

# Semantic Human 3D Shapes Annotation for Animation

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**Abstract**—The problem of identifying particular points or areas on 3D meshes is closely related to several outcomes in computer graphics: when animating virtual characters the animator must first identify which part of the 3D envelop can be assigned to which corresponding part of the animated skeleton, to obtain a visually coherent animated shape. Every shape has to be segmented to be usable after while. For instance, the CAESAR body database has been built using 3D scans plus a set of landmarks to identify body measurements. Unfortunately this is not the case when acquiring scanned data in general, and particularly for human scanned bodies. We demonstrate that it is possible to get rid of noisy and complex data so as to extract from any human body closed mesh its skeleton of animation. Assuming the joints are located where the shape has the more variations and based on a multi-scale analysis, we are able to deduce main joints positions. We also build a control skeleton and label automatically all detected joints relying on a priori knowledge on human anatomy, independently from body postures. We demonstrate our approach with several examples.

**Index Terms**—Semantic Annotation, 3D Shape Analysis, Computer Animation, Virtual Human.

## I. INTRODUCTION

A skeleton for animation is a hierarchical structure composed of joints and segments linking them. A joint stands for a possible degree of freedom of the creature's shape. Each joint is considered as a local coordinate system and its position in the world coordinate system depends on its parent joint position. The root of the hierarchy is the basin center for a human. This structure is necessary to compute efficiently the shape deformation during animation, or to evaluate body measurements and meta-data. For a human, we can consider a joint for each anatomical joint and the segments are the bones linking the different joints. In a standard animation pipeline, we consider around 20 degrees of freedom (i.e., joints). Virtual Humans are traditionally produced from a single 3D shape representing the body shape in a default posture. An articulated animation skeleton is

associated to this default shape and is used to animate the Virtual Human and adjust the 3D default shape to animated postures [1, 2]. Extracting an accurate skeleton is a tedious task. We propose to use multiscale shape analysis tools in order to automate the process.

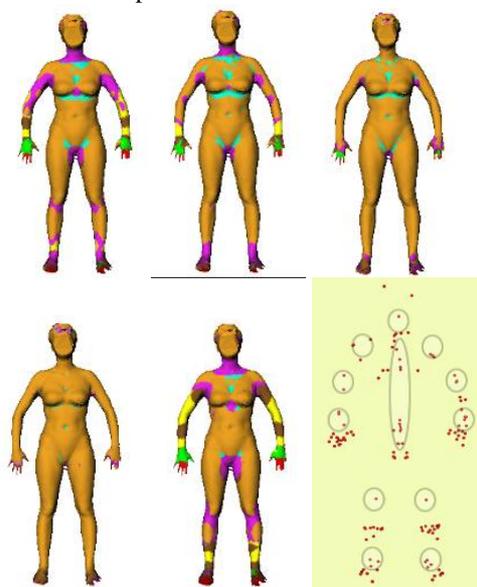


Figure 1: Detected areas on a scanned body at all scales; in the last picture, the centroids corresponding to these regions are located by the circles and they globally correspond to the anatomical joints.

## II. BODY SHAPE ANALYSIS

The *Tailor* algorithm [3] detects different kind of features (sharp protrusions, wells, dips, and branching parts) at different scales on a given shape (c.f. figure 1). Vertices are labeled with different colors according to the feature they are associated to. We performed tests on a set of bodies with different corpulence. For each labeled area of vertices, its centroid is defined as the mean of triangles barycenters. We computed them across the different scales and filtered these features points according to their position invariance. We did experiments on the average centroids displacement across scales and noticed it stays approximately located at a same position considering a set of bodies, regardless of fatness, size and morphology, which confirm our hypothesis: the anatomic joints of a human on a scanned mesh correspond to features that can be detected by *Tailor* algorithm. Some of the detected points do not correspond to real joints: we can filter them by

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taking into account only the blends and concave features. The *Plumber* algorithm [4], which builds on the vertex classification provided by *Tailor*, identifies tubular features together with their axes (cf figure 2).



Figure 2: Tubular features with their axes.

