Estimation of the Location of Joint Points of Human Body from Successive Volume Data

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Abstract

Recognizing structure of human body is important for modeling human motion. Human body is usually represented as an articulate model, which consists of the rigid parts and the joint points between them. The structure of the human body is specified by the joint points.

In this paper we propose a novel method for estimating the location of joint points from successive volume data.

Our joint point estimation method consists of three steps. In the first step, rigid parts are extracted from two successive volume data under the constraint of the rigid transformation. In the second step, the joint points are estimated based on the rigid parts. As the last step, false joint points are eliminated by using more successive data.

Applying the method to the simulated data, the locations of joint points of the human are correctly estimated.

1 Introduction

Recognizing human body is important for various applications such as visualization of human body motion in CG and VR, human engineering and biomechanical analysis for medical and sports fields.

It is usually considered that a human body consists of rigid parts and non-rigid parts between two rigid parts, and the joint points are embedded in the non-rigid parts. Generally speaking, each person has different shape of the rigid parts and different location of the joint points. A method that can estimate location of the joint points and shape of the rigid parts in the human body from volume data is necessary.

There has been several research for estimating human pose from an image or multiple images[1,2,3,4]. Using multiple images is not enough to acquire 3D human body model, because the image does not have enough shape information of human body. It needs 3D shape data of human body that has this information completely. We can obtain such data by using 3D-shape measurement equipment like a range sensor. In this paper, we propose a method that can estimate the location of the joint points of the human body from its volume data.

We use successive volume data to estimate the location of the joint points. In our method, local shape similarity of the rigid parts between two volume data is used to extract rigid parts. We also consider the constraint that the rigid parts should move under the rigid motion. Then, according to the constraint that the rigid parts are only allowed to rotate around the joint points, we extract the joint points and estimate the location of them.

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This paper is organized as follows: Section 2 describes human body model and the constraint of human structure. Sections 3,4 and 5 describe our joint point estimation method. Experimental results and conclusions are presented in sections 6 and 7.

2 Representation of human body

2.1 Human body model

A human body consists of rigid parts and non-rigid parts between the rigid parts, and the joint points. Each non-rigid parts embeds at most 1 joint point. We define human body model according to this consideration, and divide it into the fixed number of human body parts.

Fig.1 shows the human body parts and joint points.

2.2 Constraint on human body structure

In the human body model, each joint point connects one rigid part to another. the rigid part rotates around the joint point.

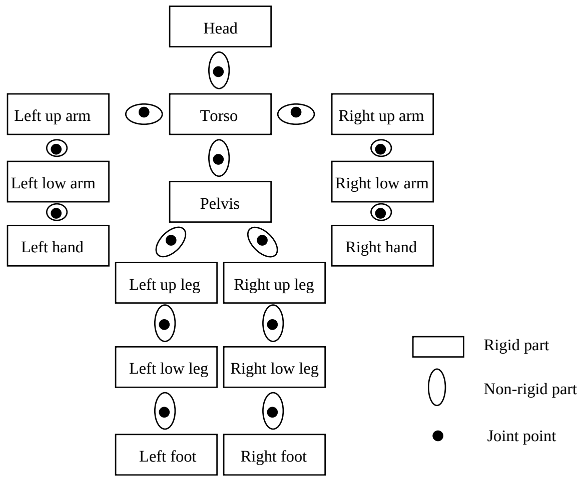


Figure 1. Human body parts and joint points

Fig.2 shows the constraint of the location of two rigid parts.

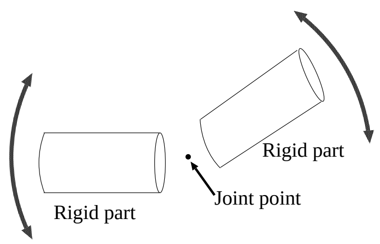


Figure 2. Constraint of the location of two rigid parts: Two rigid parts rotate around a joint point

3 Extracting rigid parts

We extract the rigid parts to estimate the location of joint points at the first step.

To determine whether a region in one volume data belongs to rigid parts or not, we measure the local shape similarity of this region against the other volume data. This measurement is based on the constraint of the location of two rigid parts.

Therefore we use two successive volume data to measure this similarity. Throughout this section and the next section, we consider two successive volume data at time t and $t+1$.

3.1 A method for extracting rigid parts

Our method for extracting rigid parts consists of four steps. In the first step, the volume data at t is divided into initial blocks. In the second step, seed blocks that can be thought as a subset of the rigid parts are selected among the initial blocks. In the third step, seed blocks are merged into a seed region so that it uniquely corresponds to the region on data at $t+1$. And the last step, the seed regions that rotate around the same joint point are unified into a seed union.

3.1.1 Dividing volume data into initial block

We divide the volume data at t into cubic regions of the same size at this step. We call each cubic region an initial block.

The size of initial block should be small enough to divide rigid parts and non-rigid parts. However as we set it small, the calculation cost in the later steps enlarge.

