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Quantification of Parkinsonian kinematic patterns in body-segment regions during locomotion

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Abstract

Purpose: Diagnosis and treatment of Parkinson's Disease (PD) are typically supported by a kinematic gait analysis. Nonetheless, the main drawbacks of the classical analysis, based on a reduced set of markers, are the loss of small dynamical changes, the invasive methodology, and the sparse representation from few points, restricting the disease analysis. **This work aims to perform a robust regional kinematic characterization, which may result in a potential digital biomarker of the disease to complement personalized analysis, treatment and monitoring of PD.**

Methods: This work introduces a markerless computational framework based on a full body-segment kinematic characterization related with PD motor alterations. Firstly, a set of dense motion trajectories are computed to represent locomotion. Such trajectories are grouped using a deep learning based body segmentation, that partitions the human silhouette into regions corresponding to the head, trunk and limbs. Each resultant region is described using *dartboard*-like kinematic histograms computed along the trajectories.

Results: The proposed approach was validated using different pre-trained classification models. The proposed method was evaluated on a set of 11 control subjects and 11 PD patients, achieving an average accuracy of **99.62%** for lower-limbs and head regions.

Conclusion: This work proved to be effective to classify Parkinsonian patterns w.r.t control gaits. A major contribution of the proposed strategy is the capability to recover kinematic patterns in different body segments, particularly, for head and trunk regions, which turned out to be a decisive PD biomarkers.

Keywords: gait analysis, kinematic analysis, dense trajectories, Parkinson's disease

Statements and Declarations

Competing interests

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- **Non-financial interests:** None.

1 Introduction

Parkinson's disease (PD) is the second most common neurodegenerative disorder, with a prevalence greater than 3% in people over 80 years old, currently reporting more than 6.9 million cases and 177 000 associated deaths worldwide [1, 2]. The PD diagnosis is strongly correlated with movement disorders of upper and lower limbs, which alter among others the gait patterns [3]. During locomotion are observed pattern alterations like arm swing and footstep size reduction, decreasing of ground clearance, slowness and rigidity on displacements, and postural instability [4]. Specifically, the walking process requires a fine balance between trunk stiffness and mobility, absorbing movement-related forces, and therefore, amplifying other motor alterations as result of typical instability of the trunk on PD patients [5]. For instance, head stability, segment stiffness and postural abnormalities, typical and co-occurrent in PD patterns, are amplified during locomotion due to the loss of dynamical stability. These patterns represent relevant but currently under-explored features in the characterization of PD [6].

The kinematic gait analysis (KGA), related with the qualitative and quantitative description of body segments displacements, allows to support diagnosis, treatment and monitoring of diseases related with motion disorders [7]. KGA usually uses several cameras placed around a walkway and a set of markers located at points of reference on the body. From the marker information, the gait is usually characterized by measures such as the bending angle of knees or hips during a gait cycle. These approaches, however, strongly simplify the complexity of PD movements to a few markers and can affect the natural gesture of gait [8]. On the other hand, the KGA of Parkinsonian gait is usually focused on the study of different measures of lower limb movements, reducing the importance of the information given by all other body segments [9, 10]. Furthermore, traditional methods ignore the hidden patterns characteristic of PD, focusing on providing general gait measurements and ignoring Parkinson's patterns that arise from the instability produced by the disease. However, some works have shown the relevance of the head, neck and upper limbs movements during walking in the characterization of PD, demonstrating that such patterns provide complementary information and are not the result of simple reflex movement [11, 12]. For instance, complementary works on KGA have shown that velocity patterns and freezing of gait initiation turn out to be highly descriptive for PD, with demonstrated statistical independence w.r.t age and health conditions [13, 14]. Also, Parisi et al. presented a comparative evaluation of leg agility, sit-to-stand and Gait tasks based on a correlation analysis, emphasizing the shorter steps and reduced velocity patterns as signature of PD patients [15].

Hence, novel approaches that capture a full description of segmented body parts during locomotion result fundamental to explore particular behaviours that could be associated to PD. In the literature have been presented different approaches as alternatives to explore dynamic during locomotion. For instance, some silhouette-based methods have managed to follow the position of some

lower limbs, as well as to compute gait speed, stride length and cadence, from sagittal gait captures [16, 17]. These approaches however are prone to self-occlusion and ignore upper limbs information. Alternatively, Parkinson quantification methods have recently focused on measuring head and pelvis accelerations, which are in turn correlated with other dynamic variables and allows to predict PD [18]. Along the same line, Buckley *et al* explored upper body accelerations to measure postural control, and reported greater magnitude in the mid-lateral direction in people with PD [19]. Such findings evidence the importance of measuring postural control in PD, however, the wearable capture systems affect the patient's natural gait and lead to a corrupted or unreliable characterization of the disease. Moreover, these methods limit exploration of other kinematics, potentially suitable for PD representation like the ground clearance, the reduction of arm swing and dragging of feet.

