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A Study on Parametric Shape Modifications of 3D Skeletal Models

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ABSTRACT

Parametric biomechanical models of the human body have a wide range of applications. Factors that make construction of such models difficult include the difficulty to model free form shapes, the existence of large shape variations, poor models for soft tissues, etc. An important step towards achieving a solution is to generate parametric skeletal models. In this paper, we introduce a new method to parametrically define shapes of skeleton components (bones). Our approach has several advantages: we require only a few sample bones of a class to construct a fairly robust template model; we do not rely on accurate identification of specific landmarks or shape features; finally, our algorithms are robust and efficient. The main tool we use is free form deformation (FFD), which we use to modify the shape of a template mesh by dislocating points of its affiliated lattice. This lattice is automatically derived by mesh simplification. Using the template bone and the values of a few parameters, an FFD based transformation automatically derives the shape of the bone instance. We evaluate the accuracy of the model and analyze the performance of our approach under different settings.

Keywords: bio-mechanical models, parametric models, shape deformation.

1. INTRODUCTION

The initial motivation for this research came from the problem of designing custom fit shoes. The design and fit of shoes depends on the shape of the shoe last that is used to fabricate them, which itself is designed using measurements made on the user's foot. The same last can be used to construct multiple pairs of shoes for a customer. However, this approach suffers if these multiple designs vary in some parameters, especially the heel height and shoe style; this is because the original measurements are made with the user standing in a particular posture. This is probably the reason that bespoke shoemakers appear to predominantly cater to men rather than women. Traditional shoe last design relies mainly on statistical models that provide guidelines on how the average foot shape varies as a function of heel height etc. This approach works well for mass produced shoes, but obviously loses its appeal if applied to custom shoe-making. Our long term goal is to investigate how to automatically generate the shape of shoe lasts for specific shoe styles based on a single set of measurements of the foot (in a specific posture).

One way to do this is by constructing a 3D bio-mechanical model of human feet, which can be used to predict the foot shape in different positions/elevations of the heel. Such a model would require a parametric constrained assembly model of the foot skeleton, as well as some quasi-static kinematics models of the joints in the foot. Statistical models can be used to instantiate the parametric model, and kinematic constraints can then be used to derive the skeletal geometry at different postures. Finally, statistical models for other soft tissues can be used to generate the shape model for the foot. If such a strategy is successfully developed, it can be used as a basis for design and manufacture of customized shoes. In this scheme, the user's foot is scanned only once, but for every subsequent pair of shoes, even with different heel heights (for instance), the modeler will be able to accurately predict the exact shape required for the best fitting shoe last. Thus, the design procedure can be optimized for mass customization of footwear.

There are various difficulties in developing this technique. First of all, there are a number of bones in a skeleton model (e.g., 26 in a human foot). Every bone of a skeleton has a unique shape. Each bone model need to be built in a way such that it can be applied on any arbitrary shape. Secondly, Magnetic

Computer-Aided Design & Applications, 11(1), 2013, 90–98, http://dx.doi.org/10.1080/16864360.2013.834147

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Resonance Imaging (MRI) or Computerized Tomography (CT) scanning of the human body is expensive; CT scans also are not totally safe. It is not cost efficient to collect a large number of samples and then use a statistical approach to build a template model. Thus, the approach should be able to capture the parameters given on a small number of samples. Thirdly, since the shape of each bone type is different, the set of parameters vary from bone to bone; further, such parameters can assume different forms, such as dimensions, angles, or curvature, depending on the shape of the bone and the requirement of the user. Finally, each bone has a unique shape for each individual. We need to consider this kind of natural variation, and capture only the typical shape features of each bone sample; otherwise, the template model would not be useful as a predictor of the shape of a new sample. In this paper, we shall restrict our focus to the sub-problem of generating and using parametric model for a particular bone in a skeleton. Informally, the problem is defined as:

We are given the geometric shape of a set of bone samples, B_i, $i = 1 \ldots n$, (e.g. the first meta-tarsal bone), one from each individual of a population. Using this sample, we wish to (a) identify/generate a nominal (i.e. a template, or exemplar) geometric model, T_B of such bones over the entire population; and (b) identify a small but sufficient set of parametric measurements, $p_{B1} \ldots p_{Bk}$, and a simple mapping, $f(p_{B1} \ldots p_{Bk})$: T_B: $\rightarrow B$ that can be used to accurately map the template model to the geometric model of an unknown shape for which we know only the parameter values $p_{B1} \ldots p_{Bk}$. By solving this problem, we would be able to construction a parametric skeleton model of a human foot.

2. RELATED RESEARCH

Bio-mechanical modeling has been an active research topic for decades, with applications in medical, ergonomics, textile design, animation, virtual reality, motion analysis, etc. We briefly discuss the different approaches that have been used by other researchers.

