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# GEOMETRIC REPRESENTATION OF AVERAGE TRAJECTORY AND ITS APPLICABILITY TO DESCRIBE A LEARNING PROCESS 

Bachelor's thesis

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Infotehnoloogia teaduskond

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# LIIGUTUSE KESKMINE TRAJEKTOOR JA SELLE RAKENDATAVUS <br> <br> ÕPPEPROTSESSI MODELLEERIMISEKS 

 <br> <br> ÕPPEPROTSESSI MODELLEERIMISEKS}

Bachelor's thesis

Supervisor: Sven Nomm,
PhD

## 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.

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#### Abstract

The human gross-motor analysis is an area widely involved in medicine and sports. The notion of average trajectory of repeating motion is yet to gain ground in this sphere.

This study has two main objectives.

The first goal is to to relax assumptions previously proposed approach of average trajectory calculation imposes [1]. For this several average trajectory computing methods are implemented. As a comparative characteristic their applicability to describe a learning process is used.

The second objective is to represent average trajectory in the way familiar to human understanding. In order to achieve this goal a simple graphical software is implemented with use of speed based plot colouring and animation of comparable single motion.

This thesis is written in English and is 34 pages long, including 7 chapters, 24 figures and 4 tables.


# Annotatsioon Liigutuse Keskmine Trajektoor ja Selle Rakendatavus Õppeprotsessi Modelleerimiseks 

Inimeste liigutuste analüüs on meditsiinis ja spordis laialt kasutatav ala. Korduva liikumise keskmise trajektoori mõiste ei saanud veel selles valdkonnas levimust.

Selle töö põhieesmärkideks on kaks sihti.

Esimeseks on kergendada eelmiselt pakutud meetodis oletatud kitsendusi esialgsete andmete kohta. Selleks neli teistsugust lähenemist on implementeeritud. Meetodite võrreldamiseks nende sobivus õppeprotsessi kirjaldamiseks on võetud. Selle hindamiseks on leitud korrelatsioonsuhed Liigutusmassi parameetrite ja meetodite esitatavate ruumalade vahel. Meetod, mis näitab parima korrelatsiooni on valitud teiste loendist.

Teiseks eesmärgiks on edastada keskmise trajektoori inimese jaoks arusaadavas vormis, milleks on valitud graafiline esitus. Lihtne tarkvara on implementeeritud. See annab võimalust võrrelda kordatavate liigutuste keskmist ühiksalvestusega, värvida joonist baseerides inimese liigeste kiirustes ja animeerida võrreldava ühiksalvestuse luukeret.

Lõputöö on kirjutatud inglise keeles ning sisaldab teksti 34 leheküljel, 7 peatükki, 24 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. |
| Python | Python 3 programming language. |
| pandas | Python Data Analysis Library. |
| MM | Motion Mass. |
| E | Euclidian distance. |
| Tm | Trajectory mass. |
| Am | Acceleration mass. |
| Vm | Velocity mass. |
| Jm | Jerk mass. |
| Cm | Curvature mass. |
| t | Time. |
| 2D | Two dimensions, two dimensional. |
| 3D | Three dimensions, three dimensional. |
| 4D | Four dimensions, four dimensional. Includes three standard |
|  | dimensions and time. |
| DTW | Dynamic Time Warping algorithm |
| NN | Nearest Neighbours rule. |

## 1 Introduction

The gross-motor motion is a set of human joint displacement in four dimensions. It can be described by numeric characteristics, which contain a lot of information and can be easily proceeded by computers, but is not so understandable to people. At the same time perception of motion can help performer to improve results or medic to describe a pattern inconsistency while neurological diseases diagnostics.

The notion of "average trajectory" of repeating motion yet to gain ground in the area of human motion analysis. The one of methods was proposed in [1]. Still this method relies on a few strong assumptions about the initial data. The first goal of this thesis is to relax these assumptions and experiment with a number of alternative approaches.

Second goal is to make the comparing of single motion average between multiple motions comprehensible for a human and to provide a software realisation.

### 1.1 Work-flow

Three main phases can be selected to define the process of the work described and concluded in this document (Figure 1). To a greater or lesser extent, phases require experimental data to be gathered, which is another task accomplished during all the work-flow.

1. Four methods of repeating motion average trajectory calculating are implemented based on previously described approach [1]. Each method supplements the previous or addresses the issues occurred in define approaches.
2. The methods are compared by their applicability to describe learning process, relying on the notion of Motion Mass parameters.
3. One of the methods is chosen and implemented into a software, which provides an opportunity to describe average graphically and to observe it together with
single motion.


