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Analysis of Alignment Influence on 3-D Anthropometric Statistics*

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Abstract: Three-dimensional (3-D) surface anthropometry can provide much more useful information for many applications such as ergonomic product design than traditional individual body dimension measurements. However, the traditional definition of the percentile calculation is designed only for 1-D anthropometric data estimates. The same approach cannot be applied directly to 3-D anthropometric statistics otherwise it could lead to misinterpretations. In this paper, the influence of alignment references on 3-D anthropometric statistics is analyzed mathematically, which shows that different alignment reference points (for example, landmarks) for translation alignment could result in different object shapes if 3-D anthropometric data are processed for percentile values based on coordinates and that dimension percentile calculations based on coordinate statistics are incompatible with those traditionally based on individual dimensions.

Key words: three-dimensional (3-D) anthropometry; alignment; percentile

Introduction

Three-dimensional (3-D) anthropometry is the quantitative study of the dimensions and certain other physical characteristics of the human body region and organ surfaces, volumes, and shape characteristics using noninvasive methods[1]. Data from 3-D anthropometry are critical to equipment and workplace design. Hundreds of anthropometric dimensions have been defined and measured for use in customized apparel design, personal care items (protective helmets, faces mask, eye glasses, knee braces, etc.) design, workstation layout, furniture and so on[2,3]. Traditional body size measuring tools are generally limited to single, independent dimensions. Currently, many specially designed 3-D scanners for human anthropometric measurements have become available for research and applications.

The advantages of the 3-D scanning method is that, in addition to obtaining traditional anthropometric measurements, a 3-D scanner can also record the surface shape, area, and volume of the entire body or body segments. For some engineering applications, this can provide the possibility for the user to realistically visualize human anthropometry in three dimensions. 3-D anthropometric data can also enable designers to accommodate a desired portion of the potential user population in their designs.

Traditionally, to utilize the collected anthropometric data, independent dimensions are measured first and then analyzed statistically to generate percentile tables. However, for most 3-D anthropometric measurements, the collected raw data is only point information in a 3-D format. Therefore, algorithms used to calculate 1-D statistics cannot be applied directly to 3-D data. The user needs to convert the original coordinate data to individual dimension data before statistical analysis. However, if only dimensions are interested in, the great benefits of 3-D scanning over the traditional 1-D measurement method are lost since large quantities of 3-D data are not exploited.

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Different alignment methods have been used by researchers to calculate the percentiles of 3-D data based on uniform references. Pre-defined landmarks are often used as alignment reference points. Hawes et al.[4] presented a method for averaging foot phantagram curves based on three well-defined anatomical landmarks that serve as reference points. The alignment axis was defined using the geometric method proposed by Katoh[5]. Other methods include aligning two scans by a common surface area[6], and using critical design elements[7]. However, no theoretical study has been reported regarding the effects of the selection of alignment methods on statistic analyses in 3-D anthropometry. Significant differences may result from the use of the various alignment methods. This paper presents an analysis to quantify such differences.

1 Method

Assume that the coordinates of three corresponding points (maybe landmarks) of n subjects, P_1, P_2, and P_3, are measured using the same 3-D scanning equipment. Denote the coordinates as P_{1i} (x_{1i}, y_{1i}, z_{1i}), P_{2i} (x_{2i}, y_{2i}, z_{2i}), and P_{3i} (x_{3i}, y_{3i}, z_{3i}) (i = 1, 2, …, n) (Fig. 1), the mean values as $\overline{x_k}$, $\overline{y_k}$, and $\overline{z_k}$, and the standard deviations as s_{x_k}, s_{y_k}, and s_{z_k} (k=1, 2, 3). These values are related as:

$$\begin{aligned}
&\overline{x_k}=\frac{\sum_{i=1}^{n}x_{ki}}{n},\ s_{x_k}=\sqrt{\frac{\sum_{i=1}^{n}(x_{ki}-\overline{x_k})^2}{n-1}};\\
&\overline{y_k}=\frac{\sum_{i=1}^{n}y_{ki}}{n},\ s_{y_k}=\sqrt{\frac{\sum_{i=1}^{n}(y_{ki}-\overline{y_k})^2}{n-1}};\qquad k=1,2,3\\
&\overline{z_k}=\frac{\sum_{i=1}^{n}z_{ki}}{n},\ s_{z_k}=\sqrt{\frac{\sum_{i=1}^{n}(z_{ki}-\overline{z_k})^2}{n-1}}
\end{aligned}\tag{1}$$

