

Automatic Feature Detection in 3D Human Body Scans

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ABSTRACT

Human body scanners generate meshes, consisting of over 100,000 points and triangles, defining a human shape model. The underlying anthropometric landmarks are not scanned, but necessary for many applications. In the CAESAR database these anthropometric landmarks have been premarked by attaching small markers to the human body. The positions of these anthropometric landmarks have been extracted semi-automatically and are available as part of the CAESAR data. Attaching markers to humans is time consuming and is therefore often omitted in other surveys. Hence, there is a need for methods for fully automated extraction of landmarks from human body scans.

We investigated three fully automatic detection methods for landmark extraction. The first method uses a function that is fitted onto the region around the marker of interest. The second method analyzes the curvature in the area around the marker. The third and last method is template matching, which has been successfully applied in other fields.

The sellion and the four malleoli were selected for evaluation. The latter landmarks are important to locate the ankle joint. For the malleoli the template matching method was best (mean deviation 15 ± 3 mm) followed by curvature calculation (15 ± 3 mm) and function fitting (28 ± 10 mm). For all methods the deviation for the sellion was considerable larger. Template matching proves to be the most consistent and furthermore has the potential of being refined.

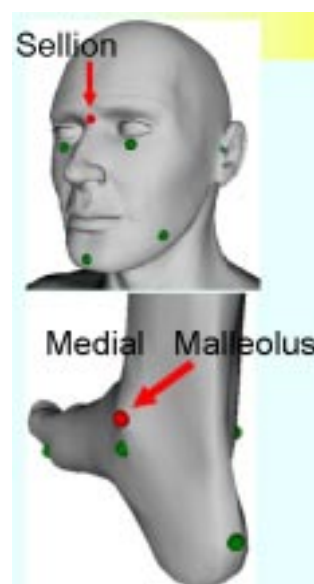
INTRODUCTION

In the CAESAR project a large-scale anthropometric survey has been conducted (Robinette et al., 2002), in which 2500 people in the United States and another 2500 in The Netherlands and Italy have participated. Each individual has been premarked with small markers attached to 73 selected anthropometric locations on the body. All individuals were scanned and the locations of the markers have been extracted semi-automatically using software displaying a global area in which the

marker should lie, and leaving it to the user to pick the exact location.

Since then more research is done to automatically detect landmarks in 3D body scans in order to fully use the benefits of 3D laser scanning, the applications of which are summarized by Jones and Rioux (1997). The amount of research dealing with feature extraction in 3D body scans is limited and primarily concentrated on face recognition. Therefore we investigate methods, which are currently applied for feature recognition in 3D, not limiting ourselves to only body scans, but also looking at the field of object recognition.

Because only limited time was available we focused our attention to five landmarks. These are the lateral and medial malleoli (ankle bones) and the sellion (located between the eyes). The former is important to estimate the ankle joint location and the latter is used for the design of gasmasks.



METHODS

The Dutch CAESAR scans are obtained with the Vitronic Vitus Pro scanner producing 16 point clouds for each scan. These clouds are only aligned by the calibration of the scanner. They proved unusable due to miscalibration errors and noise. Therefore we aligned the 16 point clouds with a software package called PolyWorks. The aligned point clouds contain (almost) all of the original points, are completely aligned and contain much less noise. The next step is to merge the point clouds into one new point cloud containing much less points than in the 16 points together (many points in the 16 point clouds overlap).

We investigated three different approaches to detect the landmarks from these scans: template matching, function fitting and curvature calculation. The results of these three techniques were compared to the results of the hand picked landmarks, which were used as a reference. In the remainder of the paper we use the phrase 'region of interest' to denote a part of the body scan containing a landmark to be detected.

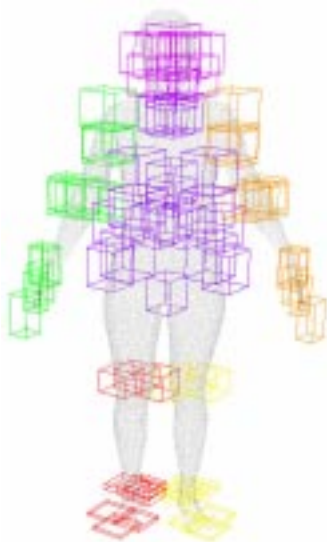


Figure 1: Bounding boxes

Bounding Boxes

First, we defined a method to obtain regions of interest for all the 73 handpicked markers from the CAESAR project. The coordinates of every landmark (x,y,z) were divided by the dimensions of the whole body bounding box. This resulted in a percentage (x,y,z) for every landmark. When this was done for all landmarks in all scans, we constructed a box for every landmark. We defined this box to contain 95% of all values, so extremes were not taken into account. The result is shown in Figure 1. The bounding boxes were used in all methods to extract the regions-of-interest in which the landmark is located.

Template Matching

There are several applications of template matching, but the applications are generally not related to landmark detection but to image registration. Nevertheless the basic principle remains the same: try to match a surface of which all relevant information is known (a template) onto another surface. The matching of the two surfaces is driven by a similarity function.