Figure 1: The work-flow markup

### 1.2 Experimental settings

The methods applicability to describe learning process is verified on example of ball throwing exercise (Figure 2). Ball throwing exercise allows to consider successful and fail trials separately. During the ball throwing the performer and basket to aim are located on the defined distance ( 3 m ). The recording equipment is capturing the movement of performer during the attempt with some frequency.


Figure 2: The model of ball throwing exercise

Two performers were captured over 15 series each consisting of 20 attempts. Both performers are right-handed and are doing exercise with right hand. Right wrist is chosen as the throwing movement representing joint. Performers showed different progress rate, which can be seen on Figure 3.


Figure 3: The success rate of two performers captured

In this study Microsoft Kinect sensor is chosen as recording equipment. Till the release of Kinect was discontinued, the official Microsoft description is no longer available. Still it is widely described in previous works on human joint movement analysis [1] [2] [3] [4]. It allows to get location of 25 human model points in the time moment with frequency of 30 s . The data is gathered with the software developed in TalTech laboratory in 2017 by J.J. Bernstein [5]. As the format of data Comma Separated Values (CSV) is used.

However all the methods described can work with trajectories defined as point chains not depending on how the initial data was gathered.

The steps explained in following sections are implemented with use of Python [6] and SciPy packages. SciPy is "a Python-based ecosystem of open-source software for mathematics, science, and engineering" [7]. Next packages are used in this work: pandas [8] for CSV format files proceeding, NumPy [9] for performing complex mathematical actions, Matplotlib [10] for graphics.

## 2 Mathematical explanations

In this section mathematical notions used in implemented methods comparison are explained.

### 2.1 Motion Mass Parameters

Motion Mass (MM) is a set of variables used to describe movement [2]. The MM vector in this analysis includes 6 previously stated and one appended parameter: Euclidian distance (E), Trajectory mass (Tm), Acceleration mass (Am), time (t) [2], Velocity mass (Vm) [3], Jerk mass (Jm) [4] and Curvature mass (Cm).

To represent the Motion Mass of the entire series of attempts (performed in one day) an average of every parameter between this day successful trajectories is computed.

$$
P=\frac{\sum_{i=1}^{n} P_{i}}{n}
$$

where $P$ represents Motion Mass parameter and $n$ is the number of trajectories.

The Motion Mass parameters of one trajectory come with following definitions:

$$
E=\sqrt{\left(x_{1}-x_{2}\right)^{2}+\left(y_{1}-y_{2}\right)^{2}+\left(z_{1}-z_{2}\right)^{2}}
$$

where $\left(x_{1}, y_{1}, z_{1}\right)$ and $\left(x_{2}, y_{2}, z_{2}\right)$ are the first and the final points of the throwing trajectory

$$
\begin{aligned}
T_{m} & =\sum_{i=1}^{n} E_{i} \\
V_{m} & =\sum_{i=2}^{n-1} \frac{E_{i}}{t_{i}}
\end{aligned}
$$

where $n$ is amount of intervals of trajectory, $E_{i}$ is distance of the interval and $t_{i}$ is
time between frame capturing.

$$
A_{m}=\sum_{i=2}^{n-1} \frac{V_{i+1}-V_{i}}{t_{i}}
$$

where $n$ is amount of velocities computed for the trajectory, $V_{i}$ and $V_{i+1}$ are initial and final velocities and $t_{i}$ is time between frame capturing

$$
J_{m}=\sum_{i=2}^{n-1} \frac{A_{i+1}-A_{i}}{t_{i}}
$$

where $n$ is amount of accelerations computed for the trajectory, $A_{i}$ and $A_{i+1}$ are initial and final accelerations and $t_{i}$ is time between frame capturing

$$
C_{m}=\sum_{i=1}^{n} C_{i}
$$

where $n$ is amount of angles of the trajectory and $C_{i}$ is curvature calculated for angle $i$ preceding interval. As a interval curvature the relation between interval length and the angle after it is taken:

$$
\begin{gathered}
C=\frac{\Delta \gamma}{\overline{a b}} \\
\Delta \gamma=\arccos \left(-\frac{\bar{a} \cdot \bar{b}}{|\bar{a}| \cdot|\bar{b}|}\right)
\end{gathered}
$$

where $\bar{a}$ and $\bar{b}$ are vectors of interval $i$ and interval $i+1$ as it is shown on Figure 4 [11].


Figure 4: The angle between two tangents of the curve

### 2.2 The volume of trajectory distribution describing shape

In [1] it was established, that during the process of learning the volume of success trajectory distribution describing shape changes. Hence it is used to mathematically represent the average computing methods.

