TALLINN UNIVERSITY OF TECHNOLOGY

School of Information Techonoligies

Dmitri Golovatš 164096IAPB

DETERMINING THE MINIMUM AMOUNT OF MOTION TO DETECT PARKINSON'S DISEASE ON THE BASES UP AND GO GROSS MOTOR TESTS

Bachelor's thesis

Supervisor: Sven Nõmm,

PhD

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Dmitri Golovatš 164096IAPB

MINIMAALSE LIIGUTUSTE KOGUSE MÄÄRAMINE PARKINSONI TÕVE DIAGNOOSIMISEKS TÕUSE JA MINE TESTI PÕHJAL

Bakalaureusetöö

Juhendaja: Sven Nõmm,

PhD

Tallinn 2019

Author's declaration of originality

I hereby certify that I am the sole author of this thesis. All the used materials, references to the literature and the work of others have been referred to. This thesis has not been presented for examination anywhere else.

Autor: Dmitri Golovatš

20.05.2019

Abstract

Up and Go gross-motor test provided to analysis human motion. Motion Mass parameters are designed to detect violations in the human gait.

The main idea of this work is to determine whether it is possible to obtain more accurate or similar data in a shorter period of time that the full test analysis.

In this study, an application for human motion analysis has been developed as a part of the research. This application works with data that was obtained by Kinect motion sensor.

To fulfill the main purpose walk forward phase of Up and Go test was separated in to 10 slices and calculated with cumulative and non cumulative periods. Moreover it was decided to use machine learning classifiers to predict class for Parkinson's disease and health controls.

Created application allows to observe movement animation in three planes: three dimensional space, (x, y coordinates), (z, y coordinates). This feature allows to detect the problems during movement data recording.

Analyzing and comparing the value obtained during the test the differences were found in a number of several points of the human body.

This thesis is written in English and is 27 pages long, including 7 chapters, 14 figures and 4 tables.

Annotatsioon
Minimaalse liigutuste koguse määramine Parkinsoni tõve diagnoosimiseks tõuse ja mine testi põhjal

Tõuse ja mine test on loodud, et ette näita inimeste liikumiste analüüsimiseks. Liikumismassi parameetrid ette näitavad inimtegevuse rikkumiste avastamiseks.

Selles uuringus töötati uuringu osana välja taotlus inimese liikumise analüüsimiseks. See rakendus töötab Kinecti liikumisanduri abil saadud andmetega.

Peamise eesmärgi saavutamiseks jagati ülemineku- ja üleminekuetapid üles ja üles kümneks osaks ning arvutati kumulatiivsete ja mittekumulatiivsete perioodidega. Lisaks otsustati Parkinsoni tõve ja tervise kontrollimiseks kasutada klassiõppijaid.

Loodud rakendus võimaldab teil jälgida liikumise animatsiooni kolmes tasapinnas: kolmemõõtmeline ruum, (x, y koordinaadid), (z, y koordinaadid). See funktsioon võimaldab tuvastada probleeme liikumisandmete salvestamisel.

Uuringu käigus saadud väärtuste analüüsimine ja võrdlemine leiti erinevates inimkeha mitmes punktis.

Lõputöö on kirjutatud inglise keeles ning sisaldab teksti 27 leheküljel, 7 peatükki, 14 joonist, 4 tabelit.

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List of abbreviations and terms

TalTech	Official abbreviation of Tallinn University of Technology.
Kinect	Microsoft Kinect sensor.
CSV	Comma Separated Values.
JSON	JavaScript Object Notation
PD	Parkinson's disease
HC	Health control
Python	Python 3 programming language.
MM	Motion Mass.
E	Euclidian distance.
Tm	Trajectory mass.
Am	Acceleration mass.
Vm	Velocity mass.
Jm	Jerk mass.

1 Introduction

At the present moment human gait analysis is in use in medicine purpose for diseases diagnostics. However it's necessary to use expensive devices and equipment for human motion capture, moreover an appropriate specialist is required to use this equipment and it may also be inconvenient for patients as it will make them adapt to new conditions which makes the analysis process more time consuming. The necessity for constant fine installation of the equipment makes it unreasonable to use it on a everyday basis. On the other hand instead of equipment it is possible to hire the appropriate human motion specialist. Nevertheless specialist assessment can take a long time, and the result can be subjective, which makes this analysis not accurate.

One of the alternative solutions for human motion analyzing can be the use of simpler and more convenient devices such as Kinect. However Kinect have a problem with the recognition of the movement of the human model, in particular the lower part of human body [1]. In addition today we have two versions of Kinect, moreover in Figure 1 we observe the different human body model captured by Kinect v1 and Kinect v2. The main difference is the various number of captured human body points. However Kinect this device is more simple to use and has free software development kit [2]

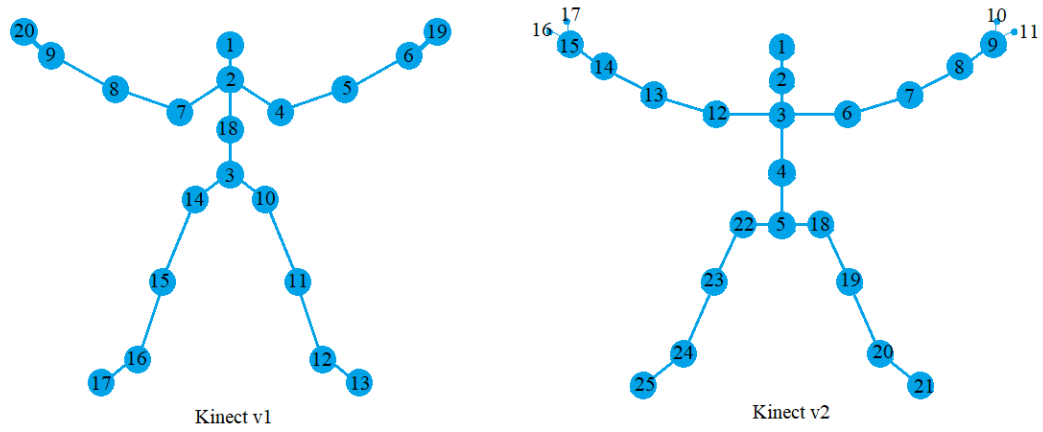

Figure 1: Human body model capture by Kinect v1 and Kinect v2

The main goal of the present research is to answer the question whether it is possible

to shorten the walking phase of the Up and Go test without loosing the accuracy of machine learning classifiers used to detect symptoms of Parkinson's disease (PD). That is, take the walk forward phase from the test and divide it into 10 equal parts.

To achieve this goal a standalone application to conduct observations and perform necessary computations was developed. Application that can make analysis of recorded data from two version of Kinect and provide the user basic tools to make analysis more easily and allows to view the recorded data. Furthermore this application need to implementation of cumulative and non cumulative data analysis to determine the minimal test duration where the difference between a Parkinson's diseases (PD) and health control (HC) groups will be the most distinguishable. To verify the concreteness of the results, it is necessary to find the values that describe the movement of a person and allow to determine the difference between the two groups (PD and C). The current approach focuses on exploring the parameters for each walk forward phase period.

