

Adaptation of cluster analysis methods to optimize a biomechanical motion model of humans in a nursing bed

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Abstract— The paper considers the optimization of a Hidden-Markov Model (HMM) based method for the generation of averaged motion sequences. To create averaged motion sequences, motion sequences of different test persons were originally recorded with a motion capture system (MoCap system) and then averaged using an HMM approach. The resulting averaged data sets, however, partly showed serious motion artifacts and uncoordinated intermediate movements, especially in the extremities. The aim of this work was to combine only movements with similar courses in the extremities by a suitable cluster analysis. For each test person, model body descriptions of 21 body elements are available, each of which is represented in three-dimensional time series. For optimization, the MoCap data are first compared using time warp edit distance (TWED) and clustered using an agglomerative hierarchical procedure. Finally, the data of the resulting clusters are used to generate new averaged motion sequences using the HMM approach. The resulting averaged data can be used, for example, in a simulation in a multilevel biomechanical model.

Keywords — Clusteranalysis, model driven development, biomechanical motion model, averaging motion pattern, TWED

I. INTRODUCTION

The modelling of human motion is becoming more and more important in various research areas, especially in robotics [1] and medicine. The focus of the research work is often on the natural look and precision of a movement, but also, for example, in the fields of sports and medicine, on the analysis and evaluation of real human movement sequences [2] or in biosignal processing on gait analysis [3] or motion strategy analysis [4]. Our research work focuses an optimization of a biomechanical human motion model.

As a basis for modelling we use a functionalized nursing bed which is equipped with four force sensors. These enable us to derive various basic parameters such as bed occupancy, center of gravity position and restlessness of the person in the nursing bed by means of signal processing methods. Furthermore, it is also possible to derive higher-value parameters such as the respiratory rate and movement patterns from the sensor signals [5]. The initial model [6] is based as already explained on a functionalized nursing bed and

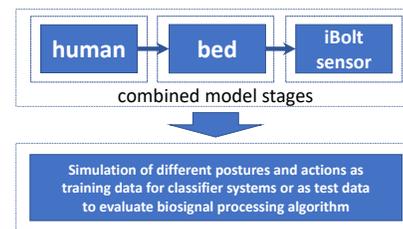


Fig. 1. Multi-stage model [6].

describes the three elements "human", "bed" and "sensor". An overview of the model is shown in Fig. 1.

The use of the model should make it possible to examine various considerations on the functionalization of furniture in the hospital and care sector. For this purpose, the number, type and design of a sensor can be examined in the model, for example. Thus, the immense effort of testing each sensor

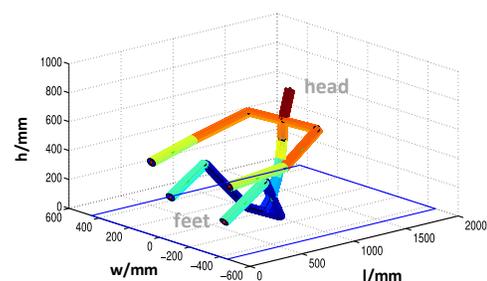


Fig. 2. Human stickman model in sitting position.

combination in various test series with different test persons can be minimized and would simplify new developments in this area. In order to enable a simulation as close to reality as possible, the focus is primarily on modelling human movement. As "human" model a stickman structure is used, which consists of 21 body elements (19 body nodes + 2 nodes for heart and lung). This model structure is shown as an example in a sitting position in Fig. 2. To make the motion sequences for the simulation as realistic as possible, a database with different motion sequences was created using the

markerless MoCap System from XSSENS [7]. The focus of the movement sequences is on movements of people in a nursing bed [8]. Since the simulation should be independent of the movement of a single person, averaged movement sequences were generated from the movements of the individual persons using an HMM-based system [9]. For this purpose, the Hidden Markov models were used in their function as a generator. Due to their structure they are particularly suitable to map time-dependent data and are also well suited for use with smaller data sets [10].

During the initial investigations into the generation of averaged motion data, the individual motion sequences from the database were not specified in detail and it has not been considered that a large number of different variations of one and the same motion sequence exist in the test data. For example, in a movement sequence "supine position, sitting, supine position" the test persons may either rest their arms next to their body to sit up or they may not move their arms at all. In the end positions the arms were either placed around the knees or next to the body, just to give two examples. The result was that in the averaged movement this leads to undesired effects. This can be seen in a visual analysis, for example, in a "trembling" in the arms. At this point, averaging does justice to both variations of movement mathematically speaking, but the resulting movement no longer corresponds to a natural movement sequence. To remedy this situation, an intermediate step is inserted into the processing chain for the generation of averaged motion sequences, in which the test data is first clustered and then averaged according to its cluster. This procedure is intended to make the resulting movements more natural, since clustering only averages data with comparable movement sequences. The entire procedure is shown in Fig. 3 and is described below according to the function groups used.