For computing the volume the shape is reviewed as sequence of ellipse pairs. The part represented by ellipse pair in its turn is divided into tetrahedrons as it is shown on Figure 5.

The volume of every tetrahedron is calculated using the next equation [12]:

$$
\begin{aligned}
& V^{2}=\frac{1}{144}\left[l_{1}^{2} l_{5}^{2}\left(l_{2}^{2}+l_{3}^{2}+l_{4}^{2}+l_{6}^{2}-l_{1}^{2}-l_{5}^{2}\right)+l_{2}^{2} l_{6}^{2}\left(l_{1}^{2}+l_{3}^{2}+l_{4}^{2}+l_{5}^{2}-l_{2}^{2}-l_{6}^{2}\right)+\right. \\
& \left.+l_{3}^{2} l_{4}^{2}\left(l_{1}^{2}+l_{2}^{2}+l_{5}^{2}+l_{6}^{2}-l_{3}^{2}-l_{4}^{2}\right)-l_{1}^{2} l_{2}^{2} l_{4}^{2}-l_{2}^{2} l_{3}^{2} l_{5}^{2}-l_{1}^{2} l_{3}^{2} l_{6}-l_{4}^{2} l_{5}^{2} l_{6}^{2}\right]
\end{aligned}
$$

where $l_{1}, l_{2}, l_{3}, l_{4}, l_{5}$ and $l_{6}$ are lengths of tetrahedron edges.


Figure 5: The shape described by two ellipses divided into tetrahedrons

### 2.3 Welch's t-test

Welch's test is statistical hypothesis test for two unequal variances [13]. It takes as null hypothesis $\left(H_{0}\right)$, that the means of samples are equal. The alternative hypothesis $\left(H_{1}\right)$ states, that means differ. The equation for Welch's $t$-test $t$-statistics calculating is following:

$$
t=\frac{\bar{X}_{1}-\bar{X}_{2}}{\sqrt{\frac{s_{1}^{2}}{N_{1}}+\frac{s_{2}^{2}}{N_{2}}}}
$$

where $\bar{X}_{i}$ is sample $i$ mean, $N_{i}$ is sample $i$ size and $s_{i}$ is its variance.

In hypothesis testing the notion of p-value is important as well. This value is representing the probability of results inaccuracy and is used to make decision on null hypothesis rejection [14]. For calculating t-statistics Python SciPy package [7] is used (Figure 6).

```
t, p = scipy.stats.ttest_ind(test_set1, test_set2, equal_var=False)
```

Figure 6: The example of Python SciPy package usage for Welch's t-test executing

### 2.4 Pearson correlation coefficient

Correlation coefficient in statistics is used to show dependence between two variables. The Pearson's linear correlation coefficient is illustrating how linear the relation is. The coefficient value lays in interval $[-1 ; 1]$. 0 points to no correlation. -1 and 1 indicate strong negative and strong positive correlation accordingly [15]. The Pearson's correlation coefficient is computed with next equation:

$$
r=\frac{n\left(\sum x y\right)-\left(\sum x\right)\left(\sum y\right)}{\sqrt{\left[n \sum x^{2}-\left(\sum x\right)^{2}\right]\left[n \sum y^{2}-\left(\sum y\right)^{2}\right]}}
$$

where $n$ is a size of sets, $x$ and $y$ are values of variables.

For calculating the coefficient value Python SciPy package [7] is used as well (Figure
7).
r, p = scipy.stats.pearsonr(motion_mass_parameter_list, volumes)
Figure 7: The example of Python SciPy package usage for Pearson coefficient calculating

## 3 Methodological explanation

In this section the average trajectory of repeating motion calculation basic approach, previously stated solution and explored modification possibilities are described. Tested suggestions are explained one after one in the order of their occurrence.

### 3.1 Previously stated approach

All the solutions considered and verified in this thesis are based on the main approach of average trajectory calculating and analysis stated in [1]. Which means that in behalf of full understanding the fundamentals of previously proposed technique should firstly be described. In next few sections either the notion of the mean trajectory, the key steps of calculating the mean as well as the previously defined approach inherent solutions and weaknesses are explained.

### 3.1.1 Basic method explanation

The method of average trajectory calculating this thesis relies on assumes getting the polygonal chain representing so called "perfect motion" and also a shape, describing a variability of analysed trajectories. The points representing the polygonal chain are computed as the means of point sets. Such sets are composed with the points of all trajectories intersecting a defined plane. The analysis of certain amount of points lying in the same plane allows also to calculate an ellipse encasing generally all the considered points (with use of right parameters). At least three trajectories are needed to calculate the ellipse. The two dimensional (2D) example is shown on Figure 8.