The secondary goal of this work evaluating achieved results of cumulative and non-cumulative analysis for Parkinson's disease and health control groups based on Kinect obtained data. The achieved result will allow to make a conclusion. Does it make sense to do an analysis of the entire test or a separate test phase can provide more information. Does the neurodegenerative disease affect the gait of Parkinson's diseases person in comparison with a healthy person and find out which features are most distinguishable by their parameters.

At the present day most of the studies concentrate attention on the whole test without taking into account the detached parts of it or consider the results of several types of joints at the same time. The main new component of this work will be to obtain data in a shorter period of time.

This work is organized as follows: Section 2 introduce the hardware and software that are used to collect data from Up and Go test for two groups of people. Section 3 provides us to algorithms and classifiers used in this work. Section 4 describes the software implementation for current work. Section 5 present the achieved results, results validation and their comparison with previous work. Section 7 describes the

conclusion of the this work.

2 Background

2.1 Hardware

2.1.1 Kinect

Kinect is a device that consists of several parts: infrared sensor, depth camera, microphone and RGB camera. However first Kinect v1 allows to capture 20 joints of human body, while Kinect v2 can capture 25 joints. Kinect was used to capture the human body. One of the main advantages of using this device is the ability to capture human body in three-dimensional space [2].

2.2 Software

To store human motion data was used TalTech laboratory developed software by Jan-Joonas Bernstein[3]. This software works with Kinect v2.

3 Methodology

3.1 Human motion analysis

3.1.1 Up-and-Go test

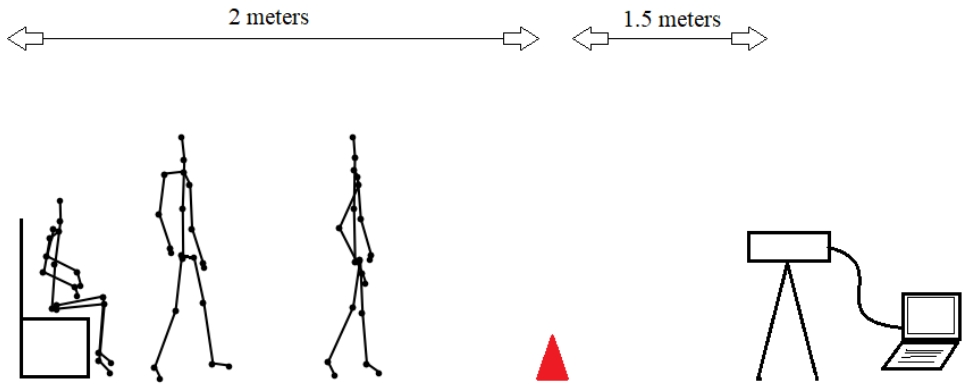

Figure 2: Up and Go Test settings

Up and Go test was conducted for two group of people. One group is people with Parkinson's disease (PD) and second group is Health control (HC). Test is based on Kinect performance restrictions. Kinect can capture human body on 1.5 to 4 meters with 30 frames per second (Figure 2). Kinect perform 20 joints of human skeleton. Up and Go contains seventh main phases.

- First phase: person are siting until the stand command
- Second phase: person stand and wait for walk forward command
- Third phase: person walk forward 2 meters
- Fourth phase: person turn around
- Fifth phase: person walk back 2 meters
- Sixth phase: person turn around

- Seventh phase: person seat on the chair

Up and Go test is provide to distinguish differences between PD and HC people. Moreover it is necessary to find minimal duration of second phase of test that can tell us, which one of people have problem with health or not. Human skeleton model that were capture by special software saved in Comma Separated Values (CSV) format.

3.1.2 Walking forward phase

For motion analysis was taken first walking forward phase of Up and Go test. This is connected with the fact that a person only adapts to what is going on and during this period the difference between a healthy person and a sick person should be most noticeable.

3.1.3 Walking forward phase separation

In accordance with the task it was decided to divide this phase into 10 equal parts for each person who passed this test. Thus, when reading files with information about the test, only those data were taken where the walk forward phase occurs. Furthermore only first walk forward phase was taken.

There is two way to store information:

- Cumulative: sum of several periods, that begin from first
- Non cumulative: calculate each slice separately

3.2 Mathematical algorithms

3.2.1 Motion Mass parameters

With a motion capture device, it's possible to present each joint (j) of human body separately. Each joint includes a set of Joints (J). Set of joints can be presented as follow:

$$J = \{j_1, j_2, ..., j_n\} \tag{1}$$

where n is number of joint. Each human body joint of interest contains number of Motion Mass parameters (MM). Motion mass parameters includes Trajectory mass, Velocity mass, Acceleration mass and Jerk mass.

$$M_j = \{Tr_m, V_m, A_m, J_m\} \tag{2}$$

Trajectory can be calculated using the difference between two points in the space, in the other words, the distance E.

$$E = \sqrt{(x_0 - x_1)^2 + (y_0 - y_1)^2 + (z_0 - z_1)^2} \tag{3}$$

where (x_0, y_0, z_o) current position of human body joint and (x_1, y_1, z_1) next position.

$$Tm_i = \sum_{n=1}^{n} E_i \tag{4}$$

$$Vm_i = \sum_{n=1}^{n} \frac{E_i - E_{i+1}}{t_i} \tag{5}$$

$$Am_i = \sum_{n=1}^{n} \frac{Vm_i - Vm_{i+1}}{t_i} \tag{6}$$

$$Jm_i = \sum_{n=1}^{n} \frac{Am_i - Am_{i+1}}{t_i} \tag{7}$$

$$t_i = t_{end} - t_{start} \tag{8}$$

where n is number of frames captured by device or selected by user.

3.2.2 Statistical hypothesis

Statistical hypothesis the assumption about the distribution of the variables or population [4]. The observable assumption may be true or not. It can be provided two types of statistical hypothesis:

- Null hypothesis (H_0): the means of two groups are equal

- Alternative hypothesis (H_1): the means of two groups are differ

To make decision on accept or reject null hypothesis it was decided to refer to the p-value. P-value show the probability of error when rejecting the null hypothesis. If the p-value less than 0.05 or 0.01 (the significance level), then we reject null hypothesis. P-value calculated with Welch's test.

3.2.3 Welch's test

Welch's test is one of statistical test and that used to compare means of two groups, however unlike Student's t-test, Welch's test is provide to compare group with different variances[5].

$$t = \frac{\overline{X}_1 - \overline{X}_2}{\sqrt{\frac{s_1^2}{N_1} + \frac{s_2^2}{N_2}}} \tag{9}$$

where $\overline{X}_1$ and $\overline{X}_2$ are means of the two groups, s_1 and s_2 are standard deviation of the two groups, N_1 and N_2 are size of the two group.