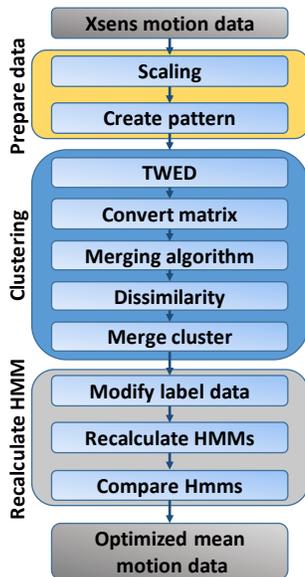


Fig. 3. Block diagram of the method.

II. PREPARE HUMAN MOTION DATA

First, the preliminary work and preparation of the data necessary for clustering is considered. The basis for the averaged data is, as already explained, the data of the MoveHN database. The data sets are available as raw data of

the XSens Awinda MoCap System. Raw data means at this point that during the recordings with the XSens system different zero points have been set despite calibration. Therefore, the individual movement sequences are first aligned. Here the arbitrary alignment of the motion data in the form of a global offset and an angular displacement is scaled by means of offset correction and rotation of the coordinate system. The alignment is carried out in such a way that the hip is fixed on the origin of the coordinate system and the basic position of the respective test person lies along the same axis of a Cartesian coordinate system. Pictorially represented, the scaling ensures that all persons have the same orientation in the room so that they can be compared. Afterwards the transformation into a pattern takes place as described in [9].

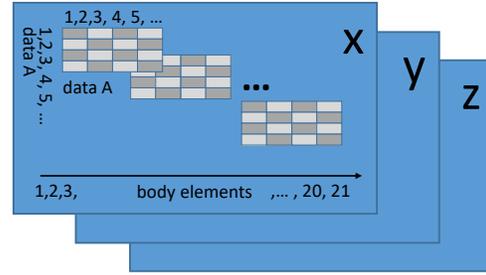


Fig. 4. Data structure of distance matrix after TWED.

III. CLUSTERANALYSIS

After the data has been prepared, the actual cluster analysis is performed in the second step (highlighted in blue in Fig. 3). For this purpose, all data records of a motion sequence are first compared with each other. The data are available as three-dimensional Cartesian coordinates, the fourth dimension is the time to map the motion sequences. Furthermore, the data are available separately for each movement. Each data record has a label file that describes the time structure of the data. Therefore, first all pattern files are searched for using the data labels from the database, in which the corresponding movement to be compared is present.

Then each of these files is compared with all other files found. This comparison is done with the Time Warp Edit Distance (TWED) [11]. TWED was used in this context as distance measure because of its elastic features. A rigid distance measure e.g. Euclidean distance cannot reasonably consider differences between the motion sequences from stretching or displacement with respect to the time axis [8]. This comparison results in a symmetrical distance matrix for each body part and each of the three axes. The structure of the data is shown in Fig. 4. Using the TWED algorithm, the optimal path with the least weight is determined in addition to the distances accordingly. The extensive analysis by TWED delivers relatively large result files that require a lot of memory. To allow an adequate processing time, the files are compressed for further processing by deleting the paths, because for the current view all distances to each other must be considered and not, as usual, only the smallest distances.

After preparation the fusion algorithm starts to merge the individual files using the distance matrix. An agglomerative hierarchical cluster procedure was used for this. In this bottom-up procedure, all data sets are combined into clusters based on their similarities to each other, up to the largest cluster containing all data sets. In comparison to partitioning

cluster methods, no resulting number of clusters has to be specified here. This is a big advantage at this point because due to the different possible variations of the movements the algorithm should initially be able to work independently of restrictions in order to achieve an optimal result. The clustering result describes the similarity of the individual body part movements of the 60 data sets. After the fusion it is possible to visualize the result of this procedure by means of a dendrogram. This will be taken up again later and used as an opportunity to evaluate the results of the clustering also by means of a visual analysis.

In the present work two different fusion algorithms were tested and evaluated to achieve an optimum for the later averaging of the motion data. One is the single-linkage method and the other is the average-group-linkage method. In the single linkage method, the minimum distance of a pair of elements of two clusters is calculated as follows:

$$D_s(A, B) := \min_{a \in A, b \in B} \{d(a, b)\} \quad (1)$$

The single-linkage method is suitable for detecting branched, curved or elongated clusters because it is sufficient if an object of one class is close to an object of another class. However, it may happen that groups are combined which are only connected to each other by a connection comparable to a bridge and are otherwise clearly separated from each other spatially. This may lead to quite heterogenic clusters. Due to its characteristics, however, the method is also well suited to filter out outliers.