Figure 8: The average point and the original points distribution describing area

The ellipse definition comes following. After computing the covariance matrix with coordinates of the plane intersection points set, its eigenvalues and eigenvectors are found. The vectors represent the ellipse radii $a$ and $b$ orientation, the eigenvalues in their turn are taken as $a$ and $b$ numeric value squares. The ellipse is represented as defined number of points distributed on its outline. Ellipse canonical equation with $a$ and $b$ as its inscribed and circumscribed circle radii:

$$
\frac{x^{2}}{a^{2}}+\frac{y^{2}}{b^{2}}=1
$$

In order to receive a volumetric shape, ellipses lying on the chosen planes are sequentially connected. The chain connecting central points of the ellipses is considered to be average motion. The methods implemented and compared in this work only differ in plane sequence choosing approaches.

### 3.1.2 Previously stated approach description and inherent weaknesses

The main idea of previously stated method is to choose planes parallel to each other and normal to one of the coordinate axes as it is illustrated on Figure 9.


Figure 9: The segment of average trajectory computed using method stated in [1] and the planes calculated

Further is given the stepwise description of plane choosing in this approach.

1. Make the decision on a leading dimension. Every three dimensional (3D) movement described by rectilinear relocation from one point to another can be decomposed to the projections on three captured dimensions. In majority of cases the vector of one of them has the biggest numeric value. The dimension relevant to the biggest change can be chosen as leading. In the case of movement described by multiple points the leading is dimension with the biggest difference between extremes. In the context of Figure 9 it is the $z$ axis.
2. Pick up the segment of leading dimension, where all the trajectories are present.
3. Define interval and for every step:
(a) Identify a plane normal to the leading dimension. With the zero as two out of four parameters, equations of the planes illustrated on Figure 9 are following:

$$
z=\text { step }
$$

(b) Find the intersection points of defined plane with all the trajectories. This includes in certain case finding the pair of points, the interval between leading coordinates of which includes step. Other two coordinates of intersection point are found in this thesis using the ratio of distances between trajectory points $a, b$ and wanted point $c$. For the Figure 9:

$$
\begin{gathered}
\text { ratio }=\frac{\text { step }-a(z)}{b(z)-a(z)} \\
c(x)=b(x)-a(x) \text { ratio }+a(x)
\end{gathered}
$$

The same comes to $y$.
(c) Compute the ellipses as it was described previously.

The main weaknesses of this approach are related to the rigid limitations the method imposes. It works well in case of unidirectional movement. However if the motion among the leading dimension achieves its extreme, it is impossible to continue analysis. As potential solution the movement trajectories can be split and each part examined separately each by its leading dimension. Still this does not allow to study the whole movement, because some parts of it are either left out, taken twice or just not related with another, which for sure can affect the results.

On the segments, where the leading dimension is dominating not so clearly, which means that difference between the coordinate changes are pretty similar, the plane normal to the dimension can capture points which are inconsistent with each other from the perspective of motion phase. For one of the trajectories captured point can already be a dimension extreme whereas for the another it is not even near. The situation in which analysis continues after the leading dimension change can also occur. This case as well leads to the scenario described in this paragraph.

Different performers are doing the same movements in different ways, so the leading dimension of the whole motion can differ. Which brings up the question of human engagement. There is a possibility of different motion phases being described by different leading dimensions, so the human being is needed to make decision of which part of motion to take into analysis. In other case the logical computer decision can turn out to be absolutely random from the motion phase perspective.

The method does not take into consideration the time. All the measures are done only in space. Yet the time taken to perform the movement in every segment of the motion is very important both in the sport exercises and motor system medical analysis.

Taking importance of the changes in one dimension higher than in the others prioritizes the one condition and reduces the impact of other circumstances. However the analysis is expected to be as impartial as possible. Which is why described limitations are tried to be relaxed in this work.

### 3.2 Changes in methodology

In order to eliminate the notion of leading coordinate the planes in the first place are captured among the movement trajectories rather than among some dimension. It turns to be possible with including of plane rotation. The idea of plane rotation and its advantages are explained in the next section.

### 3.2.1 Plane rotation

The previously stated approach assumes taking the axis defining vector as the all plane sequence unified normal vector. Considering the motion direction changes requires on its turn individual normal vectors for the planes on each step.