Promising works to characterize Parkinsonian gait have integrated spatio-temporal patterns with learning and prediction approaches. For instance Baby M. *et al.* represent feet motion information from wavelet coefficients, mapped in a neural network scheme, to classify PD and control subjects [20]. Similarly, Lee *et al.* used a neural network with weighted fuzzy membership functions as PD classifier, modelling on 40 features of vertical force records [21]. Also, Sarbaz *et al.* computed the power spectra of stride and swing signals, taking advantage of the semi-periodicity of the gait, to characterize PD patients, validating the potential of frequency analysis as biomarker of the disease [22]. A main limitation of such approaches is the significant amount of data required to learn a proper representation of Parkinsonian patterns. The variability modelling of such case could be limited then to trained patterns, with potential overfitting on boundary definition between control and disease trained samples. Additionally, these methods are based on global measurements of specific parts of the body typically considered the most descriptive. They assume that the movements of the other body segments correspond to reflex movements and overlook their potential contribution to the characterization of the disease.

This work introduces a markerless strategy that captures, models and allows to analyze body segment kinematics to obtain a PD characterization during walking, captured in sagittal video-sequences. [This strategy supports the diagnosis of Parkinson's disease \(PD\) and complement the analysis, which may be important to the management and monitoring of the disease.](#) Initially, the proposed approach performs a regional and dynamic segmentation of body segments, allowing to individualize head, trunk and limbs. Kinematic patterns are densely captured in each of the segmented regions by densely computing a set of long motion trajectories that represent per-pixel motion during displacement. The whole point-wise trajectories are summarized on a proposed gait descriptor using dartboards that encode the temporal distribution of different kinematics such as velocity, acceleration and curvature. These dartboards constitute a motion body-segment representation that allows to distinguish control and PD population, and could be a digital biomarker to quantify motion patterns at different body segments, which have remarkable correlation with the

disease. This method was evaluated on 176 gait video sequences of 22 patients, that is, 11 patients per class and 8 videos per patient.

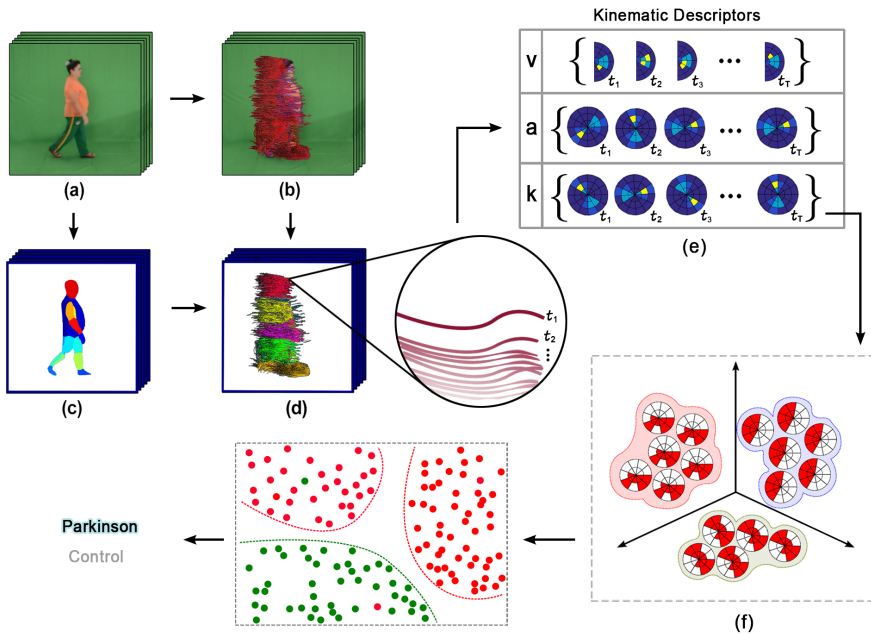


Fig. 1 a) Original video sequence. b) Dense motion trajectories estimation. c) Body segmentation masks. d) Dense trajectories grouped by body segment. e) For each trajectory t_i , the temporal distribution of the 2D displacement (velocity), its derivative (acceleration) and curvature (oriented toward radial acceleration) is encoded into polar kinematic histograms. f) Binary classification scheme.

2 Methods

A markerless strategy is herein introduced to observe and analyze regional body parts kinematics during gait. This approach makes possible to find correlations and discover particular motion patterns related to Parkinson disease and focus on particular spatial regions and specific gait stages. The method automatically recovers body silhouette and respective segmentation for head, torso, upper and lower limbs, among others (Figure 1.c). Then, motion trajectories are mapped over computed masks, obtaining a local movements description for each body segment during walking (Figure 1.d). From such segmented trajectories, a set of key kinematics are codified into polar histograms (dartboards) obtaining a comprehensive kinematic description of each body-segment (Figure 1.e). Each kinematic segment representation can be analyzed w.r.t the capability to predict and group patients diagnosed with PD. A

description of each step of our method is presented in the following subsections.