We faced two challenges for applying template matching on the regions of interest. First, a suitable template had to be created. Second, a similarity function had to be selected, so that a minimizer algorithm can align the template onto the region of interest.

For the first problem we created a set of templates for each landmark which contains information about the location of the landmark. The bounding boxes were used for the creation process to select a small subset of points from the whole body scan of a subject. This subset contained our landmark position. We added the hand picked location to this subset and stored the subset to file. This procedure was automated and repeated for some 25 randomly picked scan files. We visually verified that the hand picked locations corresponded to the location where we would expect them to be on the basis of shape. This was done because picking errors might have occurred during the landmark picking process.

For the second problem, the choice of the similarity function used by the minimizer, we selected 'average-min distance'. The value calculated with the similarity function is used to determine the goodness of fit of the template onto the region of interest. The distance between the two points of a point pair was expressed in terms of the Euclidian distance. The most commonly used function is the max-min distance, also referred to as the Hausdorff distance. We altered this Hausdorff distance slightly which resulted into the average-min distance. This was done to improve robustness, because our template and regions of interest are in fact point clouds and that can contain noise. The definition of the max-min distance and average-min distance is displayed in Figure 2.

Max-min distance definition:

$$\overline{d}(A, B) = \max(\overline{d}(A, B), \overline{d}(B, A)) \text{ where}$$
$$\overline{d}(A, B) = \max_{a \in A} (\min_{b \in B} d(a, b))$$

Average-min distance uses:

$$\overline{d}(A, B) = \text{avr}_A (\min_{b \in B} d(a, b))$$

Figure 2: Definition of max-min and average-min

The iterative alignment of the point clouds will stop when the similarity function will no longer return a smaller value. With the aid of the location of the landmark that was indicated on the template we reconstruct the location of the landmark in the region of interest.

Function Fitting

The second method is a new one. The idea is to describe the surroundings of a landmark with some (distribution) function. In a way this method is similar to template matching, only now we have a much simpler, but deformable template. We will try to adjust the parameters of the function such that a similarity function will yield a smaller value when the fit is better.

When looking at the form of the malleoli (ankle bones) for example, a Gaussian distribution can be detected. The location of the malleoli will be found by fitting an altered multi-Gaussian distribution function. The definition of the distribution function is shown in Figure 3. We will define the location of the landmark as the top of the Gaussian distribution function. The parameters of the distribution function will be estimated by non-linear regression, so that the distribution function will resemble the region of interest.

Curvature Calculation

A more conventional way of detecting features in a Modified Multi-Gaussian:

$$z = \frac{1}{\sqrt{2\pi A^2}} e^{-\frac{(x-B)^2}{2A^2}} * \frac{1}{\sqrt{2\pi C^2}} e^{-\frac{(y-D)^2}{2C^2}}$$

Figure 3: Definition of Modified Multi-Gaussian. Variables A, B, C and D are solved by non-linear regression.

surface is to compute the surface curvature (Gordon, 1992; Li et al., 2003). We chose to calculate the Gaussian curvature for each point in the region of interest (if possible). Points that will not have their curvature calculated are those that lie on a boundary. For the remainder we can calculate the curvature of a point

$$c(p) = \frac{d(p)}{a(p)}$$

$c(p)$ with the formula of Caladine (1985):

In the formula $d(p)$ is the angular defect. This is defined for the interior vertices as 2π minus the sum of the interior angles of the facets meeting at point p . The scalar $a(p)$ denotes the area associated with vertex p , where each facet contributes to $a(p)$ a part of its surface.

From the definition of the curvature formula it shows that the flatter the surface, the smaller $c(p)$ will be. If all facets are coplanar, the angular defect will be zero. If gaps occur (due to the fact that the vertex is on a boundary or a gap is present) the curvature won't be computed. An implementation which satisfies our needs already exists in the form of the open source GNU Triangulated Surface Library. When the curvatures for all points in a

point cloud are calculated, we pick the point with the smallest curvature to represent the location of the sellion. For the malleoli, the point with the largest curvature value is picked.

RESULTS

For the evaluation of our program we used a set of ten randomly selected scans from the Dutch part of the CAESAR project. We made sure that the picked scans had not been used for the creation of the templates. The locating process was done for each scan by first creating the regions of interest for the five landmarks. Then a series of recognition steps were performed on each region of interest. Each series constituted of ten tries of template matching, where every attempt a different template was used. Then a curvature calculation attempt; the points with the minimum and maximum curvature were picked from this, and finally a function fitting attempt.

The running time for the detection of the five landmarks per aligned and merged scan was just under one hour. Computation was done with a Pentium III 1Ghz with 512mb of ram. The time spent per landmark depends on the number of points in the region of interest, and for template matching, also the number of points in the template. Typical running times for an aligned and merged scan are listed in Table 1. The results for every scan are listed in Figure 4.