In application Welch's t-test was calculated using t-statistics Python SciPy package [6] is used Figure 3.

```
t, p = stats.ttest_ind(arr_type_HC, arr_type_PD, equal_var=False)
```

Figure 3: Welch's t-test calculated by SciPy t-statistic

3.2.4 Fisher's Score

The Fisher's score describes the ratio of the average interclass separation with respect to the average interclass separation [7].

$$F = \frac{\sum_{n=1}^{k} p_j(\mu_j - \mu)^2}{\sum_{n=1}^{k} p_j \sigma_j^2} \tag{10}$$

where μ_j is the mean, μ is the global mean and σ_j is the standard deviation of the group belonging to class j. p_j is the fraction of data points. Biggest Fisher's score may be select to for use with the classification algorithms.

3.2.5 Logistic Regression

Logistic Regression is one of the probabilistic classifiers that can classify problems with two outcomes. Since Logistic Regression use a specific modeling assumption to display the feature variables to a class-membership probability. Logistic Regression probabilistic model highly dependent on the data quantity and work better when input data don't contain unrelated and very similar to each other features. However Logistic regression gives probabilities for classification not only the final classification [8].

3.2.6 Decision tree

Decision tree is a tree-like structure classification methodology. Decision tree model babes on hierarchical decisions on the feature variables. Each particular node of the decision tree has the split criterion, one or more features variables. In our case decision tree has two criterion: Parkinson's diseases and health control people. To identify Parkinson's diseases decision tree need to train most valuable data, that can help us to distinguish the difference between Parkinson's diseases and health control people [8]

3.2.7 Support vector machine

Unlike Logistic regression and Decision tree Support vector machine (SVM) is defined for binary classification, that means that SVM works with numeric data. As the linear models, SVM uses to separate data between two classes [8].

3.2.8 K-Nearest neighbors

K-Nearest neighbors is classifier that provide to work with virtually any data type. Any test for k-nearest neighbors training data must be determined. On the one hand k-nearest neighbor has high efficiency with large training data. On the other hand k-nearest neighbor need to determine the number of nearest neighbors and secondly this classier does not train on the training data, but simply uses training data itself for classification [8].

4 Software implementation

4.1 Input data

Created application works with Comma Separated Values (CSV). File contains human Up and Go test information with 68 columns, which contains number of frames, timestamp, human joints in xyz coordinates and markers of test phase. Each file row include frame number, a timestamp and x, y and z coordinates for every point of human body that was captured by Kinect. Kinect motion captured speed is approximately 25 frames per second. If file structure is correct, that application allows to work with this file. In additional application works with data that was stored from Kinect v1 and Kinect v2.

4.2 Visualization

Captured Human model showing person in three planes: (x, y coordinates), (z, y coordinates) and 3D space. These views allows to observe each movement of a person in space in more detail, which helps in identifying inaccuracies in recording data. The Figure 4 shows a 3d model of a person obtained from a file with test data

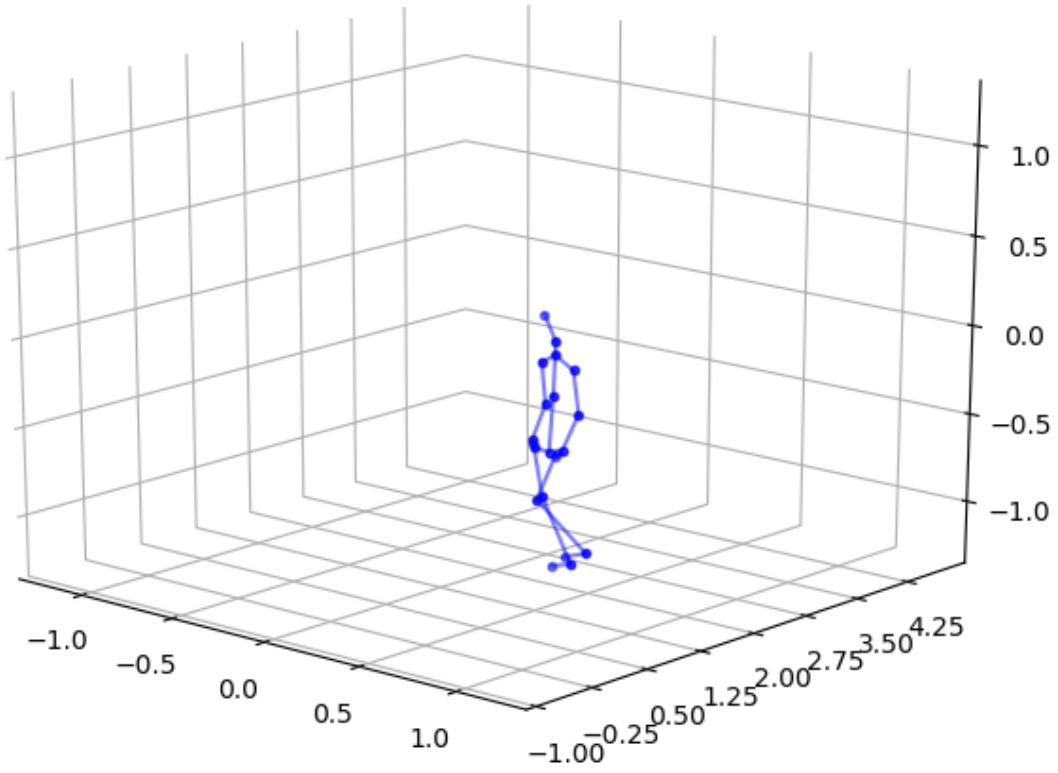

Figure 4: 3D human body model

The application show 4 Motion Mass parameters graphs. Each charts includes graphs information about each joints. Graphs coordinates show parameter changes over time (x coordinate shows number of frames, y coordinate shows the value of the parameter). In additional user choose joint to observe, this give user more valuable information about human motion. In Figure 5 presents a graph of velocity changes of the left foot (red) and head (blue).