Several schemes create models based on mechanical properties and kinematic motion of the human body for applications in virtual reality and animation [17,18,22,23,28,29]. Such models simulate motion of the entire human body, including muscle and soft tissue deformations [28]. However, these models did not focus on the detailed geometry of individual body parts, e.g., the foot. The human foot is a complex structure, with 26 bones, 33 joints and hundreds of muscles, tendons, and ligaments [11]. Besides, these models are not parametric, so the technique required to construct them cannot be easily adopted for our application.

There are also some active researchers working on building detailed foot models. In [1,4,5], 3D foot model from MRI or CT scans are used to construct a detailed 3D foot model for finite element analysis (FEA). Such models are quite detailed [27], but are static, i.e., the position and loading of the foot is fixed. Furthermore, these models are not parametric. In parametric modeling, shape design using template shapes called features is an established technology in CAD. When dealing with complex shapes within a given context, semantic features have been used successfully to define template models of sculptured forms [2]. However, their approach cannot derive the model directly from a scan of the real object.

There is some research on how to parameterize a standard foot to make a prediction model, using the measurement of the foot [19] or the 2D profile [20]. This method is fairly accurate, with a reported mean absolute error of 1.02 mm. Other researchers also have proposed frameworks for parametric human body models [3,15,26], with reported errors of 2.7%. However, they are not biomechanical models, and cannot be adopted for predicting the shape of the same foot in different postures.

Transforming a given 3D shape into another requires a mapping function with desirable properties. Free-From Deformation (FFD) [25] has proven to be the basis for many such transformation operators. Initially FFD was used to deform object by NURBS volume using a lattice of regular shape. Later, it was extended to allow deforming an object by using lattices of different shapes [7,14,16,21]. Park and Lee [24] built parametric models using FFD and an automatically generated lattice as the control mesh. In our application, accuracy of shape prediction depends on using control meshes that follow the shape of the typical samples; therefore we investigated various methods of mesh simplification [6,8–10,30] to generate our control meshes.

Finally, we mention a closely related, on-going project on human body modeling [12]. Their aim is to develop parametric human biomechanical models to support digital ergonomics. Their approach is to collect a large collection of bone specimens and analyze these using statistical techniques. Their goal is similar to ours. However, their approach is resource-intensive, and requires human experts to identify and locate anatomical landmarks. In contrast, we adopt a more geometric approach.

3. METHODOLOGY

Here we will show the process of how we build a parametric model, which can be used as a template to generate an instance of a bone given the measurements of only a few parameters. The modeling process is divided into three stages: template construction, regression and prediction. We describe these three stages at a high level before giving details of the individual steps.

In the template construction process, a number of samples B_i are collected and aligned. Next, we

measure the set of parameters $p_{D1} \dots p_{D1}$ of each of the target bone B_i. Using this, we can set up an exemplar, or a template bone mesh M_t. This mesh is too dense to be used directly for parametric shape manipulation. Using a polyhedral simplification, we create a corresponding control mesh, C. A parameterization process, based on FFD, is used to define a mapping between the template mesh M_t and C, such that when we change the shape of C, M_t is deformed accordingly. Hence, we obtain a deformable template model T_B.

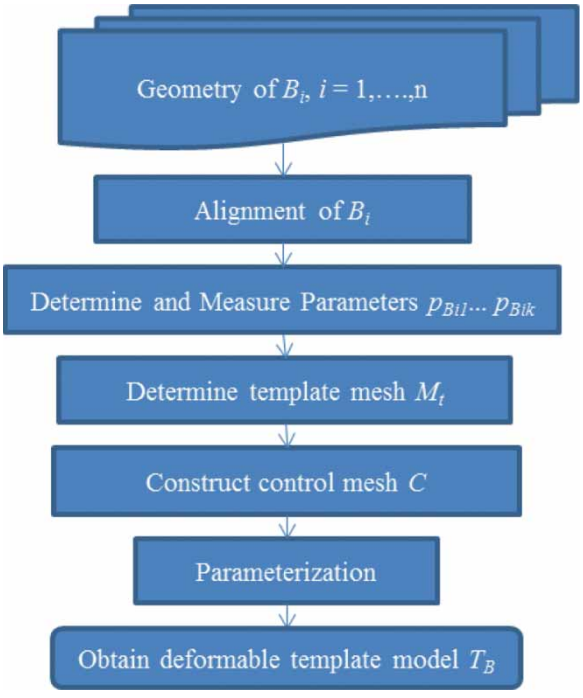

Fig. 1: Flow chart of the construction of the template model T_B.