When comparing the results of the different methods we

Landmark	Curvature Calculation	Function Fitting	Template Matching
Left Lateral Malleolus	< 1 sec.	< 5 sec.	< 2 min.
Left Medial Malleolus	< 1 sec.	< 5 sec.	< 2 min.
Right Lateral Malleolus	< 1 sec.	< 5 sec.	< 2 min.
Right Medial Malleolus	< 1 sec.	< 5 sec.	< 2 min.
Sellion	< 1 sec.	< 25 sec.	< 55 min.

Table 1: Running times for detection runs on an aligned merged scan

conclude that template matching performs best (see Figure 4). In all cases the accuracy for template matching was best (a deviation of 23 mm +/- 3 mm for the sellion, and 15 mm +/- 3 mm for the malleoli compared to the hand picked marker). It is followed by curvature calculation (a deviation of 45 mm +/- 20 mm for the sellion and 15 mm +/- 5 mm for the malleoli compared to the hand picked marker). Last is function fitting (a deviation of 80 mm +/- 20 mm for the sellion and 28 mm +/- 10 mm for the malleoli compared to the hand picked marker).

CONCLUSIONS AND RECOMMENDATIONS

We have developed and implemented a software program, which can be used as a framework for comparing different approaches for feature detection. All implemented approaches (template matching, function fitting and curvature calculation) can be visualized and the results can be exported.

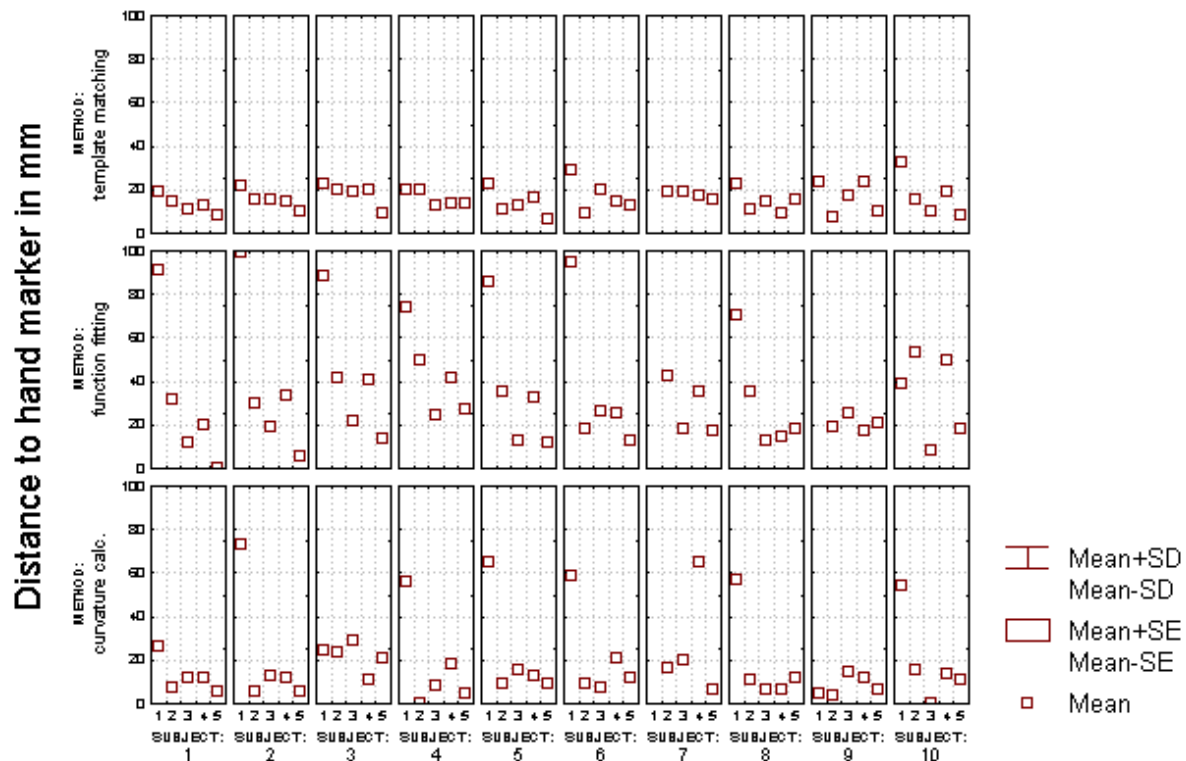


Figure 4: Distance to handpicked marker for five landmarks on ten scans, with the result of the sellion for person 7 removed. The names of the landmarks are replaced with numbers 1 to 5. '1' corresponds with the sellion, '2' with the right lateral malleolus, '3' with the right medial malleolus, '4' with the left lateral malleolus and '5' with the left medial malleolus.

When comparing the outcomes of the different approaches, template matching performed best, followed by curvature calculation and finally function fitting. However, template matching was the most time consuming method. We feel confident that the results can be improved upon by more efficient computer routines.

We would like to make some recommendations for further research for each method. For the template matching algorithm the distance measure can be improved upon and more templates may be used as a reference. For function fitting more complex functions could be tried, which would better capture the area of interest intrinsic properties. Finally for curvature calculation it could be investigated if non-Gaussian curvatures will yield better results.

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