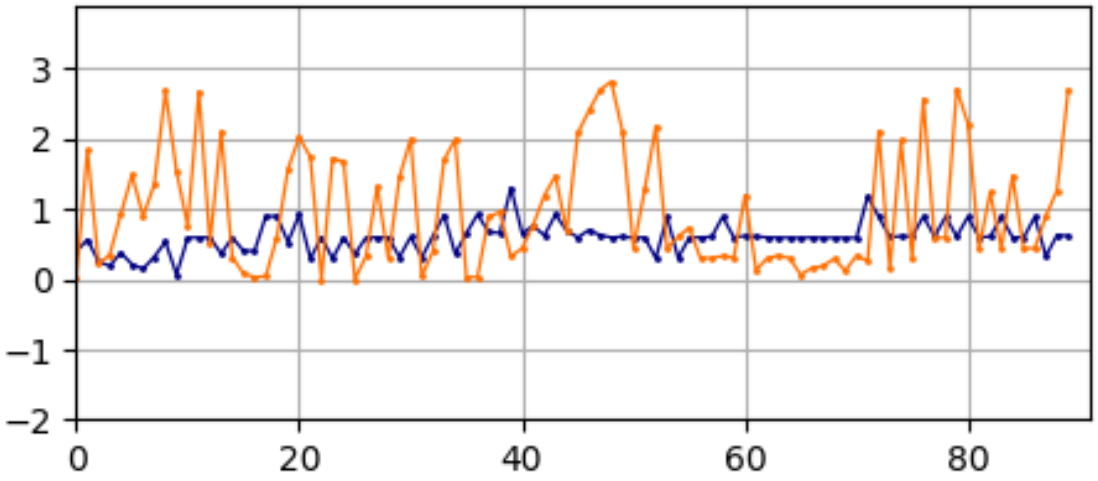

Figure 5: Velocity graph

Based on user selected joints, the application allows to calculate angles between 3 joints. For example Figure 6 shows angles between right hip - right knee - right ankle give information about right leg bending.

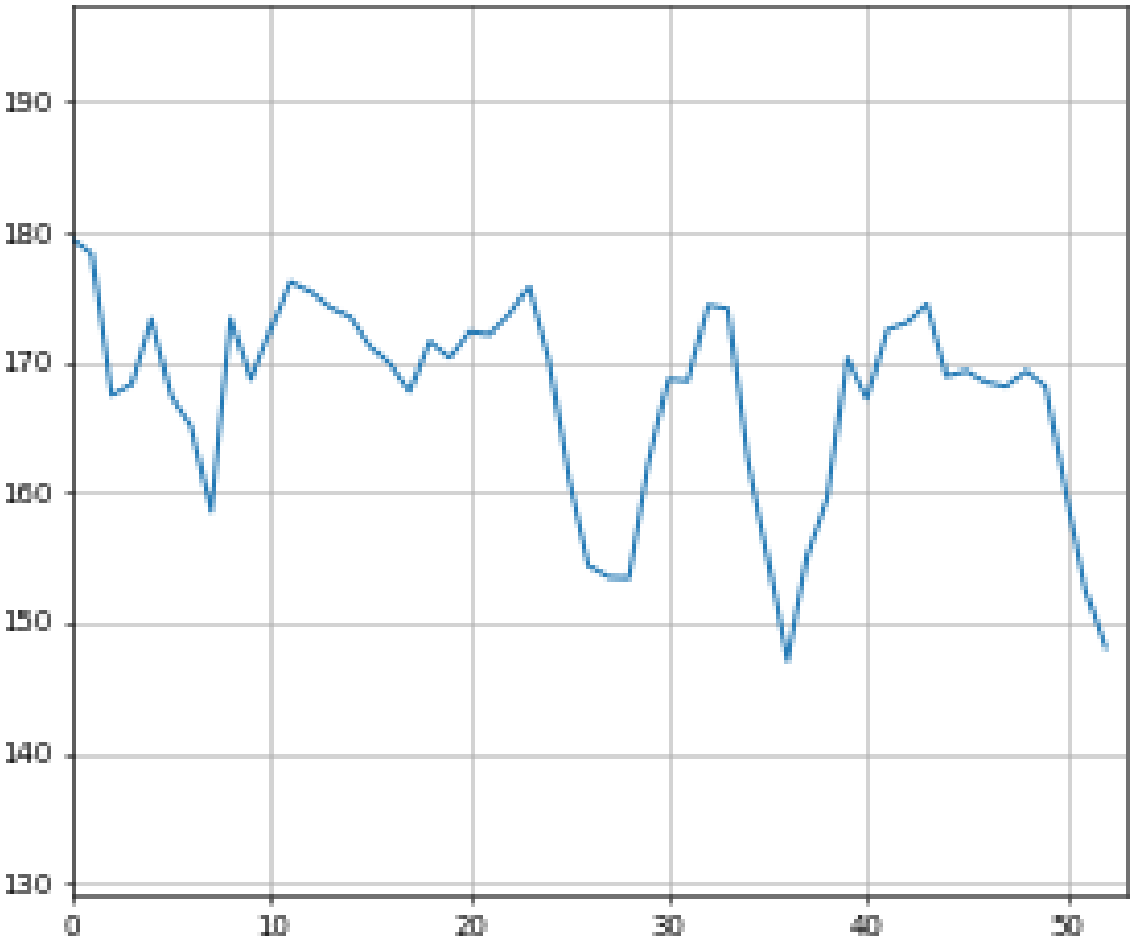

Figure 6: Right hip right knee right ankle angles

The application allows user calculate Motion Mass parameter for number of human body points at the same time. This feature allows to see sum of parameters over time. It can be used to compare different test subjects on same test phase. For example Figure 7 presents right hand trajectory mass parameters sum.