In the next stage, we use regression to create the best fitting deformation model. Assume that all samples, B_i, have been aligned as in the previous stage. Each B_i is used, iteratively, as a target bone. We deform C (into C'), and correspondingly, M_t, (into some shape M_t'), so as to minimize the error between M_t' and M_i. We record the corresponding set of parameters $p_{Bi1} \cdots p_{Bik}$. Using this data set for all bones, the relation between the set of parameters $p_{B1} \cdots p_{Bk}$ and the resulting shape of the deformed control mesh C' is established using linear regression.

In the prediction stage, we use the regression model obtained in previous stage. Given a new set of parameters $p_{B1} \cdots p_{Bk}$, we use the mapping obtained from the regression stage to estimate the control mesh C' of the (unknown) bone. Then, using the same FFD map, we generate the predicted bone mesh, M_t', by deformation of the template bone, M_t.

We now describe some of the details of the key steps of our approach.

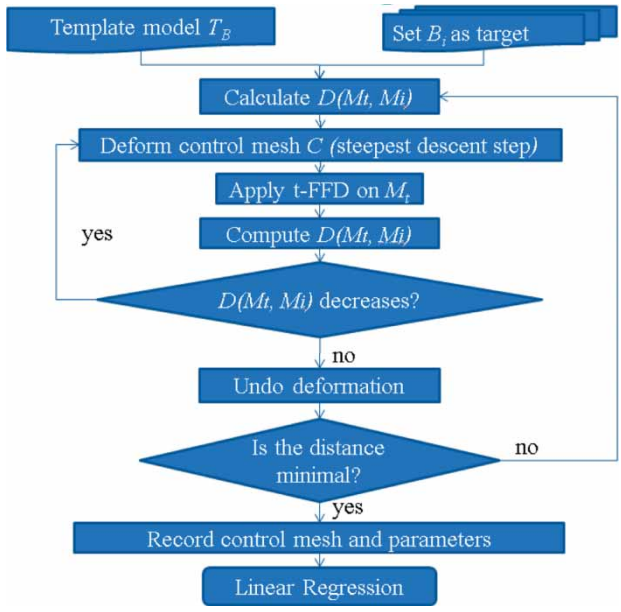

Fig. 2: The flow chart regression stage.

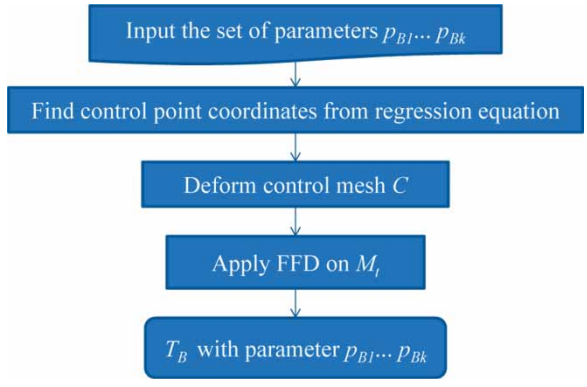

Fig. 3: Flow chart showing steps for constructing a bone model given parameter values $p_{B1} \dots p_{Bk}$.

Alignment

The sample bones differ from each other in geometry, so they must first be aligned in a common (global) coordinate frame. The local coordinate frame of the first bone sample is arbitrarily selected to coincide with this global frame. The transformation (defined by a translation and rotation) that minimizes the error between the mesh M_1 and any other mesh, M_j, is computed by solving the error function numerically. Assuming that the initial meshes are dense enough, we approximate the distance between point q and mesh M as:

$$e(q, M) = \min_{q_i \in M} \{d(q, q_i)\}$$

The error, D_H, between the meshes is defined using:

$$D_H(M_1, M_j) = \max \left\{ \sup_{q \in M_1} e(q, M_j), \sup_{q \in M_j} e(q, M_1) \right\}$$

Determination of the Template Mesh M_t

At the outset, it was unclear whether the ideal template model should be some mesh model that could adequately capture all shape features of all bones in the sample set. Such a template could be constructed, for instance, by an appropriate morphing over the sample set. However, a series of experiments showed that a randomly selected average sized bone sample assigned as the template worked equally well for our parametric shape deformations.

Constructing the Control Mesh, C

The control mesh C is a simplification of the template bone mesh model, M_t. We adopted a triangle decimation scheme that was robust, and preserved the topology of M_t even when the set of control vertexes is reduced to very small size, with, e.g., fewer than fifty vertices, based on an approach proposed in [8]. This is an edge collapse simplification algorithm based on quadric error metrics.

