GAIT QUALITY EVALUATION METHOD FOR POST-STROKE PATIENTS

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ABSTRACT

Proliferation of low-cost nonintrusive wearable sensors enables researchers to explore capabilities in monitoring physiological parameters remotely expanding healthcare delivery and reducing costs. One of the parameters that is known to be important in rehabilitation and exercise physiology is human motion monitoring, such as analysis of the walking gait and corresponding characteristics. This paper presents a robust on-line methodology for computing clinically relevant metrics for assessing quality of the walking gait in normal subjects and subjects with gait abnormalities, e.g. in patients with stroke. Furthermore, this paper proposes a metric vector that enables characterization of spatiotemporal features of walking quality evolution for post-stroke patients during and after rehabilitation. This method enables visualization of the gait improvement or changes as a result of the rehabilitation or other treatment techniques.

***Index Terms*—** Motion quality evaluation, adaptive matching, clustering, PCA

1. INTRODUCTION

The conventional assessment methods of post-stroke patients' motor functions are conducted through standard scale tests[1]. Such tests require patients to perform different tasks typical for every-day motions when in the community. The performance of patients is then scored by a physician or a qualified personnel. These tests and methods, however, suffer from the subjectiveness of physician's judgement, minor changes in specifics of the task performance or conditions in which the test is conducted.

Today, the low-cost wearable sensing devices are prosperously developing and being deployed in a variety of healthcare monitoring and assessment applications[2]. For example, motion sensors, such as accelerometers, are deployed for monitoring and analysis of locomotion or upper extremity mobility [2, 3]. The reliability and validity of accelerometer based wearable devices have been proved effective in characterizing post-stroke patients' walking[4, 5]. Wearable sensor monitoring have shown to be complementary for performance evaluation and can be deployed for monitoring in the community with feedback provided to the physicians and patients on a daily basis[2, 3].

In this paper, algorithms for detailed analysis of the motion (e.g. accelerometer) data are presented, where variations in each stride of the subject during locomotion are analyzed, providing a quantitative and qualitative description of post-stroke patient's walking. This paper has the following contributions: Firstly, an on-line methodology for computing clinically relevant metrics and characteristics for subject lower body mobility. Secondly, a metric vector, purely derived from the accelerometer data and independent of sensor orientation. Thirdly, a visualization method that indicates motion quality evolution during and after patient rehabilitation based on a longitudinal data. This enables physicians, patients and other interested parties to visualize the effects of the rehabilitation and treatment.

2. EVALUATION METRICS

The motion quality evaluation metric includes kinetic characteristics and motion variability. These metrics are independent of the orientation around the ankle placement given an ankle band mounting method described in [2] and are feasible for large scale experiment deployment. The hardware is an energy efficient platform with tri-axial accelerometers[6].

2.1. Kinetic Characteristics

Kinetic characteristics include walking speed, cadence, stride length, symmetry and swing to stride ratio (SSR). Modeling of speed, cadence and stride length has been elaborated in [2].

Symmetry is defined as a ratio of the impaired leg swing time over the normal leg swing time[7]. Fig.1 shows a stride segmentation from two legs. SSR is defined as a ratio of the swing time over the complete walking cycle period t shown in Fig.1, which is a sum of swing and stance times.

The walking cycle is identified by a peak detection algorithm, where each of the peaks correspond to the moment when heel of a foot strikes the ground - the most pronounced element of the acceleration signal. After identifying the boundary of each stride (e.g. the two consecutive peaks), an adaptive matching algorithm is applied to identify the swing phase within a stride.

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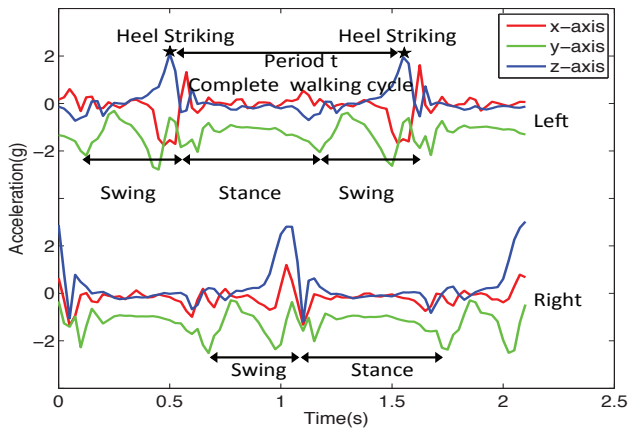


Fig. 1: Stride Segmentation

2.1.1. *Identifying Boundary of Stride Cycle*

Given a segment of walking accelerometer data (the walking state can be identified among other activities by state classification[2]), the raw data is first transformed into a vector $h = \sqrt{x^2 + z^2}$. As can be seen from Fig.1, at the point of heal striking (e.g. one of the highest peaks), h achieves maximum value during a stride cycle. In the stride cycle of Fig.1, the swing phase is comprised of the end part of one stride and beginning part of the next stride. Swing phase cannot be mapped precisely within the stride cycle if just the consecutive heal strike detection is used for defining the boundary indices.