The average-group-linkage method, however, calculates the average distance of element pairs of all elements from two clusters A and B:

$$D_A(A, B) := \frac{1}{(|A|+|B|)(|A|+|B|-1)} \sum_{x,y \in A \cup B} d(x, y) \quad (2)$$

The average group linkage method is based on the fact that objects of two groups must be similar "only on average" in order for a fusion to occur. This makes it possible to compensate for greater distances between objects by smaller distances between objects that are close together. A disadvantage of this method is that outliers are only partially eliminated. Other linkage methods such as Centroid, Median and Ward were considered but not used. This is due to the fact that a distance measure must be used as a proximity measure for the procedures. Since the TWED was used as the proximity measure here, it cannot be used, because the result of the comparison with the TWED is a distance, but in each case between two data sets and therefore not normalizable.

Following the fusion, the dendrograms for the respective test series are generated. At this point the movement "turn-supine-to-sitting" would be considered as an example.

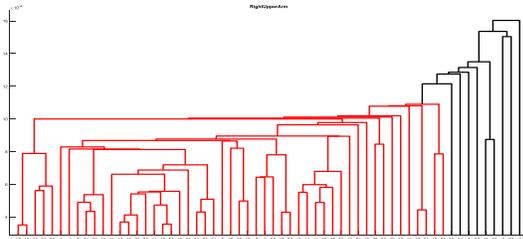


Fig. 5. Dendrogram "single linkage" result, x-axis for right upper arm

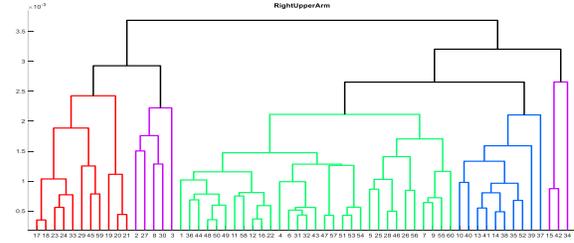


Fig. 6. Dendrogram "average linkage" result, x-axis for right upper arm

Fig. 5 shows an example of the dendrogram for the x-axis of the right upper arm using the single linkage method, while Fig. 6 shows the same data using the average-group-linkage method. It is easy to see that the two fusion algorithms result in two different cluster solutions.

When deciding on a threshold value, it is important that the individual clusters do not become too small. If the clusters are too small, the resulting HMM is not meaningful and, above all, problems can arise when training the HMMs, since the algorithms are not designed for very small data sets. From our experiments and observations, a threshold value of 70% could be empirically derived from the dendrogram as a cluster stop criterion, which was used in the further course.

To validate the two fusion algorithms and their suitability for the available data, the dissimilarity of the data sets is calculated. This value indicates how well the data set or distances are represented by the clustering. It is calculated by the Cophenetic Correlation Coefficient (CC coefficient). Here, the cophenetic correlation for a cluster tree is defined as the linear correlation coefficient between the cophenetic distances obtained from the tree and the original distances (or dissimilarities) used to construct the tree. It is thus a measure of how accurately the tree represents the differences between observations. The cophenetic distance between two observations is represented in a dendrogram by the height of the link where these two observations are first connected. This height is the distance between the two sub-clusters that are joined by this link [12]. The CC coefficient is calculated as follows:

$$c = \frac{\sum_{i < j} (Y_{ij} - \bar{y})(Z_{ij} - \bar{z})}{\sqrt{\sum_{i < j} (Y_{ij} - \bar{y})^2 \sum_{i < j} (Z_{ij} - \bar{z})^2}} \quad (3)$$

Where Y_{ij} is the distance between the data sets i and j in Y , Z_{ij} is the cophenetic distance between the objects i and j , and \bar{y} and \bar{z} are the respective average of Y and Z [12].