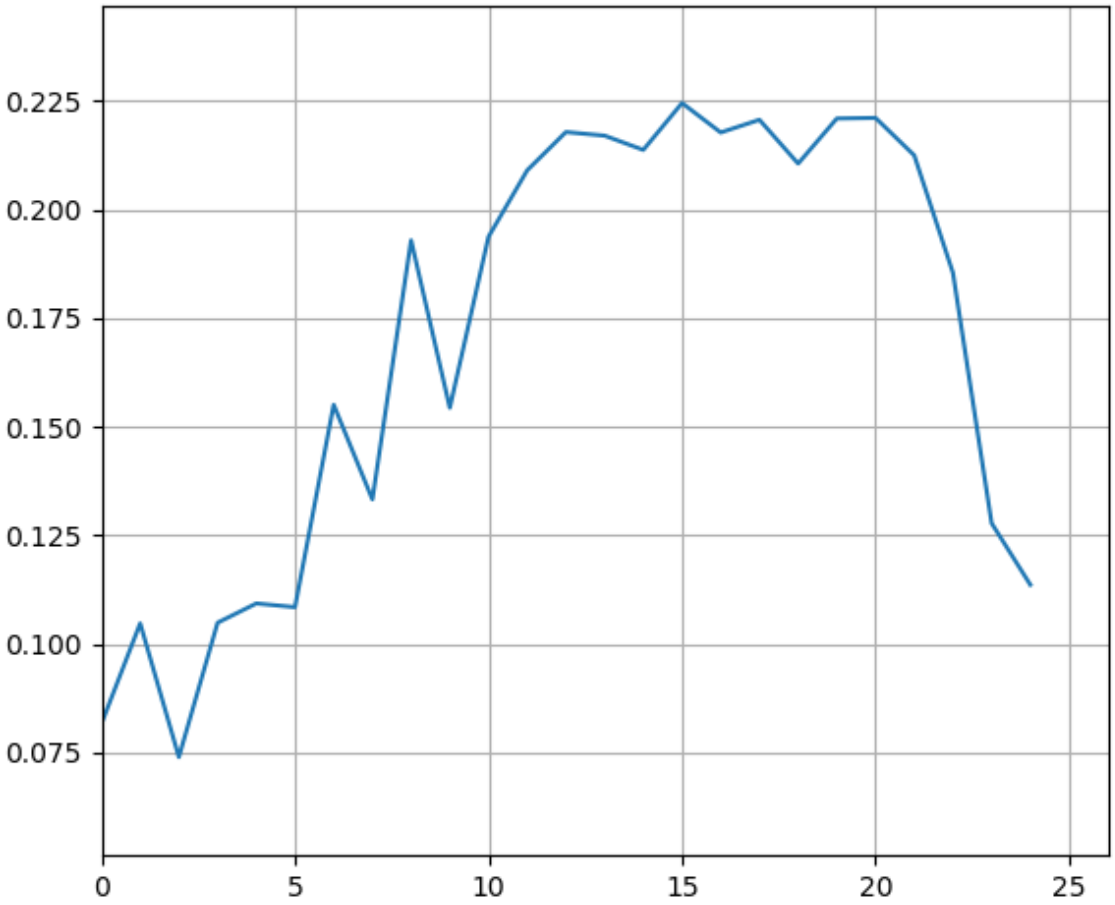

Figure 7: Right shoulder Right elbow Right wrist Right hand Trajectory mass

4.2.1 Slice analysis visualization

User select walk forward phase period. Slice analysis data created by user choices. All data separated by Motion Mass parameter type and human body point. Afterwards, the application creates 4 windows, each window present motion mass parameters with p-value and fisher's score for all human body points. The Figure 8 describes all human body points Trajectory mass for cumulative period (from 1 to 10 slice) of walk forward phase.

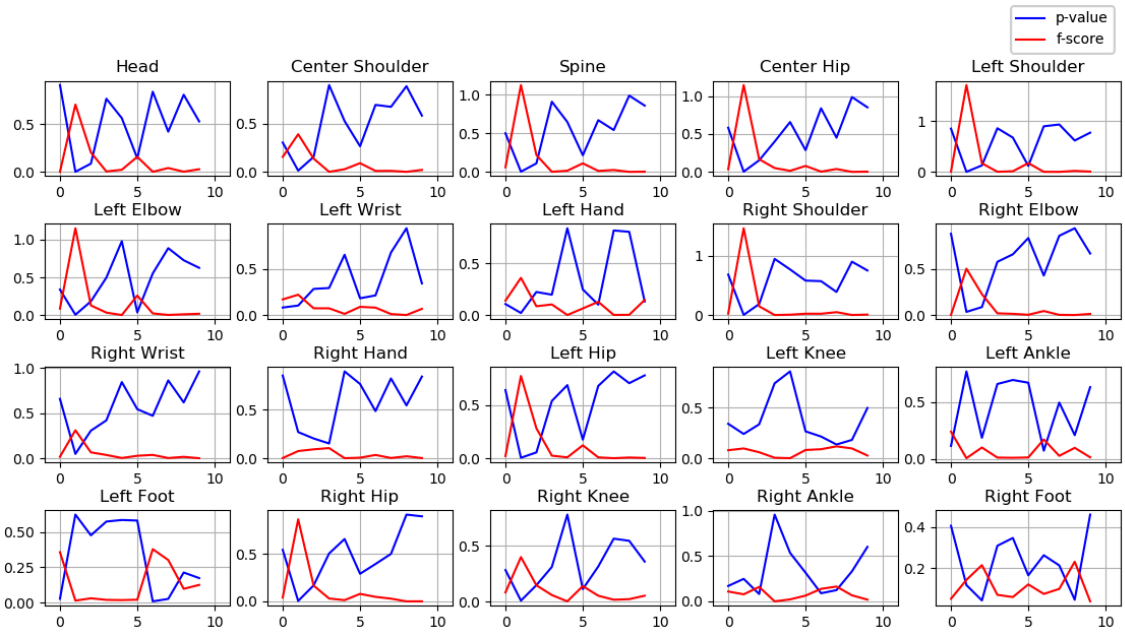

Figure 8: Trajectory mass for cumulative period

4.3 User Interface

The User Interface was created using PyQt5 (Figure 9) [9]. All graphs and animations were created with Matplotlib [10].