The relation of plane normal vector $\vec{A}$ and the plane:

$$
\begin{gathered}
\vec{A}=(a, b, c) \\
a x+b y+c z=d
\end{gathered}
$$

The plane rotation brings complexity to a intersection points finding. There is no more coordinate with value defined, which means that against every pair of points $a(x 1, y 1, z 1), b(x 2, y 2, z 2)$ in observing trajectory the following steps are used:

1. The line equation is found by $a, b$.

$$
\frac{x-x 1}{x 2-x 1}=\frac{y-y 1}{y 2-y 1}=\frac{z-z 1}{z 2-z 1}
$$

2. The intersection point $c$ of line and plane is calculated.
3. The point $c$ is checked to lay between $a$ and $b$.
4. If the previous statement is correct, $c$ is taken as the intersection point of trajectory and plane.

With the plane rotation the number of ellipses is not decided before calculation. The ellipse sequence starts from the first plane, where intersection point of every trajectory is present, and ends with the last such a plane.

The easiest way of picking direction vector is to observe the movement among the one chosen trajectory. Which heads to the concept of directive trajectory. In this study the directive trajectory is a trajectory taken to represent motion direction.

The ellipse is a 2D figure. Only two coordinates of interception points can come into covariance matrix, so the decision of which for every ellipse is made. Left out is the dimension leading on the directive trajectory current point direction vector. This dimension representing vector is the closest to be plane normal, so the changes of it are the less affected by the calculation accuracy. The coordinates of this dimension are found for each point with use of plane equation.

The understanding of step is also modified. The movement trajectories are represented as the polygonal chains, so the direction vector of trajectory is not changing constantly, but only on joints of segments. It means that every point of trajectory can be considered as step.

In the first implemented method (further the method of Directive Trajectory, DT)
the trajectory with the biggest amount of observation steps is chosen as directive.

However this approach of the plane normal vector choice leads to the dominance of one trajectory. In order to relax this dominance the plane should be corrected with considering all the other trajectories. The offered correction includes following steps:

1. For every trajectory find plane intersection point.
2. For every trajectory find the direction vector in the point.
3. Calculate an average vector.
4. Put the average vector in the step point of directive trajectory.
5. Define a new plane taking the average vector as its normal.

The Figure 10 depicts plane before correction (green), intersection points (black) and directive vectors of the trajectories in these points (colourful), average vector and plane after correction (yellow).


Figure 10: Correction of the plane


Figure 11: The method of Directive Trajectory

Figure 11 depicts surrounding shape (green), average trajectory (red), input trajectories (blue) calculated with method of directive trajectory. As it is seen, in the case of plane correction the sequential connection of the ellipses is deforming the shape of surrounding. That happens because the ellipse own coordinate axes are shifted. For preventing such a situation the connecting indexes of ellipses are chosen by the distance between connected points. Every ellipse, excluding the first one, shifts its point indexes comparing to the previous. The position with the lowest sum of distances between connected points is chosen (Figure 12).

### 3.3 Methods of choosing directive trajectory

Still the use of method of Directive Trajectory leads to the trajectories unequal affection to the result. As a possibility to prevent it the generalized trajectory is calculated and taken as directive before average trajectory finding. For implementing such a generalization several methods are tried.


Figure 12: The method of Directive Trajectory with corrected ellipse connection

### 3.3.1 Dynamic Time Warping

Dynamic Time Warping (DTW) is an algorithm for synchronizing two sequences with similar, but not fully matching pattern. It is distributed in area of speech recognition [16], for relating soundtracks and can also be applied to repeating motion. Doing an exercise, performer never repeats it in exactly same way. The speed, space orientation, phase distribution can differ. However, motion development comes generally the same. With that condition, every point of trajectory $A$ can be related by phase with some or several points of trajectory $B$, even thought their length not necessarily match. The relations definition comes following.

Let's the length of $A$ is $n$ and the length of $B$ is $m$.

$$
\begin{aligned}
& A=a_{1}, a_{2}, \ldots, a_{i}, \ldots, a_{n} \\
& B=b_{1}, b_{2}, \ldots, b_{j}, \ldots, b_{m}
\end{aligned}
$$

The distances between all point pairs $\left(a_{i}, b_{j}\right)$ compile the matrix $M$ with $n$ rows and $m$ columns. So the $M_{i, j}$ is the distance between points $a_{i}$ and $b_{j}$. The path from $M_{1,1}$ to $M_{n, m}$ is found. For every step $M_{i, j}$ the next position with lowest value is chosen out of $M_{i+1, j}, M_{i+1, j+1}, M_{i, j+1}$. The row and column indexes of chosen cells represent the relations between $A$ and $B$. The square distance $d$ can come as representative of distance between two points $a(x 1, y 1, z 1), b(x 2, y 2, z 2)$ and is calculated as following:

$$
d=(x 2-x 1)^{2}+(y 2-y 1)^{2}+(z 2-z 1)^{2}
$$

In 2010 T Kashima [17] proposed a way of average trajectory calculating using DTW. This algorithm is used as a possible for directive trajectory finding. It can be described in following steps:

1. Select the pair of trajectories.
2. Find the DTW relations for the pair.
3. Calculate an average for every phase represented as the trajectory point relation set (Figure 13).
4. Select new pair of trajectories, where one of them is calculated average and the other is next input trajectory. Repeat the steps until all the input trajectories are used.