3.1.2 Selecting seed blocks

A seed block is the block that can be regarded as a subset of a rigid part. The seed blocks are selected in the following way.

Let an initial block be $I(t)$. If $I(t)$ is a part of a rigid part, there is a corresponding block on data at $t+1$ (we call it $I(t+1)$), and the transformation between $I(t)$ and $I(t+1)$ is expressed by the rigid transformation. If such $I(t+1)$ is not found, $I(t)$ is considered to be in the set of non-rigid parts.

We adopt the template pattern matching for this selection. We set $I(t)$ as a template pattern and search $I(t+1)$ by changing transformation parameters of $I(t)$ under the rigid transformation.

We apply this search to every initial block, and obtain seed blocks.

3.1.3 Merging seed blocks

$I(t)$ may have more than one corresponding blocks when the seed block does not have enough shape feature to obtain the unique block $I(t+1)$. In this step the seed blocks are merged into a seed region so that each seed region uniquely corresponds to the region on data at $t+1$.

Let the seed block which does not have the unique corresponding block be $s(t)$. We merge one of the blocks that are adjacent to $s(t)$ (we call it $s_a(t)$) into $s(t)$, and obtain merged seed region, $S(t) = s(t) \cap s_a(t)$.

Then we search corresponding region for $S(t)$ by applying the method in the previous step. The number of corresponding region for $S(t)$ is less than that for $s(t)$. So we obtain the unique corresponding block by applying this merging recursively.

3.1.4 Unifying seed regions

As of this point, we have obtained several seed regions that have the unique corresponding region.

Some of the seed regions may belong to the same rigid part. These seed regions should be unified into one seed union.

Let two seed regions be $S_1(t)$ and $S_2(t)$, and they have unique corresponding region $S_1(t+1)$ and $S_2(t+1)$ respectively. If $S_1(t)$ and $S_2(t)$ belong to the same rigid part, the relative location from $S_1(t)$ to $S_2(t)$ is equivalent to the relative location from $S_1(t+1)$ to $S_2(t+1)$ and we can unify $S_1(t)$ and $S_2(t)$ into one seed union $A_{12}(t)$

Thus we obtain seed unions, and the number of them is at most the number of rigid parts.

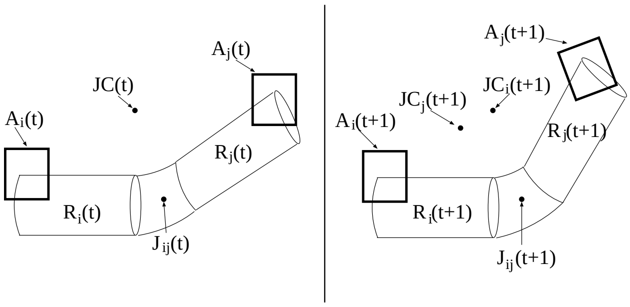


Figure 3. A relation among a joint point and rigid parts: $JC(t)$ is not a joint point, so $JC_i(t+1)$ and $JC_j(t+1)$ are not in the same location.

4 Estimating the joint points

For simplicity, we consider to estimate a joint point of any two rigid parts. These two rigid parts rotate around the joint point.

Let the region of two rigid parts at time t be $R_i(t)$, $R_j(t)$, and a joint point which connects $R_i(t)$ and $R_j(t)$ be $J_{ij}(t)$.

Since $R_i(t)$ rotates around $J_{ij}(t)$, the relative location from $J_{ij}(t)$ to $R_i(t)$ is equivalent to the relative location from $J_{ij}(t+1)$ to $R_i(t+1)$. If we know $J_{ij}(t)$, $R_i(t)$, and $R_i(t+1)$, we can obtain $J_{ij}(t+1)$. In the same way we can obtain $J_{ij}(t+1)$ from $J_{ij}(t)$, $R_j(t)$ and $R_j(t+1)$.

We estimate a joint point from these facts. Let us consider an arbitrary point $JC(t)$. The method to determine whether $JC(t)$ is a joint point or not is as follows.

Test for determining whether $JC(t)$ is a joint point Calculate the rigid motion parameters which transforms $R_i(t)$ to $R_i(t+1)$. Then transform $JC(t)$ by these parameters. We call the location of the transformed $JC(t)$ $JC_i(t+1)$. In the same way, calculate $JC_j(t+1)$ with $R_j(t)$ and $R_j(t+1)$.

If $JC(t)$ is the joint point $J_{ij}(t)$, the equation $JC_i(t+1) = JC_j(t+1)$ is satisfied.

For all the considerable $JC(t)$ between $R_i(t)$ and $R_j(t)$, this equation is checked and the points that satisfy this equation are determined as the joint points.

This test does not need the whole region of the rigid part, but a part of region (ex. $A_i(t), A_i(t+1), A_j(t), A_j(t+1)$ in Fig.3). Hence we can use the seed unions.

Unfortunately, there are some situations where false joint points are estimated. Suppose there are two rigid parts that are not connected. If these rigid parts rotate a certain point which is not a joint point, this point will be estimated as a joint point. This is called a false joint point.