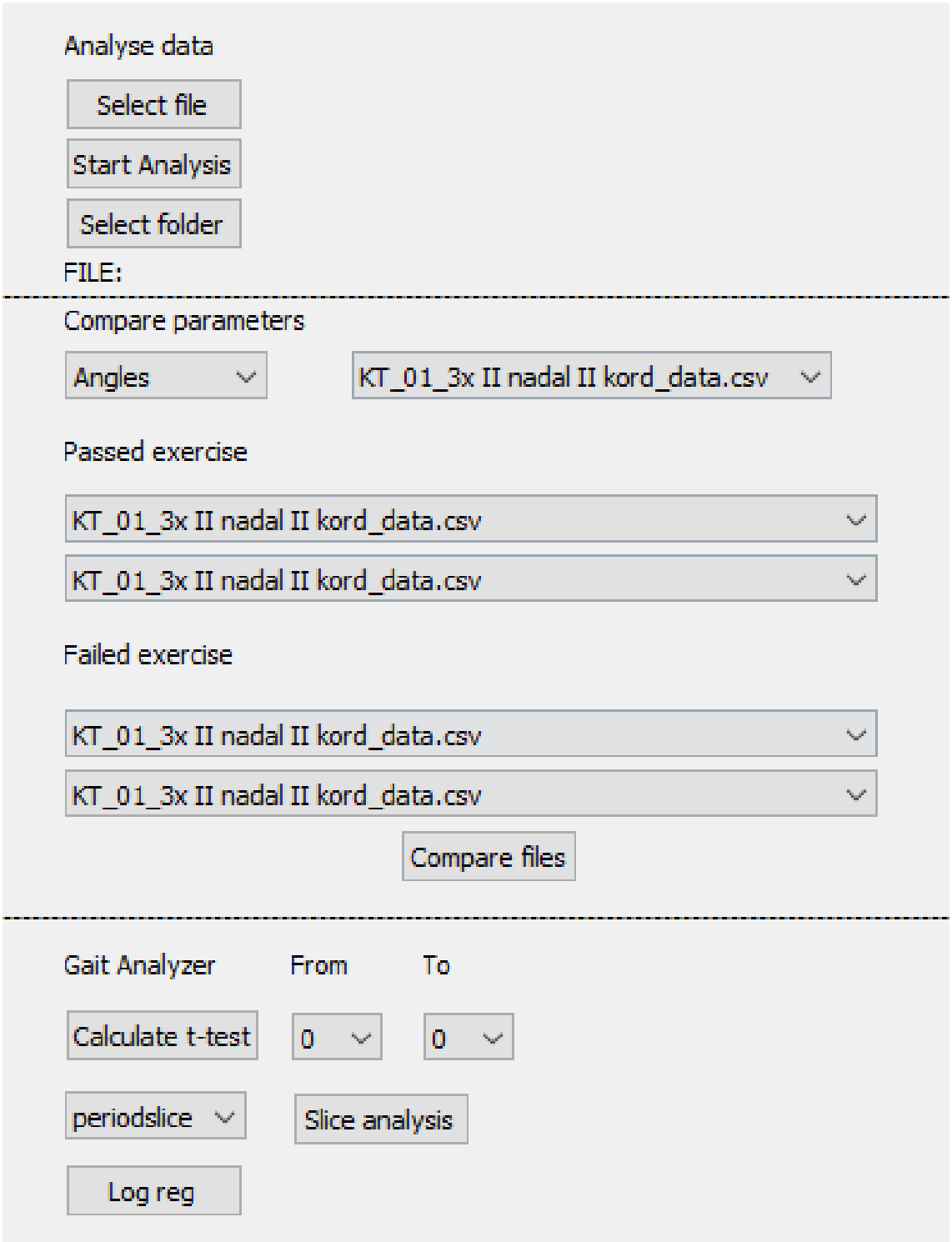

Figure 9: User Interface

4.4 Methods implementation

4.4.1 Motion Mass parameters

The application calculate 4 Motion Mass parameters for each person from two groups of PD and HC, furthermore the application takes only first walking forward phase. Motion Mass parameters for each joints: Trajectory mass, Velocity mass, Acceleration mass, Jerk mass.

4.4.2 Angles

The application allows user to select 3 different human body points to calculate angles them during test. In Figure 10

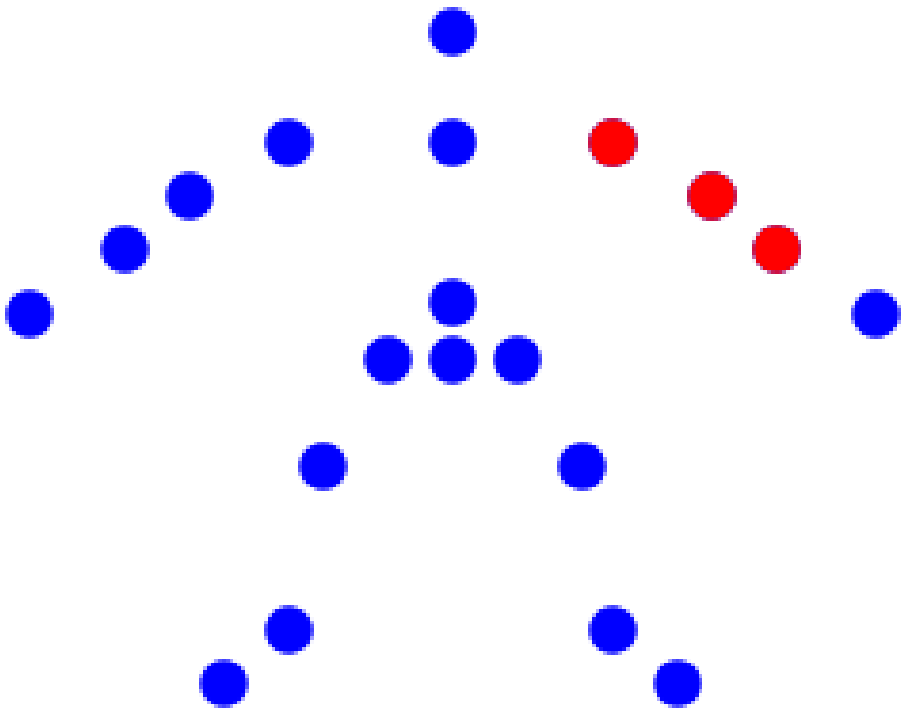

Figure 10: Select points to calculate angles between red points

4.5 Slice analysis

Each file contains number of frames for the test, based on this number it's possible to separate them into 10 slices. Afterward user can select period for analysis. For

each period application takes all files, calculate Motion Mass parameters, p-value and fisher's score for all persons, all human body points and save data in JavaScript Object Notation (JSON) format.

Information from JSON information from files can be displayed graphically. For example Figure 11 describes cumulative period for each human joint, where red line is p-value and blue line is fisher's score.