The resulting average trajectory is shown on Figure 14.


Figure 13: The DTW relations between two trajectories of ball throwing and average between these two


Figure 14: The directive trajectory calculated with DTW

### 3.3.2 Time moment including

All previously explained methods are only considering the movement in the space. However the differences in time taken to perform the exercise are also important in the movement analysis and average calculating. As the attempt to combine the movement in the space and in the time the time moment average is taken as directive in this method.

The set of points with index $i$ from every trajectory are modifying the set of points at the moment $i$. The time moment average point $i$ is calculating as the average of the set at the moment $i$. However only the set including the points from all the trajectories can be gathered. So the calculating stops, when $i$ reaches the index of final point of some input trajectory. The amount of points in input trajectories can very differ, which means that a lot of points can be left out of calculating. The Figure 15 shows the picture, when the directive (black) is much shorter, than the input trajectories (blue).


Figure 15: The average trajectory calculated with time moment including

In order to continue this directive two methods are applied:

1. Aim to the final point (further time 1). This means to take the final point of the finished trajectory $T$ into the every set of points, which moment exceeds the final of the $T$ (Figure 16).
2. Continue the movement (further time 2). This method assumes, that the movement continues in exactly same way, as the last captured interval. For every additional point it adds the vector of last movement done. If points $a(x 1, y 1, z 1)$ and $b(x 2, y 2, z 2)$ are the second-to-last and last points of trajectory $T$ in moment $i$, the assumed point in the moment $i+j$ is $c(x 2+j(x 2-x 1), y 2+j(y 2-y 1), z 2+j(z 2-z 1))($ Figure 17).


Figure 16: Directive trajectory computed with final point aiming time moment


Figure 17: Directive trajectory computed with movement continuing time moment

### 3.4 Method of choosing intersection point

With plane rotation the situation may occur, where a few point sets are intersecting the plane (Figure 18). The decision on which points to put into analysing set is made using simple Nearest Neighbour rule.


Figure 18: Plane intersecting the trajectories in a few phases

### 3.4.1 Nearest Neighbours

The idea of Nearest Neighbour rule (NN) is to choose from the group of exemplars according to their distance to the known dataset [18]. The problem of intersection points is to get point set, where belonging to a group point from every trajectory is presented. The step point of the directive trajectory is certain to be the part of needed cluster. Accordingly, the intersection point of trajectory, which is nearest to the step point is chosen into the set.

However for applying this approach all the intersection points are needed to be found before clustering. The more simple way is to define the searching area from the beginning. Which is also implemented with use of idea of NN rule. Next steps can describe the process for the one of trajectories:

1. Find the point, nearest to step point of the directive trajectory. This point serves as a graph vertex in the observing trajectory. Let it be with the index $i$
2. Examine the point pairs, as it was explained in previous sections, using Breadth-First search (BFS). BFS is a search method, which on every step observes further both directions. In other words, on step $j$ it will observe intervals starting with points $i+j$ and $i-j$.

Previously for finding the intersection points all the point pairs of trajectory should be checked with a few step analysis. That is why defining the searching area is also working faster, than method described in last paragraph. With use of this approach the process reduced the time for $20 \%$ during development.

### 3.4.2 Processing the trajectory edges

On the edges of movement the condition may occur, that the trajectory has no plane intersection point in needed cluster, yet crosses it in another place. To prevent the analysis of mismatching set the distance between the set points is restricted. For the ball throwing exercise the fourth part of trajectory as a limit has shown itself suitable in general case.

As well as in the previous section it is not necessary to receive the point before realizing it does not match the cluster. If the observation comes further than decided limit, the search stops and the set is decided to be incomplete.

### 3.5 Trajectory relocation

In the repeating motion recording one of the problems is to ensure the conditions consistency. The distance between equipment, the capturing device and the performer should remain as unchanged as possible. Even a little shift in the performer location can affect the results of analysis. It is important while recording the attempts set, which is going to be analysed as indivisible whole.