From (3) it can be seen that the more dissimilar the data are, the higher the cophenetic correlation coefficient becomes. Accordingly, high values for the correlation coefficient c are a measure for a high quality of the clustering result since in this case the links between the elements in the dendrogram correlate strongly with the distances between the objects in the distance matrix. The more similar the data are (the closer the distance values are together) the more difficult a separation becomes. The cophenetic correlation coefficient for the single linkage method is 0.67 with standard deviation of 0.027 on average for all body parts and the three axes, whereas the average for the average-group-linkage method is 0.74 with standard deviation of 0.011. For the complete-linkage and average-linkage methods, the correlation coefficient is about 0.64 and the standard deviation is 0.054 and 0.053. Therefore,

these methods will not be considered further here. In each case movement "turn-supine-to-sitting" was used. For three other motion sequences tested, similar values show that the average-group-linkage method is more suitable for these data. For this reason, the average-group-linkage method is used in further calculations: The reduced possibility to remove outliers is accepted because experiments have shown that still a large part of disturbing outliers can be removed by clustering using average-group-linkage. In the last part of the cluster analysis, the individual data sets are assigned to the clusters that remain after the threshold value has been set.

IV. RECALCULATING HMM AVERAGING

Clustering is followed by post-processing of the data. This step is highlighted in grey in Fig. 3. A list with the corresponding data records per cluster is then generated from the assignments of the individual data records to the respective clusters. All clusters below the threshold value that contain less than 10 elements are combined on a separate list, the so-called garbage-list. With this, the outliers and the very small clusters are combined to prevent separate models from being trained from these data in the averaging with HTK [13].

The new lists for the creation of the new averaged motion sequences are then prepared. For this purpose, all label files of the respective data records must also be adapted to the movement with the new cluster name. This is necessary so that the HTK function can process all associated files of a cluster during the training algorithm. The HMM algorithm for averaging the movement data is described in detail in [9].

V. EVALUATION

After the procedure for clustering of motion sequences has been described, we will finally consider how the quality of the optimization can be evaluated. For this purpose, a suitable evaluation procedure must be selected to objectively validate whether the methods used lead to the desired goal. As an initial criterion, a visual control of the generated data sequences is certainly useful. In addition, a comparison by means of TWED was used here to calculate and to visualize the differences. This approach has already been used successfully in earlier work. In the corresponding heat maps, the body parts of the model are listed on the x-axis, the number of the respective data set is on the y-axis and the distances in the plane are shown as intensity value. All representations are scaled to the same maximum value to be comparable.

The resulting HMMs as a mean motion map were compared with the original data sets to determine how large the distances to the individual data sets are. Usually, all results for the three axes x, y, and z are considered for the evaluation. For space reasons the results of the x-axis for the "turn-supine-to-sitting" movement are shown here, as this represents the main movement axis for the case under consideration, and accordingly the largest differences in the comparison of the averaged structures are contained there. Fig. 7 shows a heat map of the initial HMM of the movement "turn-supine-to-sitting" over the x-axis as baseline results. This HMM was trained from 60 data sets and it can be clearly seen that, especially in the head and the upper extremities, there are larger deviations of the data sets from the averaged courses. Fig. 8 shows the results for the TWED analysis of the four new mean motion models after clustering. These were created according to the clustering results of 31, 11, 10 and 8 data sets. In total, this gives the initial 60 data sets for the baseline results. The HMM visualizations are ordered according to the

cluster size in descending order in Fig. 8, the individual elements are referenced with HMM and the corresponding number.

If the individual HMM visualizations are compared to the baseline HMM in Fig. 7, it can be seen that the distances from every HMM to the original data are distributed over all four clusters. This point is to be expected accordingly and can be

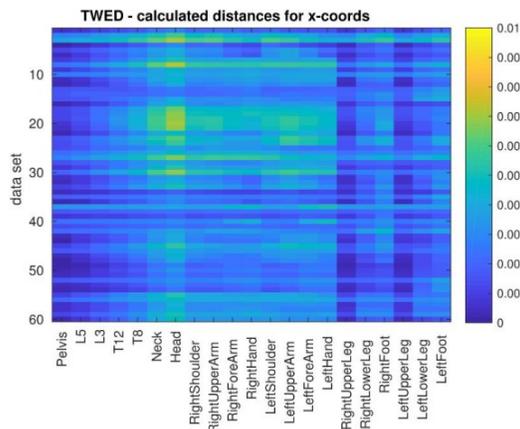


Fig. 7. TWED - calculated distances for initial "turn-supine-to-sitting" as baseline results.

confirmed by the graphical evaluation. The first and largest cluster HMM 1 shows a much more homogeneous distribution of the distances without large outliers compared to the baseline HMM in Fig. 7. HMM 2, on the other hand, has a significantly larger distance between the generating data sets and the model compared to the other new models. However, this distance distribution is relatively evenly distributed over all body parts and data sets. In comparison, HMM 3 shows much less deviation from the generating data sets in the form of a very homogeneous distance distribution with low distance values. The fourth HMM, here marked as "HMM other", is the so-called garbage HMM which was generated from the remaining clusters. Here it can be clearly seen that the distances vary strong.