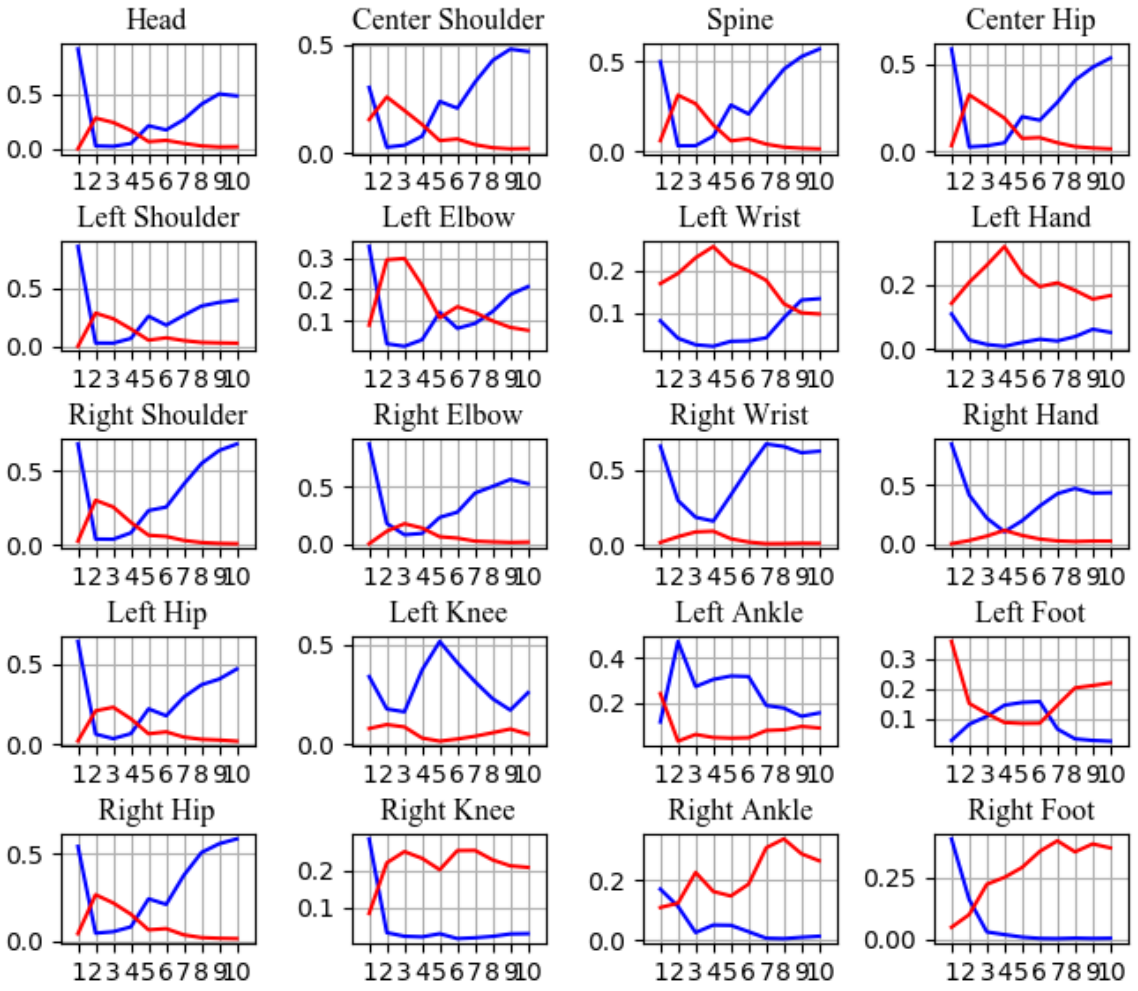

Figure 11: Cumulative graph for each human body point with p-value and fisher's score

4.6 Feature selection

Based on graphs information user can select that were shown in the previous paragraph the application allow to see three most informative human body points. The application draws 3D scatter plot, where blue dots is health control and red dots is Parkinson's disease people. 12

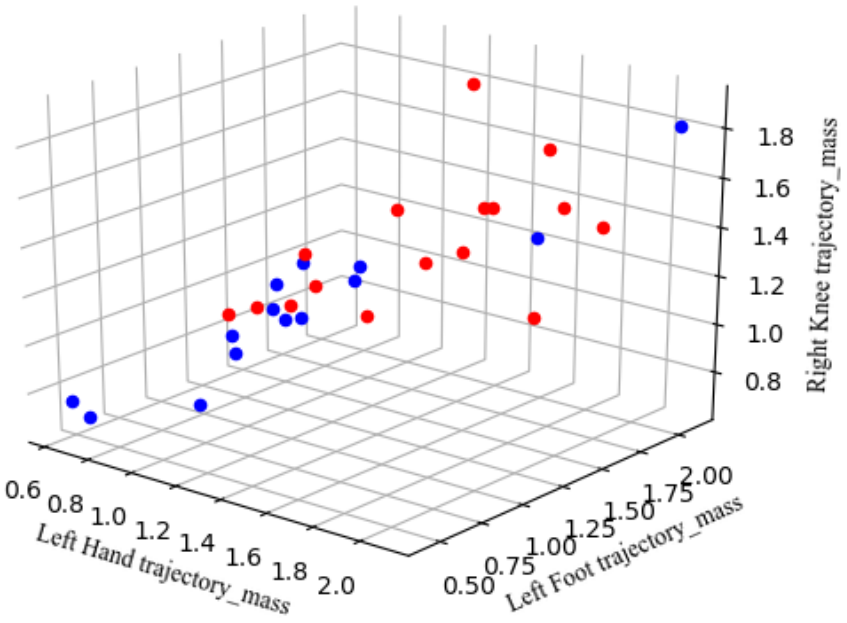

Figure 12: 3D scatter plot of three human body point for cumulative 1-8 period

5 Results

5.1 Statistical hypothesis test

The main purpose of the statistical test is distinguish the differences between Motion Mass parameters of Parkinson's diseases and health control group. In section 3.2.2 as results we have two hypotheses. The null hypothesis says that the Motion Mass parameter for human joint of the Parkinson's disease and health control groups are the same. Alternative hypothesis says that Motion Mass parameter for human joint are different for Parkinson's disease and health control groups. With the purpose of the work, it is necessary to find at what period the difference in the average of the values of the parameters of the two groups is most noticeable. Based on data quantity and test results differences was found with significance level 0.05. The Table 1 show results for cumulative results null hypothesis was rejected for 7 times at period (0 - 9) for Trajectory mass with right foot, right ankle, right knee, left foot, left ankle, left hand and left wrist. 9 times for Velocity mass with right foot, right ankle, right knee, left foot, left ankle, left knee, left hand, left wrist, left elbow. Based on table results it is possible to plot three most informative joints.

Points	Tm	Vm	Am	Jm
Head	0.28593	0.12597	0.48372	0.26614
Center Shoulder	0.38070	0.18014	0.48606	0.03911
Spine	0.33864	0.13515	0.25754	0.33070
Center Hip	0.32719	0.13402	0.28769	0.72246
Left Shoulder	0.15371	0.05574	0.10140	0.42354
Left Elbow	0.06916	0.02683	0.32862	0.79344
Left Wrist	0.04952	0.03002	0.76048	0.72832
Left Hand	0.01203	0.00738	0.73615	0.63967
Right Shoulder	0.56632	0.26841	0.38546	0.15994
Right Elbow	0.53693	0.25139	0.85003	0.85008
Right Wrist	0.60310	0.34322	0.26765	0.62671
Right Hand	0.35495	0.20019	0.38852	0.72159
Left Hip	0.24788	0.09964	0.03826	0.50497
Left Knee	0.07385	0.04256	0.92869	0.40535
Left Ankle	0.03756	0.01904	0.81061	0.22799
Left Foot	0.03330	0.02102	0.17805	0.63236
Right Hip	0.43233	0.18609	0.39043	0.94841
Right Knee	0.01482	0.01075	0.52296	0.04728
Right Ankle	0.01344	0.01173	0.79346	0.08713
Right Foot	0.00717	0.00603	0.21081	0.34847

Table 1: ρ-value for Motion Mass parameters with all joints

5.2 Feature selection

Based on results from Table 1 we can observe three most informative joints with the lowest p-value. The Figure 13, where Parkinson's diseases marked by red dots and health control marked by blue dots, shows scatter plot with Trajectory mass for Right foot, Right Ankle and Left Hand. In additional most valuable joint can be used to train model with a view to distinguish the Parkinson's diseases from the health control. Considering that a data quantity is involved in the analysis, one of the way to create train model and accuracy is use k - fold cross validation technique in all classifiers.

Training model based on two most informative joint with highest fisher's score Table 2 and used as predictors in decision tree, logistic regression, k-nearest neighbours and support vector machine classifiers. Based on 6 - fold cross validation in Table 3 can be consider the best accuracy achieved by used classifiers.