2.1 Regional Analysis

Parkinson's disease differs from other neurological pathologies by the lateral body asymmetry in symptoms, and the focus of motor alterations on specific body parts, especially at early stages [23]. Nevertheless, much of the proposed markerless strategies only perform a global shape characterization during gait, losing description of localized movements. In fact, head, trunk, upper and lower limbs describe specific Parkinsonian patterns that should be treated independently during kinematic analysis due to independent dynamic, asymmetry, and the response of specific body parts during locomotion [12, 24]. For instance, abnormal head movements produced by instability of the trunk have been shown to be significant in describing Parkinson's disease [25] but remain poorly explored. [Taking into account such considerations, the first step in this work was to obtain dynamic dense segmentation to approximate anatomical segments during locomotion.](#)

To do so, [it was implemented the *DensePose* \[26\] approach](#) that obtains dynamic pose mask with the capability to also determine specific body segment regions. *DensePose* was herein implemented to obtain general pose mask but also body segmentation parts during walking. The model was trained by its authors with around 50K images under the Mask R-CNN framework to learn correspondence between training images and body-segment labels. It achieves, in real time, a robust body part segmentation in the presence of complex background, occlusions and scale variations. In our work, only the channel that corresponds to the segmentation labels of body parts is used in order to group the motion trajectories using the body part labels. The segmentation of the body silhouette into rigid movement sections facilitates the description of patterns with semantic and symptomatic meaning. Additionally, it is effective in differentiating each side, that is, the right limbs from the left ones, allowing the identification of asymmetric PD patterns. A typical dynamic body part segmentation obtained in our work is illustrated in [Figure 1.d](#) and [Figure 4](#).

2.2 Dense Motion Trajectories

The optical flow is the most known and standard tool to capture motion patterns from videos. From such motion field it is possible to recover spatiotemporal patterns that may be representative of some particular human behaviours. Nonetheless, these patterns could be insufficient to study gait features, which are usually studied along a set of semi-periodic movements known as gait cycles (developed through multiple frames). Even worse, for Parkinson disease, where patients typically exhibit slowness of their movements [27], the optical flow could be insufficient to capture relevant kinematic patterns.

Hence, a natural way to extend the optical flow is to track local motion through the video, which results in long point trajectories, that represent the

movements of patients during walking [28]. Thus, dense trajectories are local motion primitives based on the concatenation of optical flow vectors, tracking numerous points along the video sequence, which allows a more robust representation of motion patterns [29] (see on Figure 1.b). Since trajectories span a large number of frames, they facilitate the description of temporally complex structures of Parkinson's disease. The uniformly dense sampling over the video of these trajectories provides a rich regional description of the patients' movements during locomotion. Dense trajectories extraction starts by computing the Farneback dense flow, based on polynomial expansion [30]. In this method the neighborhood value f of each image pixel is approximated by quadratic polynomial expression, defined as: $f(\mathbf{x}) \simeq \mathbf{x}^T \mathbf{A} \mathbf{x} + \mathbf{b}^T \mathbf{x} + c$, where $\mathbf{x} = (x, y)^T$ are pixel positions, \mathbf{A} , \mathbf{b} and c are the estimated quadratic (matrix), linear (vector), and constant (scalar) terms, respectively. Then, the \mathbf{d} vector field displacement is obtained from the polynomial coefficients in consecutive frames f_t and f_{t+1} , as follows: $\mathbf{d} = -\frac{1}{2} \mathbf{A}_t^{-1} (\mathbf{b}_{t+1} - \mathbf{b}_t)$. Then, the computed dense flow is smoothed by using a 2d median filter over the displacement field. In practice, the points $\mathbf{x}_t = (x_t, y_t)$ are densely sampled on a regular grid, tracked in time t at different spatial scales and rounded to integer values after the median smoothing. The matched points are finally concatenated to form a trajectory $(\mathbf{x}_{t_0}, \mathbf{x}_{t_1}, \mathbf{x}_{t_2}, \dots, \mathbf{x}_{t_n})$.

2.3 Regional kinematic representation

Based on the assumption that the motor symptoms of Parkinson's disease can be properly characterized by the computation of regional kinematics given by the velocity and its derivatives, a kinematic representation is herein proposed from dense trajectories. For doing so, a polar histogram scheme (dartboards) is proposed for coding kinematic gait behavior. The main idea of this descriptor is that local kinematics during gait can be described by the distribution of body parts movements in terms of their magnitudes and directions. Each trajectory can be seen as a series of concatenated motion vectors. As any vector, they are described from their magnitude and orientation, and within each trajectory, a vector occurrence histogram is compiled into a quantified polar histogram as depicted in Figure 2. Finally, to improve accuracy, the local histograms are normalized using L2 norm. This codification allows a statistical kinematic representation of pathological movements of PD during walking. The use of different kinematic measures can be supported according to disease findings, as:

- Bradykinesia or slowness of movement, one of the main signs of PD can be approximated by velocity patterns. This movement disorder is not caused by muscle weakness but by the incorrect transmission of neuromuscular signals. Bradykinesia can affect one limb, one side of the body, or the whole body, which can define a particular locomotion signature for each patient. In order to kinematically describe bradykinesia, let $\vec{v} = \mathbf{v}(t)$ be the 2D displacement of a video element between frames t and $t + 1$. We construct

