

Serialization of a 3D Human Body based on MoCap Data in a BVH File for Sequence Comparison



Serialización de un Cuerpo Humano Tridimensional basado en datos MoCap en un archivo BVH para la Comparación de Secuencias

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Keywords

BVH; Motion Capture; Serialization; Sequence comparison.

Abstract

This work focuses on the use of sequence alignment algorithms as validation of the results obtained in the serialization of tridimensional body using BVH file, from obtained a sequence 3D to the symbology necessary for the validation that represents the data obtained in the Pattern Recognition and Intelligent Systems Laboratory (PRIS-Lab). The procedure use steradians as the method to obtain the symbology for the sequence for the Needleman Wunsch algorithm for alignment sequence, for validation the alignment algorithm score is used.

Palabras claves

BVH; Captura de Movimientos; Serialización; Comparación de Secuencias.

Resumen

Este trabajo se enfoca en el uso de algoritmos de alineamiento de secuencias como la validación de los resultados obtenidos de la serialización de cuerpos tridimensionales utilizando archivos BVH, desde obtener una secuencia 3D hasta la simbología necesaria para la validación de los datos obtenidos en el Laboratorio de Reconocimiento de Patrones y Sistemas Inteligentes (PRIS-Lab). El procedimiento utiliza esteroreadianes como el método para la obtención de la simbología necesaria para utilizar el algoritmo Needleman Wunsch para las secuencias, y como métrica de validación se utiliza el resultado numérico del algoritmo.

Introduction and Related Work

Biomechanics studies the living beings, looking for relations between magnitudes and looking for behavioral explanations and observations. (Aguilar, 2000) The structures and forces allow the study of the movements from an anatomical or structural point of view, so that the movements are deduced from the structure in movement (skeleton, joints, etc.) applying physiological and physical properties. This science is in development due to the difficulty of establishing a normalization of the human body.

The main complication during the biomechanical analysis of the human body is comparing two different actors performing the same action, since the movement depends of the upper or lower extremities, largely on their dimensions and the mass distribution, the results obtained in the same movement can differ greatly from one person to another (Ceccarelli, M.J. Gómez García and C. Castejón Sisamón and J.C. García Prada and G. Carbone and M., 2011). Therefore, a normalization is required to be able to compare the actions of two people without the results being affected by their dimensions.

Nowadays, in order to capture the performance of people doing sports and other activities in real-time, several MOtion CAPture systems (or MoCap for short) are commercially available like OptiTrack, Qualysis, Codamotion or Vicon that offer cameras for indoor or outdoor, virtual reality systems and the accessories necessary for the task. Motion capture is a process in which the real movements of humans are obtained and used to map these to a virtual representation. Motion Capture involves the detection, digitization, and capture of the actions made by the actors to obtain the three-dimensional representation of it. (Parent, 2012).

There are different MoCap technologies, where the most commonly used is optical capture. This kind of system is based on the measurement of reflected light, mainly using passive infrared markers placed on the body to track. The main advantage of this type of system is that by using the images created from the sensors, valuable information such as the position of every sensor can be extracted. Although this information usually has a high computational cost to be able to deduce it, and its main disadvantage is that the sensors require a direct line of light from the light emission (Welch, G.F. and Foxlin, Eric, 2002). Ramos created a system to extract movement patterns using kinematic variables at the points of an individual's body using the Kinect camera. This is a depth camera system that uses an infrared emitter and for processing uses the captured images and the OpenNI software that determines the depth of the body. (Gutiérrez, 2013)

Methodology

First, it is necessary to obtain a tridimensional representation of the human movement, which is done with the optical motion capture system of PRIS-Lab. This requires the use of a suit to put passive infrared markers to obtain the information with OptiTrack Prime 13 cameras, then this representation is saved in the BVH file.

This file passes through the normalization algorithm that consist in:

- Read the file and obtain the *OFFSET* information from the BVH file.
- Obtain the biggest magnitude in the information from part one.
- Make a new file BVH normalized.

This way a new BVH file is obtained as output of the algorithm. With this file, the information from 20 points is obtained and use for the creation of a sequence that describes the movement.

Sequence N
 Head, LeftShoulder, RightShoulder, LeftElbow, RightElbow,
 LeftHand, RightHand, LeftKnee, RightKnee, LeftToe, RightToe.

Each component of the sequence is obtained by a vector sum of the points of the BVH file, then each of this need to be converted to a symbol, because the sequence alignment algorithm use symbols for the sequence not a vector. For this conversion steradians are used; this is the unit of measurement of the solid angle and can be obtained at drawing a sphere of radius R with center P, this intersects the conic surface generating a surface sector S that is described by Equation 1.

$$S = R^2$$

Equation 1. Steradian equation.

For each component, the correspondent steradian is calculated, this way a sequence of eleven symbols is obtained that represented the human movement. The alignment algorithm uses letters as part of the sequence, because it is used mainly for ADN and ARN; so for better results is necessary to obtain a sequence that uses letters as the symbol. As the dimensions of the body are normalized, the maximum results of the steradian are 1, we can use the alphabet letters and each of those has a value of 1/27 (using ñ). The results can be validated using the metric of the sequence alignment algorithm. If both sequences are the same the result of the Needleman Wunsch algorithm is zero.