Points	Fisher's score
Head	0.02789
Center Shoulder	0.01865
Spine	0.02238
Center Hip	0.02347
Left Shoulder	0.05088
Left Elbow	0.08490
Left Wrist	0.09870
Left Hand	0.16432
Right Shoulder	0.00791
Right Elbow	0.00917
Right Wrist	0.00647
Right Hand	0.02062
Left Hip	0.03289
Left Knee	0.07921
Left Ankle	0.10862
Left Foot	0.11500
Right Hip	0.01495
Right Knee	0.15166
Right Ankle	0.15724
Right Foot	0.19229

Table 2: Fisher's score for Trajectory mass with all human body points

	1	2	3	4	5	6	average
decision tree	0.5	0.5	0.375	0.625	0.625	0.5	0.52
logistic regression	0.625	0.875	0.625	0.625	0.875	0.667	0.72
k-nearest neighbours	0.5	0.75	0.375	0.75	0.75	0.667	0.63
support vector machine	0.375	0.5	0.5	0.625	0.5	0.5	0.50

Table 3: Classifiers accuracy for 6 - fold cross validation

Right knee and Left arm Trajectory mass the accuracy of the logistic regression classifier predictor is 0.72 and this give us confusion matrix Tab 4, where we can observe health control (HC) and and Parkinson's diseases (PD) groups.

	Predicted (HC)	Predicted (PD)
Actual(HC)	3	4
Actual(PD)	1	4

Table 4: Confusion matrix for logistic regression classifier

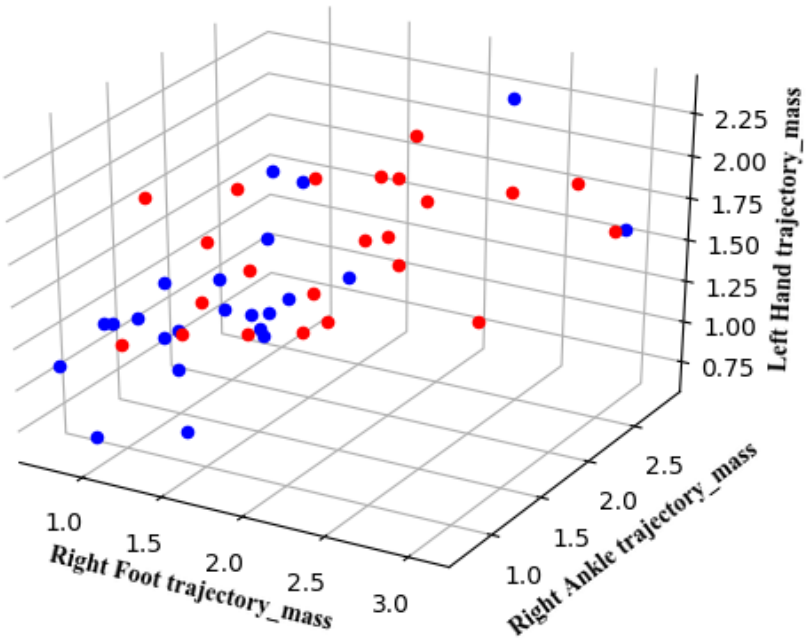

Figure 13: 3D scatter plot with three most informative human body joints

In additional it's was decided to compare same results with the previous work [11]. After calculation with the same features as [11] Right knee, Right shoulder and Right hip, the following scatter plot was obtained Figure 14, however Parkinson's diseases marked by red dots and health control marked by blue dots.

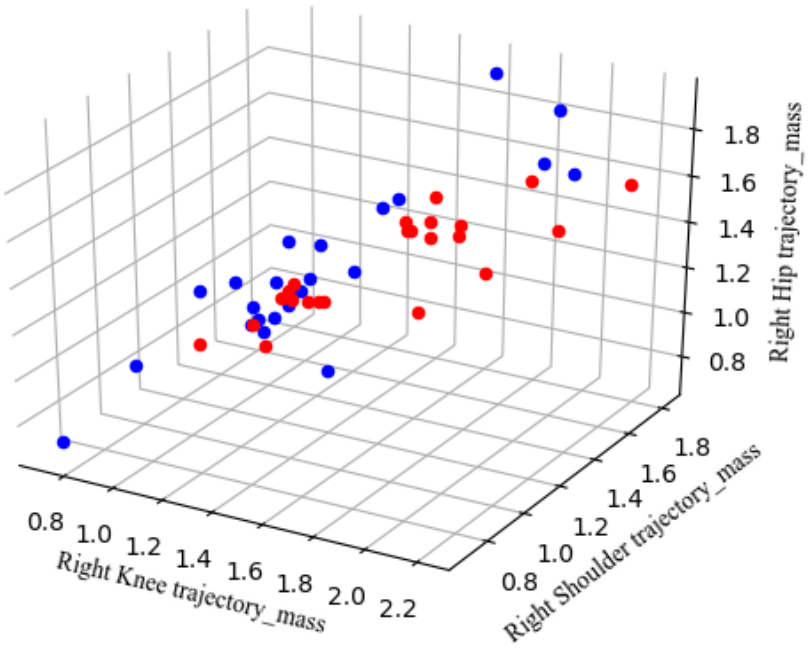

Figure 14: Scatter plot with right knee, right shoulder and right hip trajectory mass

6 Discussion

The present results of this work research were made for walk forward phase cumulative and non cumulative period with 10 intervals. However it is possible to separate period into other number of intervals. In additional it is necessary to consider other phases of this test. Consequently, there are many more options for analyzing the movement of a human body.

Usually walk forward phase of Up and Go test by steps. However each person can make different numbers of steps on the same distance, in this case it's not possible to divide phase on same number of steps, as results there no way to make objective results.

7 Conclusion

The main goal of this work was to prove that the separation of the walk forward phase can provide more information or an equal amount of information for distinguishing a healthy and Parkinson's disease person by analyzing the entire test. For this purpose the walk forward phase of Up and Go test was divided into 10 slices and separated in cumulative and non cumulative intervals. This separation was done to describe the changes of human body points during the walk forward phase.

Each slice of cumulative and non cumulative analysis provide difference Motion Mass parameters results. Based on this analysis it was selected more informative features.

The cumulative and non cumulative methods do not take into account the number of steps taken by each person who made Up and Go test, however, it all divides the walk forward phase into 10 parts. This method makes it possible to consider in more detail the phase of walk forward phase and analyzing the variability of data at smaller distances.

For all features at each period of cumulative and non cumulative analysis were calculated a Motion Mass parameters and these parameters were used to compute the p-value that was use in statistical test and fisher's score. P-value gives the probability of error occurring when rejecting the null hypothesis which means that the means of two group are not equal. Most informative method was cumulative analysis with period from 1 to 9, that contains a large number of p-values that were approached the significance level (0.05). As result statistical tests confirmed that the difference between two groups of people can be distinguished.

Highest fisher's scores were used as a predictors for classifiers. Were used two feature with highest fisher's score. After that these these features were used in k - fold cross validation. Analysis of the classifiers with cross validation for right foot and left hand demonstrate that motions of these features are differ for Parkinson's disease and health control groups.

Finally results demonstrates that cumulative analysis of walk forward phase provide

us information that in a fairly short period you can find the differences between a Parkinson's disease and healthy person. These results provide new direction for further analysis of human motion.

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