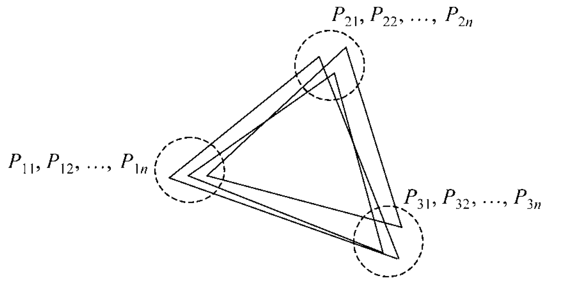

Fig. 1 Distribution of the sample points

Consider the case when all samples are aligned by translation (without rotation transformation). By first selecting P_{11} as the alignment reference point, the points can be translated so that all the P_{1i} (i = 2, 3, …, n) are moved to point P_{11}. The new coordinates are then: P_{1i} (x_{11}, y_{11}, z_{11}), P_{2i} ($x_{2i}-x_{1i}+x_{11}$, $y_{2i}-y_{1i}+y_{11}$, $z_{2i}-z_{1i}+z_{11}$), P_{3i} ($x_{3i}-x_{1i}+x_{11}$, $y_{3i}-y_{1i}+y_{11}$, $z_{3i}-z_{1i}+z_{11}$), (i =2, 3, …, n). The new mean values and standard deviations are as follows.

For point P_1

$$\overline{x_1'}=x_{11},\ \overline{y_1'}=y_{11},\ \overline{z_1'}=z_{11},$$
$$s'_{x_1}=s'_{y_1}=s'_{z_1}=0\tag{2}$$

For point P_2,

$$\overline{x_2'}=\frac{\sum_{i=1}^{n}x'_{2i}}{n}=\frac{\sum_{i=1}^{n}(x_{2i}-x_{1i}+x_{11})}{n}=\overline{x_2}-\overline{x_1}+x_{11},$$

$$s'_{x_2}=\sqrt{\frac{\sum_{i=1}^{n}(x'_{2i}-\overline{x_2'})^2}{n-1}}=\sqrt{\frac{\sum_{i=1}^{n}(x_{2i}-x_{1i}+x_{11}-\overline{x_2})^2}{n-1}}=$$
$$\sqrt{s_{x_1}{}^2+s_{x_2}{}^2-\frac{2}{n-1}\sum_{i=1}^{n}(x_{1i}-x_{11})(x_{2i}-\overline{x_2})}=$$
$$\sqrt{s_{x_1}^2+s_{x_2}^2}\tag{3}$$

In Eq. (3), the point coordinates are independent of each other, so the covariances are equal to zero. Denote $\sqrt{s_m{}^2+s_n{}^2}$ as $s(m,n)$ and $\overline{a_m}-\overline{a_n}$ as $\overline{a_{m,n}}$. Note that $s(m,n)=s(n,m)$, $\overline{a_{m,n}}=-\overline{a_{n,m}}$ and $\overline{a_{m,n}}=\overline{a_{m,l}}+\overline{a_{l,n}}=\overline{a_{m,l}}-\overline{a_{n,l}}$. Now Eq. (3) can be written as:

$$\overline{x_2'}=\overline{x_{2,1}}+x_{11},\ s'_{x_2}=s(x_1,x_2)\tag{4}$$

Similarly,

$$\begin{aligned}
&\overline{y_2'}=\overline{y_{2,1}}+y_{11},\ s'_{y_2}=s(y_2,y_1),\\
&\overline{z_2'}=\overline{z_{2,1}}+z_{11},\ s'_{z_2}=s(z_2,z_1),\\
&\overline{x_3'}=\overline{x_{3,1}}+x_{11},\ s'_{x_3}=s(x_3,x_1),\\
&\overline{y_3'}=\overline{y_{3,1}}+y_{11},\ s'_{y_3}=s(y_3,y_1),\\
&\overline{z_3'}=\overline{z_{3,1}}+z_{11},\ s'_{z_3}=s(z_3,z_1)
\end{aligned}\tag{5}$$

For the p-th percentile when n ≥ 30, the corresponding percentile positions of the above points are $P_{1(p)}$: (x_{11}, y_{11}, z_{11}); $P_{2(p)}$: ($\overline{x_{2,1}}+x_{11}+z_p s_{x_1,x_2}$, $\overline{y_{2,1}}+y_{11}+z_p s_{y_1,y_2}$, $\overline{z_{2,1}}+z_{11}+z_p s_{z_1,z_2}$); $P_{3(p)}$:($\overline{x_{3,1}}+x_{11}+z_p s_{x_1,x_3}$, $\overline{y_{3,1}}+y_{11}+z_p s_{y_1,y_3}$, $\overline{z_{3,1}}+z_{11}+z_p s_{z_1,z_3}$).

Here, z_p is the standard normal value corresponding to the p-th percentile.