However, consecutive heal striking of left leg provides the boundary index information for the right leg and vice versa. As can be validated by [8], the walking cycle of left leg will affirmatively include a complete swing phase of the right leg (however, not necessarily include the right leg stance period). The algorithm switches the heal striking indices between left leg and right leg as stride boundary information. Maximum of h is derived by applying a peak detection algorithm.

For patients with hemiparesis, the transformed vector h may not achieve maximum at heal striking from the impaired limb data and thus cannot provide reliable index information for the boundary of the normal stride. Typically multiple local maxima are found (caused by both swing and heal striking) by applying just the peak detection. According to the stride boundary of impaired limb derived by peak detection from the normal limb, a local maxima array that belongs to the same stride is known. Since heal striking happens after swing, the local maximum that is the end of local maxima array is natural to be heal striking from the impaired limb. In this way, boundary indices for the normal leg are derived.

2.1.2. *Adaptive Swing Matching*

With a stride that contains a complete swing phase, an adaptive matching algorithm is applied to precisely identify its location.

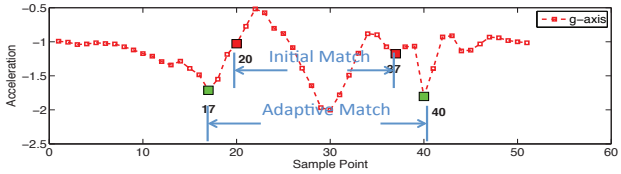


Fig. 2: Swing Phase Adaptive Matching

This algorithm first performs a search within the stride data S through all of its sub strings to identify the one that has the smallest distance compared to the template, shown in Eq.1. substring$^-$ represents the initial match result. The distance metric is calculated by the Dynamic Time Warping[9]. This provides an estimate of the similarity between the stride substring and template. Motion data signal warping caused by different walking speeds are adjusted accordingly.

Next, substring$^-$ is extended and shrank on both ends of the boundary indices and the distance array is searched to find the minimal distance. The corresponding substring is the final match.

$$\text{substring}^- = \arg\min(\text{Dist}(\text{stride}, \text{template})) \quad (1)$$

$$\text{substring} = \min(\text{Dist}, \text{Dist}_{shrink}, \text{Dist}_{expand}) \quad (2)$$

Algorithm 1 shows the process. The input is a data vector of a stride and a swing phase template, that has been precomputed. Lines 1-7 show the initial matching process. $startind$ and $endind$ in Alg.1 are the start and end indices of the initial match.

Lines 8-17 show the adaptive searching part of the algorithm, where lines 8-12 and lines 13-17 expand and shrink the sub string length of stride S separately. Finally, line 18 finds the minimum distance of the three distance vectors and line 19 obtains the proper swing length by adjusting the $startind$ and $endind$. Fig.2 shows an example of expanded matching.

2.2. Variability

Variability is an important qualitative measurement of stroke patients' walking functionality[10]. We define an entropy parameter to characterize variability and randomness in the walking data.

Algorithm 2 shows the process to calculate entropy. Input is a vector of stride signals and a threshold value. The stride signals are automatedly delimited by method proposed in 2.1.1. The output of the algorithm is the entropy value. In Alg. 2 lines 1-7 generate a lower-triangle distance matrix of the stride vector, that is, a distance matrix for every two strides. Each item in the distance matrix is a measurement of signal similarity between the two strides.

The distance matrix is then compared against the input threshold. The input threshold is determined by the mean value of the distance matrix precomputed from a population

Algorithm 1: Adaptive Swing Phase Matching

Data: $s, template$
Result: $swinglen$
begin
  for $n = 1 : len(s) - len + 1$ **do**
    $d(n) = dtw(s(n : n + len - 1), template)$
  end
  $ind = find \min(d)$
  $startind = ind + 1$
  $endind = startind + len(template) - 1$
  $start_{expand} = startind - 5 > 0?startind : 1$
  $end_{expand} = endind + 5 < len(s)?endind + 5 : len(s)$
  for $n \in [start_{expand} : end_{expand}$ **do**
    $d_{expand} = dtw(s(n), template)$
  end
  $start_{shrink} = startind + 5$
  $end_{shrink} = endind - 5$
  for $n \in [start_{shrink} : end_{shrink}$ **do**
    $d_{shrink} = dtw(s(n), template)$
  end
  $shiftind = find \min(d, d_{shink}, d_{expand})$
  adjust $startind$ and $endind$ with $shiftind$
  return $swinglen$
end

Algorithm 2: Entropy Calculation

Data: $S = (s_1, s_2..., s_i, ...s_j)$,$threshold$
Result: $Eval$
begin
  for $n = 1 : j$ **do**
    for $m = 1 : j$ **do**
      if $m \geq n$ **then** continue
      else $Dist(n, m) = dtw(s_n, s_m)$
    end
  end
  for *n=1:j* **do**
    $index\{n\}$=find $Dist(n, :) < threshold$
  end
  for $index\{i\} \in index\{1 : n\}$ **do**
    if $index\{i\}\&index\{j\}! = 0$ **then**
    merge index{i} and index{j}
  end
  for $n = 1 : len(merg\_cluster)$ **do**
    $prob(n) = len(merg\_cluster(n))./len(S)$
  end
  $Eval = -1 * sum(prob. * log(prob))$
end

of the healthy subjects. The algorithm then clusters the strides by their mutual distance. That is, if $D(i, j) < threshold$, then stride i and stride j are defined as connected and thus merged into the same cluster. Lines 11-14 show this process. The algorithm stops looping when the number of clusters does not change.