Not less significant it is while capturing the motion in a few series with the goal of comparing its location. However the question of fixity guarantee is complex. The
impact of two possible approaches for shift neutralizing are checked in this paper:

1. Single trajectory relocation. In other words, unifying the beginning points of comparable trajectories, which means that every point of trajectory $T$ is shifted on the vector of displacement. Let $T_{0}\left(x_{1}, y_{1}, z_{1}\right)$ be the input trajectory beginning point and $\left(x_{2}, y_{2}, z_{2}\right)$ be the decided unified beginning point. Hence vector $\overrightarrow{\text { shift }}=\left(x_{2}-x_{1}, y_{2}-y_{1}, z_{2}-z_{1}\right)$ is vector of displacement for $T$. Replaced trajectory $R$ point $R_{i}=T_{i}-\overrightarrow{s h i f t}$.
2. The whole human model relocation. Which means unifying the beginning placement of performer solar plexus of comparable recordings.

## 4 Results

In this section the outcome of the different method comparison is stated.

### 4.1 The learning process

In this study Welch's t-test is used to ensure, that volumes of successful trajectories distribution describing shape computed with proposed methods differ in the beginning and the end of experiment. Otherwise the volume can not be interpreted as learning process describing parameter.

For the learning process analysis two participants are considered separately. For each of them the successful trajectory combination samples are picked up from the first three and the last three days. Each sample contains fifteen combinations of five trajectories.

The Table 1 and Table 2 depict that the Directive Trajectory basic method (DT) and DT Dynamic Time Warping based method (DTW) in the case of both persons show changes in volume of shapes between beginning and end of learning process. Time moment including methods are not crossing the threshold of 0.05 level of significance considering Person 1. Since the purpose of the analysis is to find out, which method describes the process of learning better, the time moment including methods are on the lower position after this test. However the further analysis will include all four methods in order to confirm the results.

| method | hypothesis chosen | p-value | t-statistics |
| :--- | :--- | :--- | :--- |
| DT | 1 | 0.0379 | 2.2734 |
| DTW | 1 | 0.0475 | 2.1750 |
| time 1 | 0 | 0.0538 | 2.1110 |
| time 2 | 0 | 0.0535 | 2.1143 |

Table 1: The Welch's test results of training influence, Person 1

| method | hypothesis chosen | p-value | t-statistics |
| :--- | :--- | :--- | :--- |
| DT | 1 | 0.0010 | 3.8106 |
| DTW | 1 | 0.0002 | 4.4098 |
| time 1 | 1 | 0.0097 | 2.9044 |
| time 2 | 1 | 0.0092 | 2.9295 |

Table 2: The Welch's test results of training influence, Person 2

### 4.2 Correlation between volume and Motion Mass parameters

In this work Pearson's correlation coefficient is used to define relations between Motion Mass parameters and the shape volume during the learning process. The biggest correlation is witnessing the best applicability to describe the learning process. The periods with the biggest measure of learning are chosen for every person. The most illustrative results are shown in the Table 3 and Table 4. In the both cases the Dynamic Time Warping including method clearly dominates over the others.

| method | $\mathbf{p}$-value | Pearson's coefficient |
| :--- | :--- | :--- |
| DT | 0.1249 | -0.8750 |
| DTW | $\mathbf{0 . 0 0 4}$ | $\mathbf{- 0 . 9 9 5 4}$ |
| time 1 | 0.2679 | -0.7321 |
| time 2 | 0.2469 | -0.7531 |

Table 3: The correlation between Curvature Mass and average describing volume, Person 1

| method | p -value | Pearson's coefficient |
| :--- | :--- | :--- |
| DT | 0.0470 | -0.9530 |
| DTW | $\mathbf{0 . 0 1 7 1}$ | $\mathbf{- 0 . 9 8 2 9}$ |
| time 1 | 0.0528 | -0.9472 |
| time 2 | 0.0211 | -0.9789 |

Table 4: The correlation between Acceleration Mass and average describing volume, Person 2

### 4.3 Trajectory relocation

The further analysis of the methods of trajectory relocation has shown that any tried relocation of the trajectories has too significant influence on the volume of
the tube. As an illustration the changes in volume throughout all the 15 days of Person 1 are shown on Figure 19. Unlike the volumes of not moved trajectories distribution shape, the moved ones show no relation between successful, fail and full set of attempts. In addition to that no correlation between volumes and Motion Mass parameters is found as well.