Then the percentile dimensions (point distances) can be calculated by:

$$P_1P_{2(p)}{}^2 = (\overline{x_{1,2}} - z_p s_{x_1,x_2})^2 + (\overline{y_{1,2}} - z_p s_{y_1,y_2})^2 + (\overline{z_{1,2}} - z_p s_{z_1,z_2})^2,$$

$$P_1P_{3(p)}{}^2 = (\overline{x_{1,3}} - z_p s_{x_1,x_3})^2 + (\overline{y_{1,3}} - z_p s_{y_1,y_3})^2 + (\overline{z_{1,3}} - z_p s_{z_1,z_3})^2,$$

$$P_2P_{3(p)}{}^2 = (\overline{x_{2,3}} - z_p (s_{x_1,x_3} - s_{x_1,x_2}))^2 + (\overline{y_{2,3}} - z_p (s_{y_1,y_3} - s_{y_1,y_2}))^2 + (\overline{z_{2,3}} - z_p (s_{z_1,z_3} - s_{z_1,z_2}))^2 \tag{6}$$

If P_{21} is selected as the aligning reference point, then by the same process:

$$P_1P_{2(p)}{}'^2 = (\overline{x_{1,2}} + z_p s_{x_1,x_2})^2 + (\overline{y_{1,2}} + z_p s_{y_1,y_2})^2 + (\overline{z_{1,2}} + z_p s_{z_1,z_2})^2,$$

$$P_1P_{3(p)}{}'^2 = (\overline{x_{1,3}} + z_p (s_{x_1,x_2} - s_{x_2,x_3}))^2 + (\overline{y_{1,3}} + z_p (s_{y_1,y_2} - s_{y_2,y_3}))^2 + (\overline{z_{1,3}} + z_p (s_{z_1,z_2} - s_{z_2,z_3}))^2,$$

$$P_2P_{3(p)}{}'^2 = (\overline{x_{2,3}} - z_p s_{x_2,x_3})^2 + (\overline{y_{2,3}} - z_p s_{y_2,y_3})^2 + (\overline{z_{2,3}} - z_p s_{z_2,z_3})^2 \tag{7}$$

Take $P_1P_{2(p)}$ and $P_1P_{2(p)}{}'$ as examples. The difference between the two alignment methods is

$$\Delta = P_1P_{2(p)}{}'^2 - P_1P_{2(p)}{}^2 = 4z_p(\overline{x_{1,2}} s_{x_1,x_2} + \overline{y_{1,2}} s_{y_1,y_2} + \overline{z_{1,2}} s_{z_1,z_2}) \tag{8}$$

Normally, $s_{x_1,x_2} > 0$, $s_{y_1,y_2} > 0$, and $s_{z_1,z_2} > 0$, and since ($\overline{x_i}$, $\overline{y_i}$, $\overline{z_i}$) (i = 1, 2, 3) represents the coordinates of the three points, in many cases $\overline{x_{1,2}}$, $\overline{y_{1,2}}$, and $\overline{z_{1,2}}$ are all negative or positive. Thus, only z_p=0 (50th percentile or average) will always give Δ=0. Larger distances between the points or larger variances of the points will result in larger differences. Differences can also be found in the two other distances. Therefore, the use of different alignment reference points will result in different object shapes if the 3-D anthropometric data is processed for percentile values based on the coordinates.

With the traditional dimension statistic method, the distance between P_1 and P_2 is calculated as:

$$d_{12(i)}{}^2 = (x_{2i} - x_{1i})^2 + (y_{2i} - y_{1i})^2 + (z_{2i} - z_{1i})^2,$$

$$\overline{d_{12}} = \frac{1}{n}\sum_{i=1}^{n} d_{12(i)}, \quad s_{d_{12}}^2 = \frac{1}{n-1}\sum_{i=1}^{n}(d_{12(i)} - \overline{d_{12}})^2,$$

$$d_{12(p)} = \overline{d_{12}} + z_p s_{d_{12}} \tag{9}$$

Since $d_{12(p)}$ is normally different from $P_1P_{2(p)}$, statistics based on 3-D coordinates are incompatible with those based on traditional dimensions.

2 Discussion

The analysis implies that the alignment reference points for 3-D anthropometric statistics should be carefully chosen. If statistics based on coordinates have to be calculated, the alignment reference points should be selected according to the particular needs for each application. Also, the validity of the results is limited to a particular application and will not be compatible with traditional dimensional statistics. As an example, in the study by Hawes et al.[4], the results based on the authors' suggested alignment method cannot necessarily be adapted to other applications. The average digitized phantagram curve may not change with the selection of the alignment axis, but other percentile curves will do. When several scans are aligned by their common surface areas, the aligning references between each two scans may be different[8]. Hockstra[7] pointed out that since 3-D scans implicitly contain the spatial relationships between anthropometric variables, they could expand the notion of percentiles and transform it into something that has some aspects of a density function. It is apparent that density will change with the aligning method. Sizing by shape has also been proposed for 3-D anthropometric statistics[9-11] with only a few case studies. This method is so complicated that very few engineers can use it correctly and alignment is still a sensitive issue.

3 Conclusions

The use of 3-D anthropometry has become more popular in product design and workplace layout. 3-D anthropometry has many advantages in comparison to the traditional parameter measurement method. However, the data processing is extremely complex. This paper analyzes the selection of alignment

reference points. The object shape resulting from statistical analysis of 3-D data will depend on the selection of the alignment reference points. Anthropometric statistics based on coordinates are not compatible with those based on dimensional data. Therefore, when generating statistics based on coordinates, extra caution should be paid in selecting the alignment references to avoid unintended errors.

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