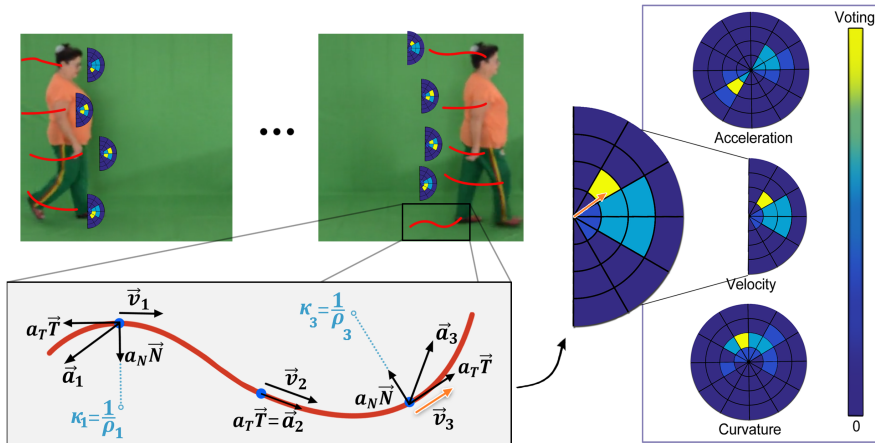


Fig. 2 Building of the trajectory level descriptor.

a half-dartboard quantization of vector \vec{v} in terms of its magnitude and direction, since the gait is supposed to be in the same direction for the whole sequence, as depicted in Figure 2.

- Some typical symptoms of PD such as tremor, and others like dyskinesia (involuntary and uncontrollable movements) or dystonia (simultaneous contraction of opposing muscles) are characterized by the sudden variation in the speed or direction of movements, *i.e.*, by acceleration patterns. Additionally, instability of the trunk and head leads to the emergence of abrupt compensatory movements to maintain balance and avoid falls. Moreover, Parkinsonian symptoms often varies from time to time, that is, good quality of movement can quickly be followed by poor quality. A reasonable way to kinematically describe these symptoms is by computing the local acceleration of the body segments: $\vec{a} = \frac{d\vec{v}}{dt}$. Analogous to velocity coding (but symmetric to support negative accelerations), a dartboard quantization of acceleration vectors is made in terms of magnitude and direction.
- Finally, the rigidity or the stiffness, causes muscles to become rigid because of their inability to relax, fact that could be represented from trajectories by measuring curvature patterns. This typical symptom can prevent muscles from stretching and relaxing as they should. As a consequence rigidity may be experienced as: stiff and/or inflexible muscles, the stooped posture commonly associated with PD, pain and muscle cramps, difficulty to turn, reduced arm swing, among others. The curvature information of body segments movements can accurately describe all these symptoms. Mathematically it can be written as $\kappa = \frac{a_N}{\|\vec{v}\|^2}$, where $a_N = \frac{\|\vec{v} \times \vec{a}\|}{\|\vec{v}\|}$. As the direction also makes sense, we use a vector with normal direction to the displacement (*i.e.* direction of the radial acceleration, that points toward the center of osculating circle to the trajectory), and with magnitude given by the curvature.

2.4 Global encoding and prediction

After describing each trajectory by a set of dartboards representing the distribution of the kinematics along the trajectory, a regional descriptor is built, by spatially aggregating, for each region, the trajectory-level descriptors to form a unique motion descriptor for each region. In this work were explored three different versions of regional descriptors, described as follows:

- In the first version, for each region, a clustering algorithm is run on the trajectory-level descriptors, to obtain N groups using a k-means approach. The centroid of each group is then considered as representative atomic information. The descriptor of each region is then defined as the set of N centroids. This version is referred to as KC in the results section.
- The second version is a bag-of-words approach, where a N -word dictionary is built for each region, using a clustering algorithm on the trajectory-level descriptors extracted for a particular body segment. Then each region descriptor is built as a histogram of occurrence over the Regional Dictionary. This version is referred to as RD in the results section.
- The third version also uses a bag-of-words approach, to form regional descriptors, but this time one unique global dictionary is built, and the same dictionary is used to code every regional descriptors by histogram of occurrences. This version is referred to as GD in the results section.

These temporal region-wise histograms constitute the final descriptors which allow to describe rigid parts during locomotion, and emphasize kinematics that statistically describe the type of gait. Each resulting descriptor is mapped to a learning strategy to perform an automatic classification. In this work was implemented a Support Vector Machine (SVM), a technique widely used in many problems of supervised learning thanks to an attractive trade-off between accuracy and computational cost [31]. Here the classes are "Parkinson" and "Control", and the optimal hyper-planes separate them using a classical maximum-margin formula. A parameter sensitivity analysis (γ, C) was performed using a k-fold cross validation scheme and selecting the parameters with the highest number of true positives. As an alternative classification scheme, Random Forest (RF) [32] was also evaluated.

2.5 Experimental setup

Video sequences were recorded at the foundation **FAMPAS** (*Fundación del Adulto Mayor y Parkinson Santander*) and at the nursing home *Asilo San Rafael*, under semi-controlled conditions. This study was approved by the Ethics Committee of the Universidad Industrial de Santander and counts on a written informed consent. The dataset consists of a set of videos captured with a RGB camera, from 22 participants, being 11 control patients and 11 patients diagnosed with Parkinson's disease. [The PD patients were in stages of the disease between 2.5 and 3.0 according to the Hoehn and Yahr scale estimated by a physical therapist during the video recording of the study. Moreover, the](#)