Experimental Results and Discussion

For this experiment we take data from two different subjects, the subject N has a height of 1.7m and the subject R of 1.5m (figure 1). Using the software Blender to obtain the graphical representation and the Ruler tool to measure the height.

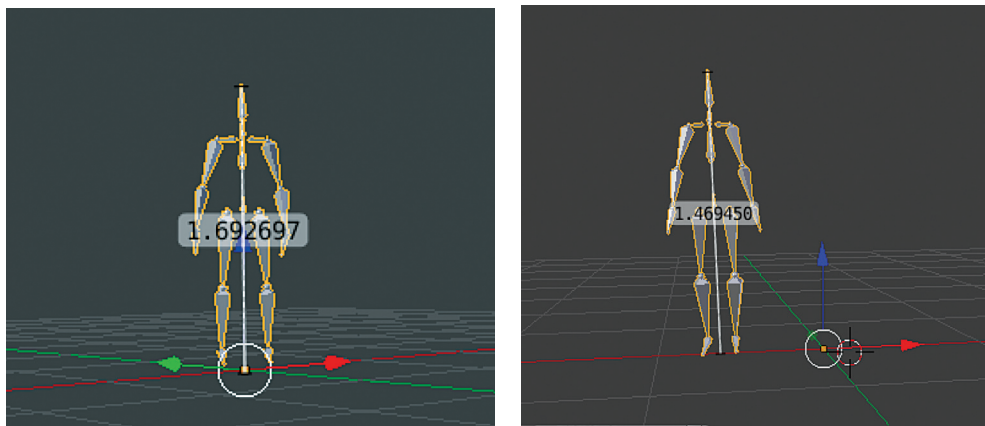


Figure 1. Normal position for the subjects.

Each of the representations was passed through the algorithm, as maximum magnitude for the normalization and creation of the new file 0,447347 was obtained for the Subject N and 0,365281 for the Subject R. Using each of these maximum the new data for each subject and its graphical representation shows in the figure 2.

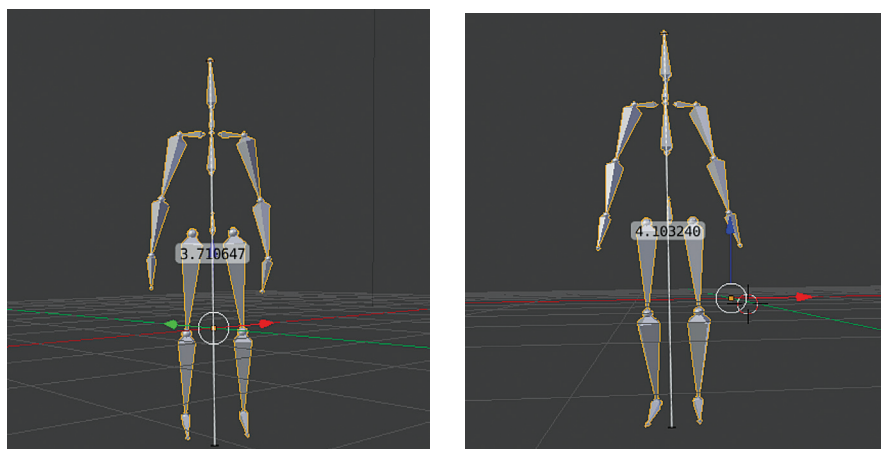


Figure 2. Normal position for the subjects after the algorithm

For a quantitative result in the comparison of the movement, after the creation of the new BVH file is necessary to define the N sequence. The file contains the position of 20 points of the body, with these points the sequence was defined which is obtained by a vector sum. This results in a sequence composed of vectors, but the alignment algorithm only allows sequences composed of letters to obtain desired results. Therefore, it was decided to use steradians as a symbol for each vector. The sequence using the corresponding symbology is shown in table 1.

Table 1. Sequence N for each subject.

Subject N	Subject R
0,0	0,0
0,459548	0,465821
0,459283	0,465811
0,620894	0,56875
0,620317	0,568725
0,77471	0,65134
0,773961	0,651305
0,457493	0,359617
0,457493	0,359617
0,919838	0,791834
0,919838	0,791834

Each of the components of the N sequence is matched with the corresponding letter, using this convention the N sequence is shown in table 2.

Table 2. Sequence N using letters for each subject.

Subject N
A M M P P T T M M X X
Subject R
A M M O O Q Q J J U U

When both sequences are obtained the sequence alignment algorithm is used to obtain a quantitative result, when passing it through the Needleman Wunsch a result of 8 is obtained.

Conclusions and Future Work

The serialization of the human body was used to create the normalization data. For each BVH file, the maximum magnitude was found to perform the normalization and create the output BVH file. Then the creation of the N sequence was made with the use of the steradian as symbols and each of them was matched with its respective letter. The metric of the Needleman Wunsch sequence alignment algorithm was used to obtain a quantitative result. This algorithm creates a symbology to pass it through to have a quantitative comparison of a movement made by two people with different physical characteristics. The quantitative result gives us an idea that the difference between the movements are bigger than what was expected, that is zero because the movements are the same. One way that this can change is using another symbology for the sequence instead of the steradians, and compare the results obtained with different symbology. Using different symbology allows the comparison of them to obtain the smallest result with the sequence alignment algorithm for the same movement.

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