This raises the question of how the result can be evaluated and whether the newly created averaged motion sequences represent better or more real motion sequences. As discussed before, the distance values are a good guide to compare individual HMMs in terms of their similarity to the input data, but they do not provide any statement on the resulting movement path. Correspondingly, the assumption would be that HMMs allow a very clean and real motion image with the smallest possible distances. This was verified by a visual analysis in which the motion sequences were displayed and analyzed as 3D Stickman with its temporal changes (see Fig. 2). For HMM 1 a comparatively well-suited motion sequence resulted which shows little of the motion artifacts in the form of twitches etc. of the original motion sequence of the baseline HMM. The small areas in which the distance values are increased can be attributed to the determination of the clusters using the average linkage method. In this method, the transaction data is combined by averaging the distances to the clusters. Accordingly, small outliers may be present in the observation. To avoid this, a more restrictive division into more clusters would be necessary. Furthermore, when looking at the movement sequence of HMM 2, it can be observed that the movements are much more "restless" compared to HMM

1 and that at the end of the sequence a kind of disturbance occurs, which can be described by an incorrect posture. HMM 3, in turn, allows a relatively clean sequence of movements which, however, is not quite as optimal as HMM 1. The "HMM-other" motion sequence does not represent a usable sequence as already assumed. The observation is supported by the evaluation of the underlying dendrogram for clustering (see Fig. 6). This shows that the two HMMs 1 (green colored

of elements in the dendrogram that are very dissimilar to each other.

VI. CONCLUSION

In this paper it was shown that the clustering of motion data using a hierarchical agglomerative approach leads to an improvement of averaged motion sequences. The thresholds etc. were intentionally chosen in the context of the current work in order to analyze and discuss the different clusters and their resulting movement patterns. For a further application it should be considered to adjust the cluster size and, contrary to the first assumption, to combine rather smaller clusters with very similar data sets to averaged models. In the following, it would still be useful to find a measure that allows to determine the quality of the new HMMs compared to the initial HMM. For this purpose, we are working on four quality criteria, to be able to compare and evaluate the averaged movements with real human movements by means of mathematical criteria.

ACKNOWLEDGMENT

The authors would like to thank the voluntary participants for their contributions to the test series in order to create suitable records for our recognition tests.

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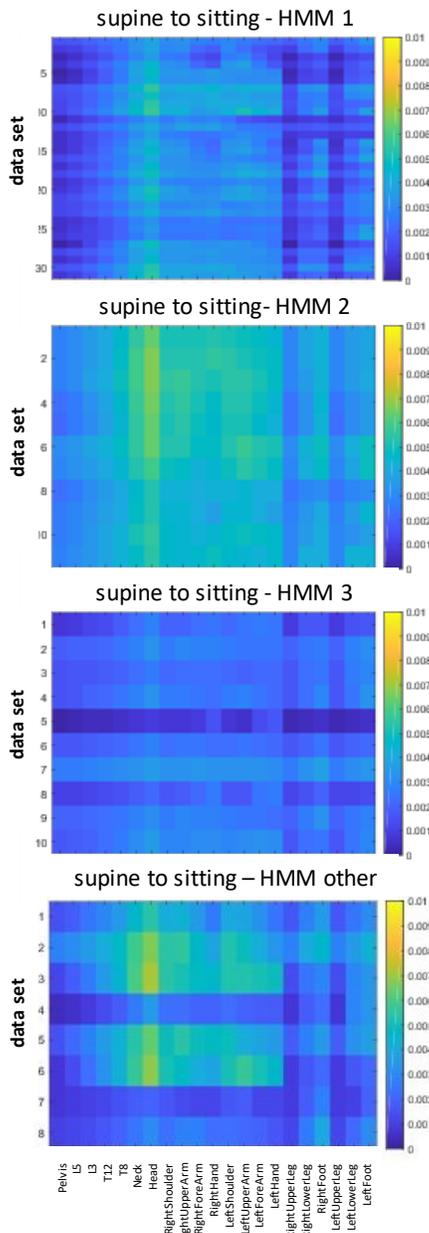


Fig. 8. TWED – x coordinates - distances for new clustered HMMs.

path in Fig. 6) and 3 (blue colored path in Fig. 6) show a comparable similarity, which is reflected in the observation of the motion sequences. The HMM 2 (red colored path in Fig. 6) has a lower similarity, this also became clear in the motion sequence, as already shown. The HMM other (purple colored path in Fig. 6), which is used as a garbage model, also consists