patient's condition was initially diagnosed by a treating neurologist, which served as basis for the observation of the therapist during the video recording. Each subject in the study was recorded 8 times while performing a natural markerless walking, 4 times to the right and 4 times to the left, for a total of 176 video sequences. The patients were medicated with Levodopa, and during the study the medication was not suspended. Regarding capture conditions, the gait trial was carried out in a bidirectional way, freely, and without any time restriction. In fact, before each capture, it was asked to each patient to walk as naturally as possible, with conventional speed and without any extra condition. The videos show patients that are already walking, *i.e.*, start and stop periods were suppressed. This dataset is age matched, *i.e.*, the mean age is 72.2 ± 6.1 for control patients and 72.3 ± 7.4 for PD patients. The subjects are 12 men and 10 women distributed as follows: 2 women and 9 men in PD group and 8 women and 3 men in control group. The whole set of videos was recorded indoor, with a static camera, a colored background and the patients wearing different clothes. The average duration of the videos is 4 seconds. For the experiments the videos were sub-sampled to 60 frames and cropped to 520×520 pixels. Samples of video captured in this study are illustrated on figure 3.

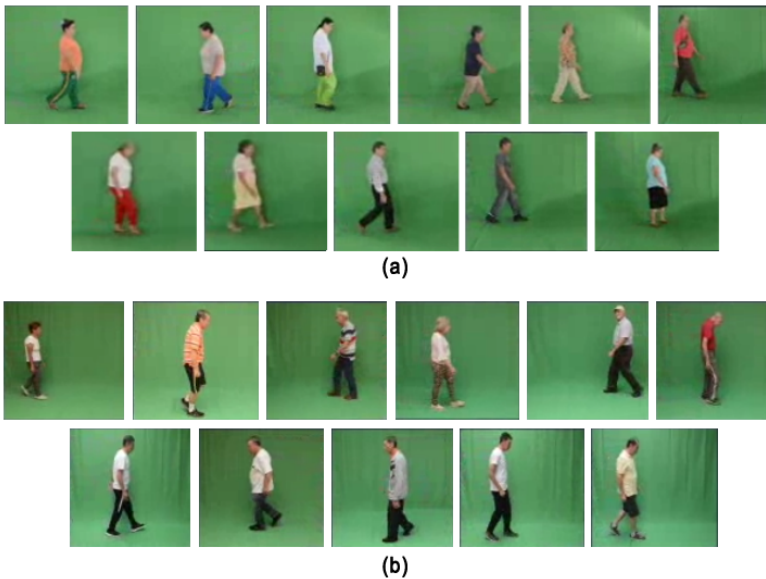


Fig. 3 Parkinsonian gait dataset. A sample frame of each control subject (a) and PD patient (b).

2.5.1 Comparison between *DensePose* and a clustering algorithm

One contribution of this work is the regional grouping using *DensePose* during locomotion video sequences. To this end, we ran the *DensePose* algorithm previously trained on a public dataset (the COCO dataset [33]). This general domain dataset represents a challenge regarding the multiple pose configurations, the multiple point of views, and the multiple actors in the scene. As a consequence, the original training was sufficient to segment the sagittal silhouettes that are required in our study. To evaluate the real benefit of *DensePose* segmentation, we also used an alternate grouping strategy using a clustering algorithm. We used the k -means algorithm, that group objects into k clusters by following a neighborhood trajectory criterion on a Euclidean multidimensional space. Then, a set of five clusters, that coarsely correspond to spatial body segments, were defined as an alternative region split. To perform k -means clustering, all trajectories were aligned temporally and then an affinity similarity matrix was computed among the corresponding points of each trajectory. The distance of similarity herein implemented to compare trajectories is described in [34], and expressed as:

$$d(a, b) = \left(\max_{n \in [1, L]} d_{spatial}[n] \right) \left(\frac{1}{L} \sum_{n=1}^L d_{velocity}[n] \right), \quad (1)$$

where L is the length of trajectories, $d_{spatial}[n] = \mathbf{x}_a[n] - \mathbf{x}_b[n]$ is the spatial distance between the trajectory points and $d_{velocity}[n] = \mathbf{v}_a[n] - \mathbf{v}_b[n]$ is the distance between point velocities. Such distance penalizes trajectories that are spatially far apart and associate trajectories with similar velocity patterns. An affinity matrix \mathbf{W} is then obtained by $\mathbf{W}(a, b) = \exp(-d(a, b)/1000)$ computed at each trajectory pair. The affinity matrix has dimension $T \times T$, where T is the number of trajectories in the video. To ensure the spatial group compactness, trajectories that are not spatially close are forced to zero (we used the condition $\max(d_{spatial}) \geq 120$ pixels in our experiments).

2.5.2 Method configuration

The proposed approach was evaluated with a fixed length motion trajectories of 16 frames, computed on a grid spaced by 5 pixels and tracked in 8 different spatial scales. This configuration was set as a trade-off between accuracy and computational cost. Once the final motion descriptor was obtained from any of the three coding schemes, two different classifiers were implemented: The SVM and the RF. An evaluation of best parameters was carried out to tune best classification performance. Additionally, the performance of the *DensePose* trajectory grouping method was compared with a classic k -means clustering. Finally, the relevance of the proposed regional approach was tested comparing it with a global classification over the whole body without clustering.

