

Statistical Analysis of Joint Determination for Skeleton Driven Animation of Human Hands

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Abstract: Skeleton driven character animation is the most popular animation technique. It has been widely applied in the current computer animation industry. Correct determination of joint positions plays a very important role in creating realistic skin deformation of character animation. Current various approaches of skeleton driven character animation have not addressed this issue. In this paper, we propose a statistical method to determine the correct joint position using the statistical data analysis of different X-ray joint images. First, we measure different joint positions from sample X-ray images. Then, we statistically analyse the data, and obtain relative mean and maximum and minimum positions together with the relative range of joints which are used to determine correct joint positions.

1 INTRODUCTION

Skeleton driven character animation is most frequently applied in computer animation since various commercial animation packages use the technique of skeleton driven character animation. Skeleton driven skin deformation is essential for realistic character animation as the realism of an animated character depends on the appearance and motion of the character. Skeleton driven character animation involves the following steps. First, a skin surface for the virtual character is created. Then this surface is mapped onto the skeleton. The animator spends a lot of time and effort to deform the skin surface realistically in relation to the motion of the skeleton. The realism of an animated character depends on the correctness of this relationship between skin and skeleton movement. Most character animation is driven by skeleton. The quality of skeleton driven character animation depends on correct joint positions. Currently, joint determination is a manual process where animators place joints on to a 3D model without any reference data. Hence this manual process may not produce correct joint positions leading to an unrealistic skin deformation.

The concept of joint-related skin deformation was first explored by Thalmann et al. (1998). The basic concept of skeleton subspace deformation was,

later on, explained by Lander (1998, 1999). The problem of shrinkage around a joint during bending or twisting was discovered by Weber et al. (2000). Wang and Philips (2002) proposed a multi-weight envelop technique to overcome this problem. Mohr and Gleicher (2003) proposed to add additional joints. Kavan and Zara (2005) introduced spherical blend skinning. Yang et al. (2006) suggested curve skeleton skinning approach. The research work carried out by Yang et al. (2006) used influence joints and blend weights as a solution to this problem. Vertices are transformed by using a number of weights for smooth transformation of bones around the joints of character's skeleton. This method is quite interactive and uses minimum animation data.

In order to address this issue, in this paper, we will develop a method which presents the relative mean, maximum and minimum positions together with the relative range of joints from the statistical analysis of available X-ray images. These data can be used to determine the positions of joints correctly.

2 STATISTICAL ANALYSIS OF JOINT DETERMINATION

The basic idea of our proposed method is to find out the statistical data from the X-ray images of joints

available from internet and hospitals and use these statistical data to guide the placement of joints of character models. Figure 1 shows the five X-ray images of a human right hand.

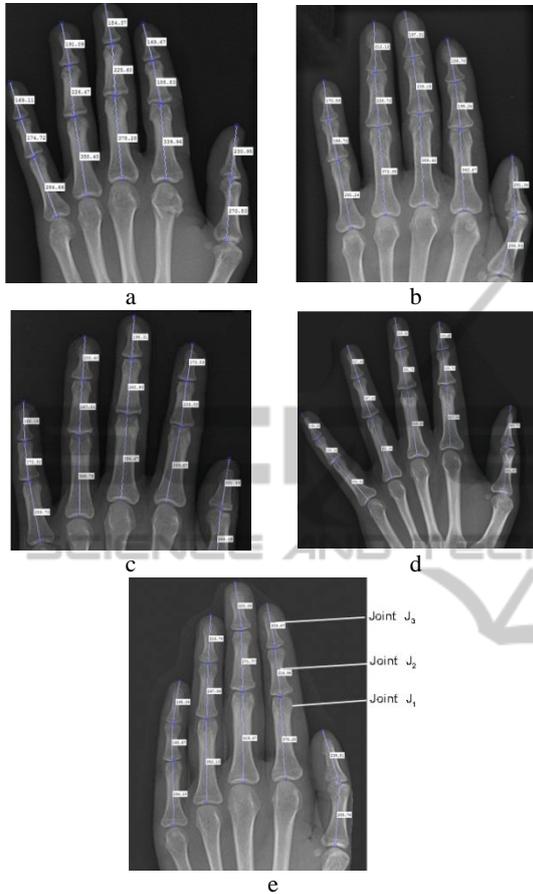


Figure1: X-ray images of the fingers of a human right hand from five different persons.