Figure 19: The volume changes calculated with relocated and not relocated trajectories, Person 1

## 5 Implemented software

The implemented software allows to calculate average trajectory of right wrist of multiple movement recordings using Dynamic Time Warping Directive Trajectory finding method. Up to two average trajectories can be placed on one plot. The option to compare average with chosen single motion exists as well.

As an input the program takes directory with .csv files with Kinect similar structure.

### 5.1 Visual additions

As the one of the main thesis purposes, graphical visual part of the analysis is important. To make the visualisation more demonstrative, a few additions are added.

### 5.1.1 Colouring

The calculated average represents the so called "perfect movement" and the distribution of input trajectories. The moment of motion speed can be understood by the intervals between capturing, but this way is not evident and requires too much effort.

A basic method of giving an additional information with graphical data is colouring. Suitable choice of colouring can recall abundant associations, which help to come to right conclusions without mathematical calculations, complex judgements made by receiving party.

For higher speed representation red colour $(\# \mathrm{f} 00)$ is used relying on [19]. Green colour ( $\# 008000$ ) was chosen for lower speed representation as complimentary of red and according to personal associations.

The gradient from green to red represents the speed change from minimum to maximum captured. Ten different values of colours are used. For receiving the
gradient values Python colour library [20] is used (Figure 20).

```
gradient = list(colour.Color("green").range_to(colour.Color("red"), 10))
```

Figure 20: The example of Python colour library usage

The frames are captured with the same interval, so the distance between points is taken as speed representative. For every segment of average trajectory mean distance of intersection point containing input trajectory segments is calculated. The average speed is changing permanently during the ball throwing movement and reaches its maximum on the end of trajectory (Figure 21).


Figure 21: The speed based colouring of the trajectory distribution shape

### 5.1.2 Animation

Comparing average trajectory with another motion in order to notice the difference with so called "perfect motion" can be statically reproduced by simple covering as it is shown on Figure 22. However it is complicated to find, how exactly should movement be performed for matching the perfect. Especially because what is done
wrong is not seen.


Figure 22: The success trials distribution describing shape and the fail trajectory

To make it easier, the animation of comparable recording is added. The human is represented by so called "skeleton" - joints connected in time moment. The joint of trajectory is marked with point and is tracing the comparable trajectory.

Every joint is taking part in speed calculation. The connection of joint pair is coloured speed based, as it was described in previous section. The maximum speed of joint pair is taken as connection representative speed (Figure 23).


Figure 23: Two frames from ball throwing animation

### 5.2 User Interface

The UI for the software is implemented with use of Tkinter module [21] (Figure 24). Graphical part is appearing separately as Matplotlib plot window.


Figure 24: User Interface

## 6 Discussion

The Dynamic Time Warping based method has shown itself as the most suitable to describe the changes in gross-motor activity, based on example of learning process. However only four methods were examined. Obviously, there is a huge area to improve results.

Still Dynamic Time Warping is considering motion only in 3D, while actual motion is taking place in 4D. The methods which further can be explored may contain time based analysis as well.

The simple human skeleton used to represent the comparable motion provides basic information about movement. Nevertheless imposing analysed average to the video recording could describe the differences better. Still this considers video proceeding area more than data analysis, which was the main sector of interest of this study.

## 7 Conclusion

The first goal of this thesis was to relax the limitations on initial data the previously stated method of average calculating [1] assumes, which are the dominance of one dimension and the need of human involving. For this purpose four approaches were implemented and tested on their ability to describe changes in repeating motion. The method with Dynamic Time Warping algorithm used to define the direction of the motion has shown biggest correlation between Motion Mass parameters and calculated average volume.

The dominance of chosen approach was clearly seen in the results of performed verification. It has shown the best results in case of both test participants with Pearson' correlation coefficient deviating from the extreme less than to $2 \%$ in the most illustrative cases.

This method is not selecting the dimension to trace motion through, the analysis is performing across the motion direction. Chosen approach also considers all the trajectories while making decision on movement direction in time moment. For this purpose it finds average trajectory by motion phases. It also solves itself the problem of analysis start and end steps decision taking as mentioned the first and the last with analysis be possible to perform.

The finding of the points considered in analysis is performed with use of Nearest Neighbour rule, which decreases the speed of the process by $20 \%$.

Second goal was to graphically describe these method and make possible to illustrate the differences between average motion of multiple recordings and single motion. For this the simple software was implemented. The main function of which is to plot the calculated average and compare it with single motion. It allows as well to trace the changes of speed by colouring and to monitor the animated movement of skeleton model. Animation and the colouring vividly show the differences in speed and direction between "expected" average movement and the single performed. The plot can depict the throwing movement from desired angle.

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