After this step, the strides are merged into different clusters on the basis of their similarity. Finally, the entropy value is calculated according to the definition. The entropy is upper bounded by $\sum \frac{logn}{n}$ and lower bounded by 0.

3. EXPERIMENTS

For the experimental evaluation of the proposed algorithms, 20 subjects have been recruited. Nine of these subjects are healthy individuals with subject IDs 1-9, and the other 11 are stroke patients with different severity of the condition and IDs of 11 to 17. An appropriate UCLA IRB and the subject consent approvals were obtained before the experiments. Of the 11 stroke patients, seven have records for only one time evaluation and the other four have longitudinal records including evaluations of four and more times over the period of several weeks. Those four patients are participants of the SIRRACT[11] project (with IDs 17 to 20). The experimental data includes 36 unique data records and observations in total.

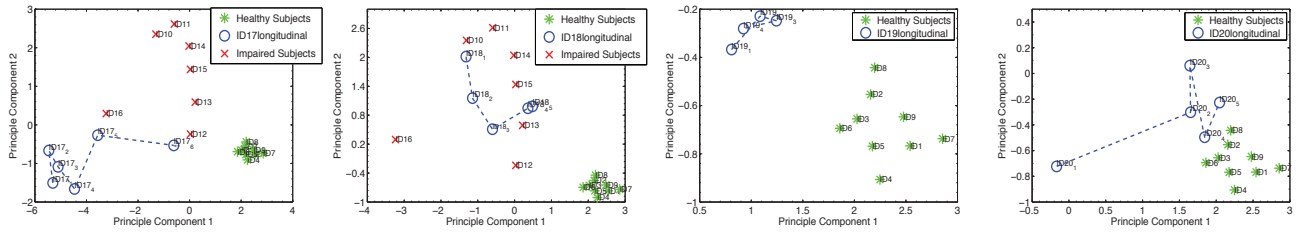
Each subject was instrumented with two triaxial accelerometer devices, MDAWN[6], one around each ankle. Both MDAWNs of every patient are time synchronized before the data collection and monitoring. Each subject is instructed by the physician to walk with three different speeds (fast, average and slow) moderated by the subjects themselves, traversing a distance of 33 to 50 feet.

The complete metric vector includes $entropy_{left}$, $entropy_{right}$, $symmetry$, SSR_{left}, SSR_{right}, $speed$, $cadence$ and $stridelen$, and is calculated for each subject. The kinetic parameters are averaged during the test.

A matrix of 36 by 8 is generated (e.g. number of observations vs metric vector). In order to provide effective visualization of the recovery evolution for these patients, the matrix is subjected to the principal component analysis (PCA). Eight principle components are generated and the first two explain 84.78% of the variance. The algorithm then projects the observations onto the first two dominant principle components for the data from the four longitudinal patients, as shown in Fig.3.

The green stars in the Figure represent the data cluster for the nine healthy subjects. The red crosses represent the seven stroke patients that have only one-time record, and the corresponding cluster. These are the two control groups. The linked blue circles in each figure represent the evolution route of the individual patients from the moment they are first admitted to the hospital until discharge with comparison to the control group data overlaid.

Fig.3a-d have different resolutions according to the performance of the patient. Patient ID17 and 18 are generally



(a) Patient ID 17 (b) Patient ID 18 (c) Patient ID 19 (d) Patient ID 20

Fig. 3: Patient Gait Evolution Visualization

weaker, while patients ID19 and ID20 have better performance initially. Thus, in the last two subfigures, the control group of the nine stroke patients is not shown. In these cases the goal is to emphasize the distance between the healthy control group and the patient recovery evolution route.

4. CONCLUSION

In this paper, we explore the methods to derive metrics of variability, swing ratio, swing stance time, speed, stride length and cadence from pure accelerometer data, and decompose the signal to visualize the evolution process of patient recovery.

This method is not limited to stroke patients. It can be applied to other communities, such as patients with Parkinson's or Multiple Sclerosis conditions. The metric value itself provides a physician with the relevant information about the patient on a frequent time basis (for example daily), and can alarm when abnormal events occur. Furthermore, some of the metrics, for example entropy, can provide physician with prognostic inference about a likely fall.

The visualization provides macroscopic view of the patient performance over a longer period of time and can aid physicians to better understand recovery process.

The visualization also provides clustering based on the performance of the patients. However, with limited observations, it is too early to draw conclusions. In the near future, with more patients recruited to the SIRRACT[11] project, the project is on its way towards data analysis for a larger group of stroke patients.

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