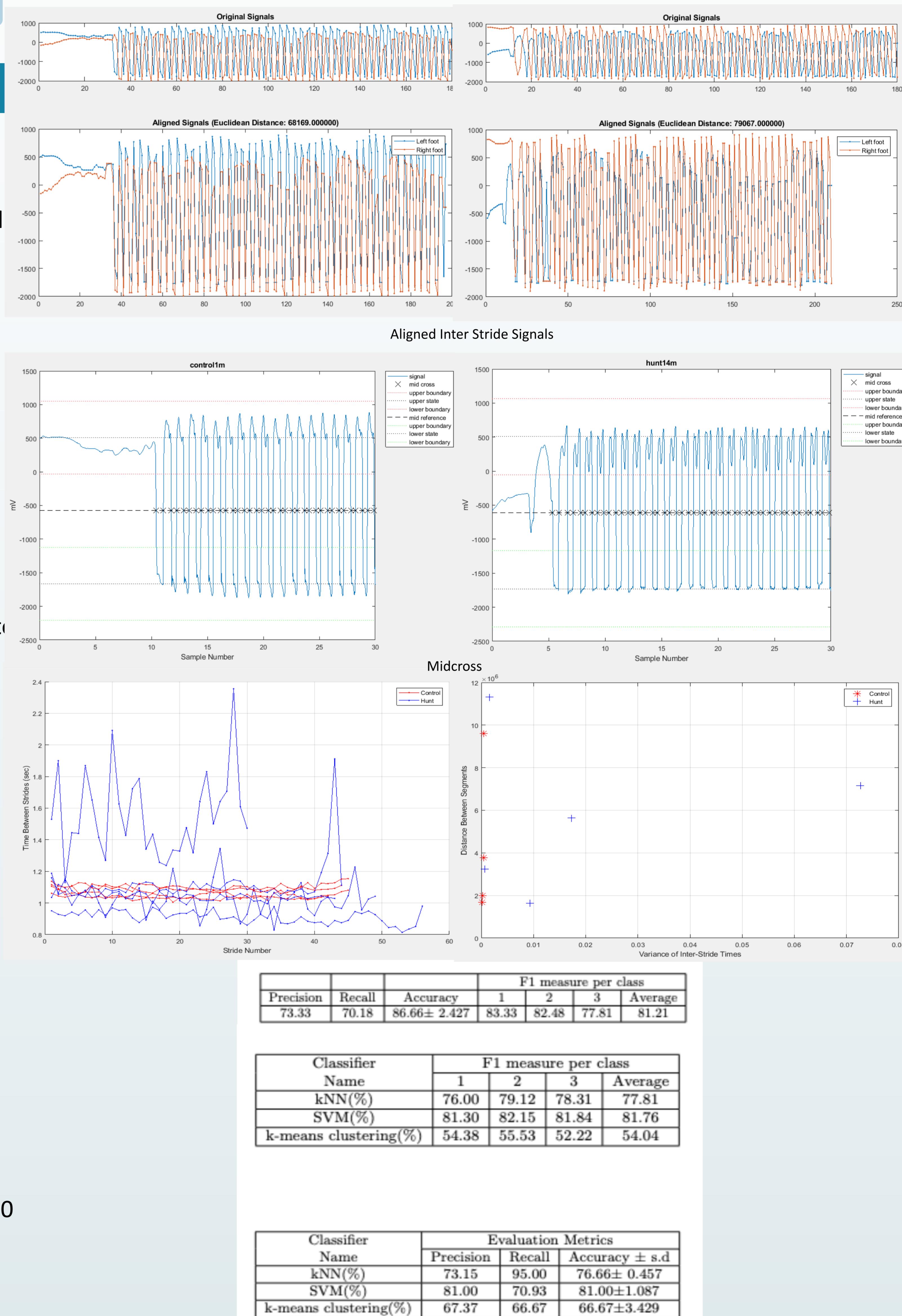
Due to the heterogeneity of the transitions between each stride of gait, a single corresponding hidden state was insufficient. The initial Markov Chain was extended and the following exceptions were made to the conventional HMM:

- A transition can occur between the final (absorbing) and the first state; the final state of ordinary HMMs are often absorbing hence cannot be left once entered.
- The transition sequence can start and end at any state

### Merging the two Models

The two models were concatenated to produce a uniform HMM to determine the stride borders of the HMM and classify strides and transition states simultaneously. The respective transition matrices were concatenated, creating a new transition matrix with dimensions  $(m+n \times m+n)$  where  $m =$  number of states in the transition model and  $n =$  number of states in the stride model. The combined transition probabilities were the weighted mean of the corresponding distributions for the merged states. As the emission distributions have already been optimised and trained using the BW algorithm, the original emission distributions were retained. The most likely sequence of gait phases was re-estimated using the Viterbi algorithm.

### Results



### Conclusion

Clinical gait analysis has played a significant role in early diagnosis of neurodegenerative diseases. The use of artificial intelligence and various machine learning techniques has yielded promising results. In this work, we observed that despite the lack of training samples, the HMM still demonstrated its strength as the number of records it processed increased, especially in terms of its accuracy. Further improvement is needed to enhance the model's precision by conducting meta learning on the two individually trained HMMs.