For validation, it was used a "leave-one-patient-out" classification method (k -fold cross validation), where at each iteration, one patient is left out for

testing and the remaining ones (21 subjects in our particular experiment) are used for training. The Parkinsonian patients correctly classified were counted as true positive (TP) and the correct control patients as true negative (TN). The global descriptors for each region were evaluated separately and identified as follows: $C1$ - head and torso, $C2$ - upper arms, $C3$ - lower arms and hands, $C4$ - upper legs, and $C5$ - lower legs and feet, which corresponds to the main rigid movements of body segments from a sagittal point of view as depicted in Figure 4. The final descriptor, for all the experiments, was set to 200 elements long. This value was obtained from a previous global tuning.

3 Evaluation and results

Figure 4 illustrates the observational results achieved by the proposed approach. In such case the body segmentation (second row) and recovered motion trajectories (third row) can be used as observational tool during clinical evaluation. An integrated visualization is illustrated in fourth row, in which kinematic information (extracted from trajectories) is spatially differentiated, according to its body localization. From such last plot, occurrence motion patterns, expressed from trajectories, at specific body part could suggest associations with Parkinson disease.

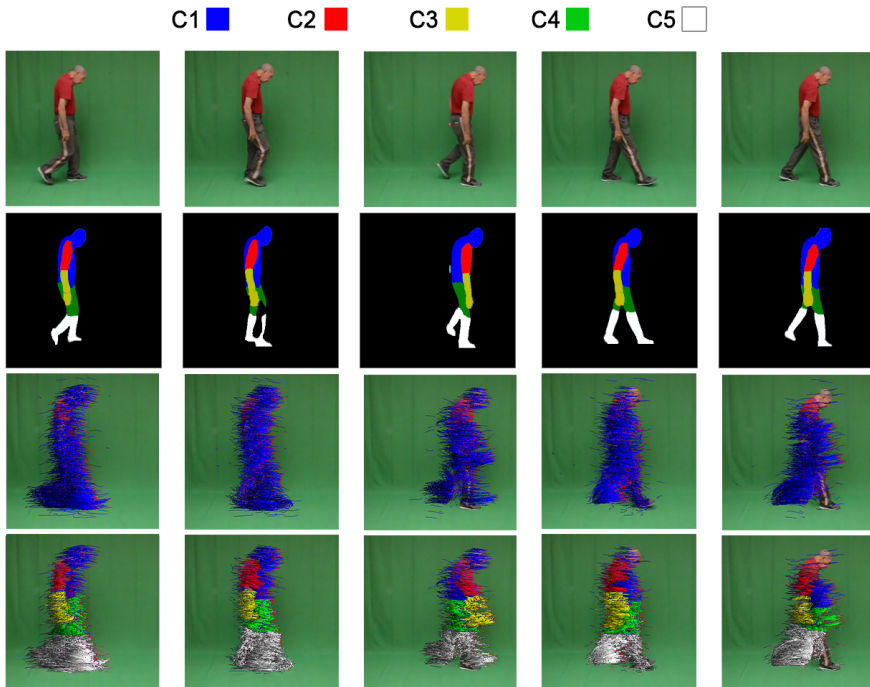


Fig. 4 First row: Original video sequence. Second row: DensePose mask. Third row: Dense motion trajectories. Fourth row: Clustered motion trajectories at current frame.

Table 1 Summary of the performance of different classification methods for each cluster using velocity description. Global Dictionary (GD), Regional Dictionary (RD), K-means Centroids (KC).

	C1		C2		C3		C4		C5	
	RF	SVM	RF	SVM	RF	SVM	RF	SVM	RF	SVM
DP-GD	94.73	92.05	94.73	92.61	98.86	94.32	99.62	94.89	99.62	97.73
DP-RD	98.83	93.18	98.69	90.91	98.86	88.64	98.86	84.66	99.62	97.73
DP-KC	77.22	72.02	75.02	72.32	68.82	70.20	71.20	66.26	67.29	73.22
KM-GD	96.56	96.59	97.73	96.59	98.86	94.32	97.73	96.59	98.86	90.34
KM-RD	93.13	79.66	93.07	91.02	92.90	89.32	93.45	89.32	93.40	87.05
KM-KC	72.02	70.52	71.20	66.82	70.80	67.29	72.54	66.26	72.48	66.62

Table 2 Kinematic evaluation per cluster using the best performance classification method (DP-RD with RF).

	C1	C2	C3	C4	C5
velocity	98.83	98.69	98.86	98.86	99.62
acceleration	90.31	88.28	91.45	88.28	89.39
curvature	99.62	97.80	96.74	93.89	94.30

Tables 1 and 2 present an ablation study of the proposed approach, using different configurations, baseline components and evaluating the capability of motion descriptors, coded at each body segment, to classify automatically PD patterns. For each video, a set of kinematic trajectories was extracted, and for each trajectory, dartboards were computed with a number of radial bins set to 4 (each bin being 6 pixels wide) and 18 angular bins (9 for the velocity) of 20 degrees. We also evaluated the best regional coding descriptor, regarding the three defined schemes: the bag of words (BoW) with global dictionaries (GD), BoW with regional dictionaries (RD) and K-means Centroids (KC). Each regional descriptor was evaluated with body-part segmentation, obtained from two different strategies: 1) using the dense pose approach (DP) and 2) using a spatial k-means trajectory clustering (KM). Besides, to analyze regional correlation of motion patterns with the PD, the evaluation was carried out independently for each of the considered segments.