In the next section, we present a method to eliminate these false joint points.

5 Eliminating the false joint points

Generally, the situations that bring the false joint points do not last for a long time. Therefore we can eliminate the false joint points by observing a long time sequence of volume data.

We decide whether a joint point $J_{ij}(t)$, which is estimated from two successive data at time t and $t+1$, is a false joint point or not. The test is the following.

Test for finding false joint points Let the seed unions that are used for estimation of $J_{ij}(t)$ be $A_i(t), A_i(t+1), A_j(t)$ and $A_j(t+1)$. And let us suppose that we have three successive volume data at t, $t+1$ and $t+2$.

At first we estimate $A_i(t+2), A_j(t+2)$ from two successive volume data at $t+1$ and $t+2$ by using the method in section 3. Then we estimate $J_{ij}(t+1)$ from $A_i(t+1), A_i(t+2), A_j(t+1)$ and $A_j(t+2)$. If no joint point is estimated from $A_i(t+1), A_i(t+2), A_j(t+1)$ and $A_j(t+2)$, we can decide $J_{ij}(t)$ is a false joint point.

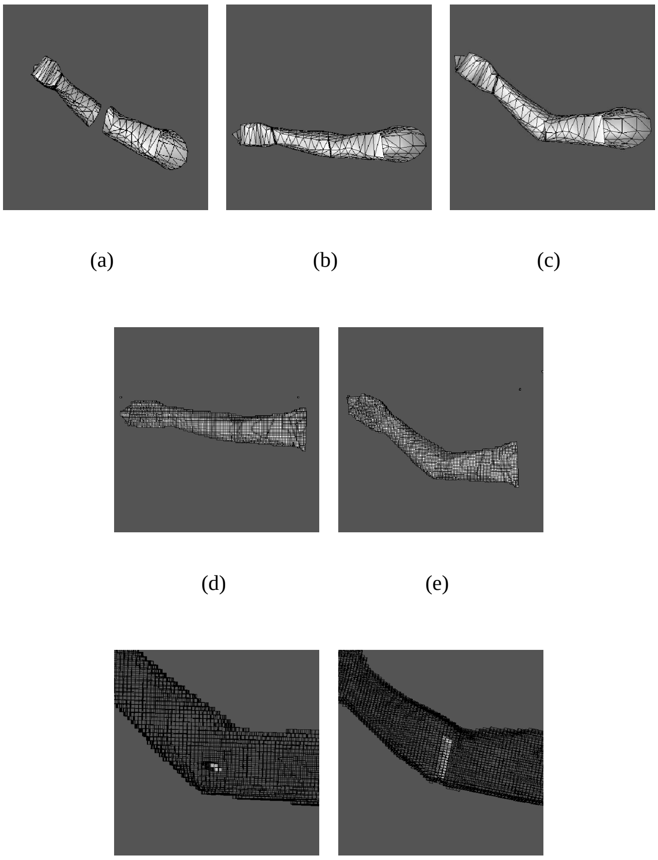
6 Experimental results

We conducted two experiments with computer generated successive volume data of a human body.

The first experiment was designed to evaluate estimation procedure of joint points from two successive volume data.

At first we made two rigid parts (Fig.4(a)), and obtained two shape data by merging them (Fig.4(b)(c)). Then we converted these shape data to voxel data (Fig.4(d)(e)), and set the size of each voxel to $5mm$ cube. Finally we estimated the joint points from these voxel data.

Fig.4(f)(g) show the estimated joint points, plotted on the data shown in Fig.4(e). Because two rigid parts rotate around one axis, a line segment of the joint points are estimated.



(a) (b) (c)

(d) (e)

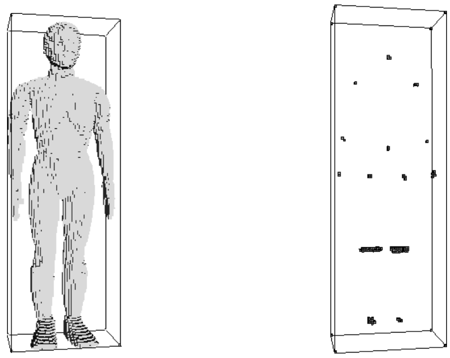
(f) (g)

Figure 4. Experimental results from two successive volume data

The second experiment was designed to evaluate the joint point estimation method described in section 4 and 5.

In this experiment, we used a sequence of 7 volume data and gave the seed unions manually.

Fig.5(a) shows the estimated joint points, plotted on one of the 7 volume data (Fig.5(b)).



(a) (b)

Figure 5. Estimated joint points from a sequence of 7 volume data

7 Conclusion

In this paper, we proposed a novel method to estimate the location of joint points from successive volume data. We extracted the rigid parts under the constraint of the rigid transformation. We estimated the location of joint points under the constraint of the location of two rigid parts. And we eliminated false joint points by using a long time sequence of successive volume data.

We plan to apply our method to real data, and evaluate the performance of it in future.

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