The lengths between the joints are calculated by using Image Processing tool in Mat lab. For each of grooming, middle, ring and little fingers, the length between the first joint and the second joint from the root of fingers is marked as J_1 , that between the second and third joints was marked as J_2 , and the length beyond the third joint was marked as J_3 . For the thumb, the length between the first joint and the second joint from the root of the thumb is marked as J_1 , and that beyond the second joint was marked as J_2 . The obtained values of J_1 , J_2 and J_3 for all the fingers shown in Figure 1 were given in Table 1. In the table, the numbers indicate the length between two adjacent joints of a same finger. For example, the numbers 339.96, 188.83 and 169.97 for the grooming finger of Figure 1a indicate $J_1 = 339.96$,

$J_2 = 188.83$, and $J_3 = 169.97$.

The total length J of each of the fingers is the sum of J_1 , J_2 and J_3 , i. e.,

$$J = \sum_{i=1}^I J_i \tag{1}$$

where $I=2$ for the thumb, and $I=3$ for all other fingers.

Then we determined the relative value of each of J_1 and J_2 . Since the position of the first joint will be determined by its relative position to the wrist joint, we only consider the second and third joints which are determined by J_1 and J_2 . The relative values \tilde{J}_1 and \tilde{J}_2 of J_1 and J_2 are:

$$\begin{aligned} \tilde{J}_1 &= \frac{J_1}{J} \\ \tilde{J}_2 &= \frac{J_2}{J} \end{aligned} \tag{2}$$

Taking the grooming finger in Figure 1a as an example, the total length of the finger is:

$$\begin{aligned} J &= J_1 + J_2 + J_3 \\ &= 339.96 + 188.83 + 169.97 = 698.76 \end{aligned} \tag{3}$$

and the relative values \tilde{J}_1 and \tilde{J}_2 of J_1 and J_2 of the grooming finger are:

$$\begin{aligned} \tilde{J}_1 &= \frac{J_1}{J} = \frac{339.96}{698.76} = 0.4865 \\ \tilde{J}_2 &= \frac{J_2}{J} = \frac{188.83}{698.76} = 0.2702 \end{aligned} \tag{4}$$

One of the advantages using the relative values \tilde{J}_1 and \tilde{J}_2 of J_1 and J_2 is the obtained results can be easily extended to other models. For example, one built grooming finger model has a total length of 1000. According to the relative values \tilde{J}_1 and \tilde{J}_2 of J_1 and J_2 given in Eq. (4), we can find J_1 and J_2 of the built grooming finger model to be $0.4865 \times 1000 = 486.5$ and $0.2702 \times 1000 = 270.2$.

With the same method, the obtained total length J , and relative values \tilde{J}_1 and \tilde{J}_2 of J_1 and J_2 of the grooming finger are 724.41, 0.4728, and 0.2695 for Figure 1b, 739.78, 0.4862, and 0.2792 for Figure 1c, 826.53, 0.5047, and 0.2731 for Figure 1d, and 793.68, 0.4728, and 0.2708 for Figure 1e.

If there are M X-ray grooming finger images, the relative mean values \bar{J}_1 and \bar{J}_2 can be determined from the relative values \tilde{J}_1 and \tilde{J}_2 of the M X-ray grooming finger images through the following equation:

$$\begin{aligned}\bar{J}_1 &= \frac{1}{M} \sum_{m=1}^M \tilde{J}_{1m} \\ \bar{J}_2 &= \frac{1}{M} \sum_{m=1}^M \tilde{J}_{2m}\end{aligned}\quad (5)$$

where \tilde{J}_{1m} and \tilde{J}_{2m} are \tilde{J}_1 and \tilde{J}_2 of the m^{th} X-ray grooming finger image.

According to Eq. (5) and the five X-ray grooming finger images given in Figure 1, $M=5$ and the relative mean values \bar{J}_1 and \bar{J}_2 of the grooming finger are:

$$\begin{aligned}\bar{J}_1 &= \frac{1}{5} \sum_{m=1}^5 \tilde{J}_{1m} = \frac{1}{5} (0.4865 + 0.4728 + 0.4862 \\ &\quad + 0.5047 + 0.4728) = 0.4946\end{aligned}\quad (6)$$

$$\bar{J}_2 = \frac{1}{5} \sum_{m=1}^5 \tilde{J}_{2m} = 0.2726$$

We also give the maximum and minimum relative values among all the values of \tilde{J}_k of the M X-ray images through the following equation:

$$\begin{aligned}\tilde{J}_{k \max} &= \max\{\tilde{J}_{k1} \ \tilde{J}_{k2} \ \tilde{J}_{k3} \ \dots \ \tilde{J}_{kM}\} \\ \tilde{J}_{k \min} &= \min\{\tilde{J}_{k1} \ \tilde{J}_{k2} \ \tilde{J}_{k3} \ \dots \ \tilde{J}_{kM}\}\end{aligned}\quad (7)$$

where $k=1$ is for the thumb, and $k=1$ and $k=2$ are for all other fingers.