Finally, each video descriptor was classified using either Random Forest (RF) or Support Vector Machine (SVM). As shown in Table 1 the proposed approach has a stable performance w.r.t. the different configurations, and using different classifiers. It should be noted that the best spatial clustering is achieved from *DensePose* (DP), using a regional dictionary (RD) and RF. The better performance of Random Forest can be explained by a finer boundary construction of the model based on the set of discrete trees. As expected, the lower limb regions provide the best results, with major discriminative performance to classify PD patterns, achieving an average accuracy of 99.62% (see Table 1).

Interestingly enough, the proposed approach exploits the kinematic description of various body regions, which could be determinant in PD diagnosis. For

instance, the head region achieves by itself an average accuracy of 94.73%, using the best approach configuration. C3 (region that includes lower arms and hands) also achieves a remarkable accuracy of 98.86%. These regions can then be integrated in a clinical analysis to better understand a particular stage and progress of the disease, fact that could be key to understand early stages of the disease.

In Table 2 is carried out a second experiment, from which the best classification setup was analyzed regarding the three different kinematics computed for each cluster. The purpose is to determine the kinematic patterns that are most relevant w.r.t. the disease. The velocity patterns appear to have major description capability on lower limbs, which in fact is related with a well know PD pattern. In fact, the use of only velocity patterns obtains an almost perfect score on classification. Regarding head patterns, the curvature coded from trajectories could be strongly correlated with PD. This can be related to rigidity of the head and part of the trunk. Finally, the velocity and curvature reach the best classification performance with an average accuracy of 99.62% for C5 and C1, respectively. Also worth mentioning is the region C3, related with hands, that is the most discriminant when the descriptor is formed from acceleration only. This could be related with hand tremor and suggest to combine complementary patterns to better differentiate among PD and control patients.

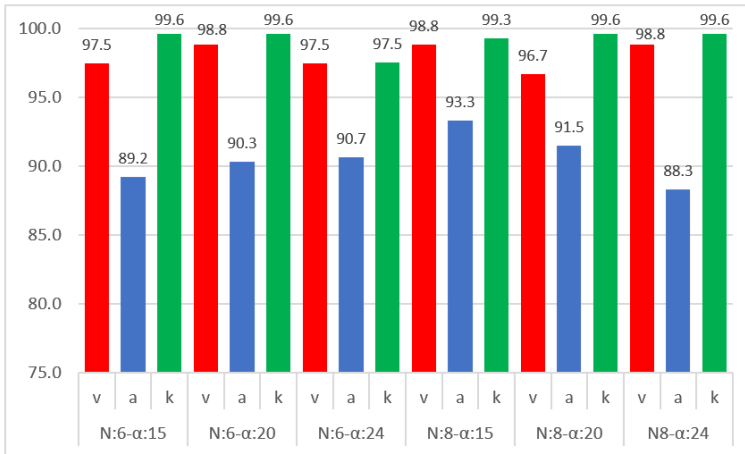


Fig. 5 Kinematics evaluation. Accuracy for cluster C1 (head and torso) for different parameters values where N represents the number of radial bins and α represents the angle of each angular bin.

Figure 5 shows a more detailed analysis w.r.t. the dartboard parameter tuning. For this purpose cluster C1 was chosen, due to the capture of two of the most relevant biomarkers for PD, *i.e.*, head motion rigidity, and trunk stability. Confirming previous experiments, all kinematics obtain fair performance, and the curvature reports the highest accuracy. Parameters selection seems to

be dependent on each kinematic. On the one hand, in general, both the curvature and the velocity present good results, above 95%. The acceleration on the other hand, varies around 90% of accuracy and reaches its maximum value with the configuration N:8- α :15, achieving a 93% score.

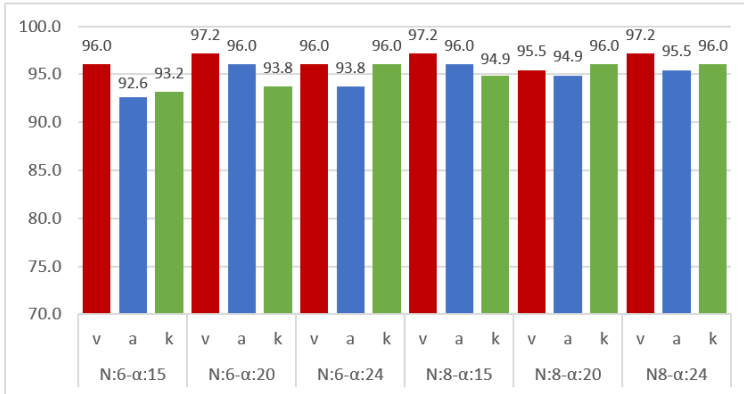


Fig. 6 Global Motion Descriptor. Accuracy for the whole set of trajectories without segmenting the body in regions, and with Dartboard parameters variation where N represents the number of radial bins and α represents the angle of each angular bin.

In a final experiment, the motion representation from dense trajectories was obtained without taking into account body segments. The purpose is both to assess the interest of body part segmentation and to check the capability of a global pattern to represent PD. Figure 6 summarizes the obtained results, for different kinematics, and using different dartboard configurations. It turns out that the global motion representation achieves a remarkable result, where velocity in general has the best and more stable performance. Interestingly, the analysis of motion descriptor over specific body regions (previous experiments) result in a better representation, even considering that there are less trajectories to carry out the analysis.