### III. SKELETON EXTRACTION

Our strategy relies on the observation that the shape variations match areas corresponding to skeletal joints. Intuitively, we expect that the areas where we detect small variations lay in the same location with bigger variations. Since the skin is thinner where we have natural articulations, it produces small concavities and variations at small scales. There are also less fat tissues and no muscles around joints, so it induces variations at bigger scales among body parts[5].

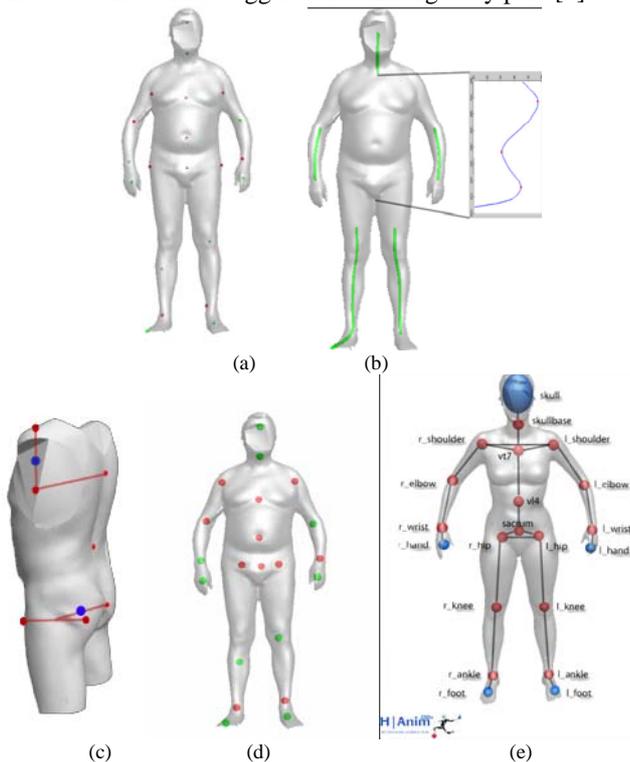


Figure 3: (a) Landmarks extracted from the 2 steps shape analysis; (b) tubular limbs axes and spine curve; (c) estimated hip and shoulder joints location from (a) and (b) and (d) final joints estimation corresponding to H-ANIM joints in (e).

Our proposed approach is based on two main steps: 1) an initial segmentation is applied on 3D scanned data with *Plumber* to extract tubular (limbs) and non-tubular parts of the body (trunk); 2) a multi-scale shape analysis is further applied

with *Tailor* onto tubular and non-tubular segments to extract potential location of joints. These results are combined with a priori knowledge on human anatomy in order to select the best candidates. The first segmentation provides arms and legs, which are tubular. Each part contains only 2 joints: in the case of arms, we have bends and wrists. In the case of legs, we have ankles and knees. *Tailor* centroids are then filtered in order to extract for each limb the 2 best candidates corresponding to the joint location. For the trunk, *Tailor* allows extracting the spine curve. This curve is used to estimate the height of the shoulders and hip joints. Extracted landmarks are further projected onto the axes of the *Plumber* tubes in order to estimate the joints locations.

### IV. RESULTS

In order to correct possible incoherencies due to bad scan data, we use the symmetry property: since the human skeleton is symmetric, the lengths of symmetric bones segments should be the same. We also use anatomic proportions, according to statistical data: proportions between long bones of the skeleton are very stable with a negligible variation. We present in figure 5 three different scanned bodies with different morphotypes.

The experiments on various morphotypes demonstrate that the resulting method is able to handle noisy 3D input data for variable 3D body shapes and postures and to extract with a reasonable accuracy the main 16 joints and the 5 tip joints corresponding to a simple H-Anim [6] hierarchy (c.f. figure 3-e).

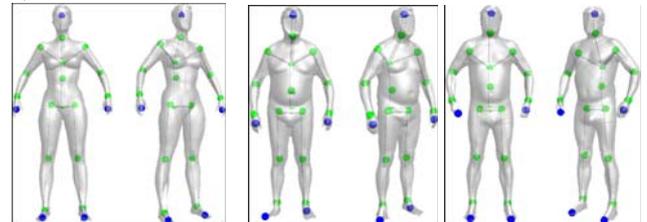


Figure 4: Skeleton extraction for different morphotypes.

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