According to Eq. (7) and the five grooming finger images given in Figure 1, the maximum and minimum relative values $\tilde{J}_{1 \max}$ and $\tilde{J}_{1 \min}$ for the five X-ray grooming finger images are:

$$\begin{aligned}\tilde{J}_{1 \max} &= \max\{\tilde{J}_{11} \ \tilde{J}_{12} \ \tilde{J}_{13} \ \dots \ \tilde{J}_{15}\} \\ &= \max\{0.4865 \ 0.4728 \ 0.4862 \ 0.5047 \ 0.4728\} \\ &= 0.5047\end{aligned}\quad (8)$$

$$\begin{aligned}\tilde{J}_{1 \min} &= \min\{\tilde{J}_{11} \ \tilde{J}_{12} \ \tilde{J}_{13} \ \dots \ \tilde{J}_{15}\} \\ &= \min\{0.4865 \ 0.4728 \ 0.4862 \ 0.5047 \ 0.4728\} \\ &= 0.4728\end{aligned}$$

The relative range can be easily found by considering the difference between the maximum and minimum relative values, i.e.,

$$R_k = \tilde{J}_{k \max} - \tilde{J}_{k \min}\quad (9)$$

According to Eq. (9), the relative range for J_1 of the five X-ray grooming finger images is:

$$\begin{aligned}R_1 &= \tilde{J}_{1 \max} - \tilde{J}_{1 \min} \\ &= 0.5047 - 0.4728 = 0.0319\end{aligned}\quad (10)$$

With above method, we calculated the relative mean values and maximum and minimum relative values together with the relative range of J_1 and J_2 of grooming, middle, ring and little fingers and those

for J_1 of the thumb from the five images in Figure 1, and listed the obtained statistical data.

Once a finger model is built and its total length J is known, we can use the statistical data determine the mean, maximum, minimum and range.

Taking J_1 of a built grooming finger model as example, if the total length of the model is $J = 1000$, the mean value of J_1 is $\bar{J}_1 \times 1000 = 0.4946 \times 1000 = 494.6$, the maximum value of J_1 is $J_{1 \max} = \tilde{J}_{1 \max} \times 1000 = 0.5047 \times 1000 = 504.7$, the minimum value of J_1 is $J_{1 \min} = \tilde{J}_{1 \min} \times 1000 = 0.4728 \times 1000 = 472.8$, and the range of J_1 is $R_1 \times 1000 = 0.0319 \times 1000 = 31.9$ which is the same as $\tilde{J}_{1 \max} - \tilde{J}_{1 \min} = 504.7 - 472.8 = 31.9$.

3 APPLICATION EXAMPLE

It can be seen clearly from Figure 2c and 3c that different skin deformations were generated by different joint positions. The skin deformation caused by the joints determined with the statistical method given in this paper creates a more realistic appearance than that caused by the manually specified joints.



Figure 2a: Human rigged model.



Figure 3a: Human rigged with correct joint positions.

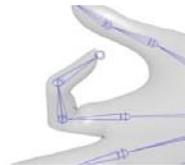


Figure 2b: Human finger animated.



Figure 3b: Human fingers animated by our method.



Figure 2c: Problem of limbs crossover which gives un-realistic skin deformation.



Figure 3c: Correct joint positions gives realistic skin deformation.

4 CONCLUSIONS AND FUTURE WORK

In this paper, we have presented a statistical method to determine the positions of joints based on available X-ray images and statistics. We have also obtained the statistical data of the joint positions of human fingers.

For our future work, we will use more X-ray images of human fingers to obtain the statistical data and extend our proposed method to a whole human model. We will also investigate the statistical data of people with different age and sex groups and provide more useful statistical data for correct determination of joints of skeleton driven character models.

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Table 1: Data from X-ray images.

	Grooming			Middle			Ring		
	J_1	J_2	J_3	J_1	J_2	J_3	J_1	J_2	J_3
Figure 1a	339.96	188.83	169.67	375.28	255.60	184.37	358.40	226.47	191.09
Figure 1b	342.47	195.24	186.70	389.42	239.15	197.31	372.98	226.72	212.12
Figure 1c	359.67	206.58	173.53	394.47	260.98	195.31	366.78	247.01	200.40
Figure 1d	417.16	225.70	183.67	446.49	261.72	209.62	442.49	267.65	227.06
Figure 1e	375.25	214.96	203.47	419.47	271.77	223.35	382.13	247.86	219.75
	Little			Thumb					
	J_1	J_2	J_3		J_1	J_2			
Figure 1a	284.66	174.72	169.11		270.83	230.95			
Figure 1b	291.24	166.72	170.56		259.53	251.34			
Figure 1c	289.73	172.52	180.18		264.05	231.33			
Figure 1d	334.51	180.32	196.25		301.67	264.72			
Figure 1e	294.10	168.67	195.09		285.76	239.81			