4 Discussion and concluding remarks

This work introduced a novel markerless approach that exploits dense beams of trajectories, grouped and analyzed at each body segment, that allows to finely characterize motion alterations related with Parkinson's disease. This model is able to obtain a multi-level motion representation, starting from a description of each trajectory by its distribution of local kinematics, computing dartboards (polar histograms) which encode velocity, acceleration and curvature features. In a second motion-representation level, using the body segmentation provided by *DensePose*, the method uses clustering to obtain regional locomotion patterns. Finally, those motion patterns are used in a supervised learning framework to predict and automatically classify Parkinsonian conditions. The

proposed approach, on a dataset with 22 patients, demonstrated a high discrimination power with respect to disease classification. In fact, during the evaluation, and using only the lower body segments, the proposed approach achieves an average classification score of 99.62%. This result was obtained by only using the velocity as basic kinematics. Interestingly enough, the proposed approach properly captures head and trunk motion patterns, achieving for both regions 94.73% of classification accuracy. Such fact results very relevant, since recent works have determined the head and trunk patterns as major biomarkers of the disease. In fact, the proposed method exploits the augmentation of tremor and postural instability during locomotion, which could be key to model patterns on early stages of the disease.

In clinical routine, Parkinsonian, and motion alteration patterns in general, are quantitatively captured from classical gait analysis, that includes the approximation of body dynamic from a set of markers. This markers methodology has standard protocols that allows an easy interpretation of a particular patient analysis. Nonetheless, this approach is invasive, alters the natural gesture, and its coarse dynamic analysis can limit the description of PD. In fact, several motion patterns like trunk instability (stationary feature), as well as hand and head tremor motions, could be easily undetected or associated to control patterns. Hence, novel approaches that capture the natural movement and recover a major dynamic description, are needed, to better characterize PD. For instance, Verlekar *et al* [17] achieved 98.8% of accuracy classifying control gait and three emulated impairments on nine male and one female persons. They achieved a right and left feet differentiation using a silhouette-based method. On the other hand, our method shows kinematic complementary in the regional description of movement. Acceleration, for example, turns out to be particularly useful to characterize the motion patterns of the upper body. This has already been suggested in other works such as Latt *et al* [35]. They model acceleration using the root mean square of torso signals of PD patients with fall history, PD patients without a fall history control subjects, and conclude that acceleration patterns of the upper body during gait differ between older people with and without PD. This approach however, performed a visual analysis of the measures and did not evaluate their utility in the prediction of the disease.

The proposed approach was quantitatively assessed, and proved to be effective to classify Parkinsonian patterns w.r.t control gaits. A major contribution of the proposed strategy is the capability to recover kinematic patterns in different body segments, particularly, for head and trunk regions, which turned out to be decisive PD biomarkers. Also, the characterization of lower limbs segments resulted totally effective to determine abnormal patterns. **In such sense, this strategy may be introduced on clinical protocol and Parkinsonian index complementing observational assessments to support clinical diagnosis as a digital biomarker of the disease.** In fact, the proposed strategy carried out a kinematic analysis at different body parts, including upper limbs that may be key to understand disease asymmetry, as well as the trunk rigidity patterns,

that have been widely documented as correlated with PD [36]. Besides, this strategy may be adjusted to monitor other locomotor diseases, by including a related population into the study. In such case, we need to re-train the local kinematic analysis and the machine learning algorithms to predict new classes or face a multiclass problem. It should be noted that the proposed approach only requires 200 scalar values to represent a global gait descriptor, which is a guarantee of computational efficiency.

The proposed approach coded a set of dense trajectories that capture dynamic of each body segment, contrary to the gait laboratory that follows specific and well-suited trajectories in specific joints. In such sense, we are dedicated to exploit motion descriptors that allows an automatic classification of PD patterns with respect to control motions. In contrast, the gait lab gives a complete kinematic description of each joint trajectory, which allows to analyze angular anomalies during gait cycle, for a wide spectrum of locomotor diseases. We consider that the proposed methodology may complement the classical gait analysis, achieved from optical marker system, and may contribute with dense kinematic patterns obtained for different body segments. These kinematic descriptors may help to analyze disease in more early stages or into personalized setups to discover the main affected body side. The proposed methodology is limited to analyze PD patterns, during locomotion of autonomous patients that do not have any extra requirement to carry out the displacement, *i.e.*, any mobility aid. Nonetheless, the patients with these limitations are already in an advanced stage of the disease, and therefore this type of diagnostic support tools is not required. Future works will include additional studies to compare the effectiveness of the method by considering the medication (or non-medication) of patients in the experiments. Perspectives of this work also include the effect of integrating kinematic patterns that result from different body parts, to establish a more personalized signature of each patient with respect to PD progression. The Parkinsonian patients involved in this study were characterized in stages 2.5 and 3 of the disease. Further works will test this descriptor in early stages and make a longitudinal study to characterize the evolution of the disease.

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Declarations

- Conflicts of Interest: None.

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- Ethical Approval: This study was approved by the Ethical Committee of the Universidad Industrial de Santander (session held on July 19th, 2019) and counts on a written informed consent.

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