Parameterization

The relationship between the control mesh C and the bone mesh M is established using a parameterization. Several variations of parameterization methods have been proposed in the last couple of decades. We adopted an approach based on triangular free form deformation (t-FFD) [16], as described below. Let C consist of N triangular facets, T_i, where $i = 1$ to N. Each facet has vertices v_{i1}, v_{i2}, v_{i3}. For each triangular facet T_i, we establish a local coordinate system Ξ_i.

$\Xi_i = \{v_{i1}; U_i, V_i, W_i\}$ where U_i, V_i, W_i are the coordinate axes

$$U_i = v_{i2} - v_{i1}, V_i = v_{i3} - v_{i1}, \text{ and } W_i = \frac{U_1 \times V_1}{\sqrt{|U_1 \times V_1|}}$$

Each vertex q in M_t is parameterized by each Ξ_i as (u_i, v_i, w_i): $q = v_{i1} + u_i U_i + v_i V_i + w_i W_i$. The influence of each facet T_i on q depends on the size of T_i and the distance of q from T_i. This is quantified as a weight, k_i, defined as:

$$k_i = \begin{cases} 1 - \dfrac{|q - G_i|}{\beta r_i} & (0 \le |q- = G_i| < \beta r_i) \\ 0 & (\beta r_i \le |q - G_i|) \end{cases}$$

where $r_i = (|v_{i1} - G_i| + |v_{i2} - G_i| + |v_{i3} - G_i|+)/3$ is the size of the facet, and G_i is the centroid of T_i. The parameter β controls the effective range of T_i; when the value of β is low, the deformation is more local. In our model, we set $\beta = 2$, so the effective range of T_i is two times of its size r_i.

As a result, given the vertices v_{i1}, v_{i2}, v_{i3} of T_i and each of the vertex q in M_t, we obtain the value of u_i,v_i, w_i and k_i which will be used in the next step.

Deformation

Suppose that a vertex $v = [v_{i1} v_{i2} v_{i3}]$ of C moves to a new position, $v' = [v'_{i1} v'_{i2} v'_{i3}]$; the local coordinate system Ξ_i of each T_i are updated to $\{v'_{i1}; U'_i, V'_i, W'_i\}$ using the above equations. The corresponding updated position, q', of a vertex q of M is given by:

$$q' = \frac{\sum_{i=1}^{N} k_i (v'_{i1} + u_i U'_i + v_i V'_i + w_i W'_i)}{\sum_{i=1}^{N} k_i}$$

Deriving the Mapping between the Parameters and Control Mesh Vertices

Given only a set of parameters, how can we predict the shape of the control mesh C that can deform the template model to get an accurate mesh representing the corresponding bone? Here, we have to find the relationship between the set of parameter $p_{B1} \cdots p_{Bk}$ and the shape of the control mesh. As the vertices, v_j, of the control mesh C of M_t move, the error $D(M'_t, M_i)$ changes. So our problem amounts to obtaining a solution for the system $\partial D(M'_t, M_i)/\partial v = 0$. We use a numerical steepest descent algorithm to solve for this system for each bone.

Given a set of parameters $p_{n+1,1} \ldots p_{n+1,k}$ for a new bone B_{n+1}, we wish to determine the control mesh C' such that the corresponding modified template, T'_B approximates the bone B_{n+1}. We use a regression model to define the relation between each vertex v_j of C and the parameters $p_{B1} \ldots p_{Bk}$

$$v_j = f_j(p_{B1} \ldots p_{Bk})$$

We tested linear as well as some non-linear (polynomial) regression models; linearly regression was finally adopted, since it gave us the best compromise between quality and speed.

Using matrix notation, $V_r = AP, r \in \{1, 2, 3\}$, where

$$V_r = \begin{bmatrix} v_{1r} \\ v_{2r} \\ \vdots \\ v_{nr} \end{bmatrix} \quad A = \begin{bmatrix} a_{1,0} \cdots a_{1,k} \\ \ddots \\ a_{n,0} \cdots a_{n,k} \end{bmatrix} \quad P = \begin{bmatrix} 1 \\ p_{B1} \\ \vdots \\ p_{Bk} \end{bmatrix}$$

This linear regression model and the data of the first n bones is used to determine the matrices A for each coordinate axis r.

4. EXPERIMENTAL RESULTS

We tested our approach on two sets of bones. Animal bones were used in these tests instead of human bones, since the former are readily and inexpensively available. The first set was made up of 13 left metatarsus bones from chicken legs, and the second set of ten femur bones from pig's legs. All bones were cleaned, painted with a thin coat of non-reflective paint, and scanned using a Minolta laser scanner to generate the input meshes.

Model number	1	2	3	4	5	6	7	8	9	10	11	12	13
# control facets	15	15	15	29	29	29	29	29	29	29	29	29	100
# control vertices	9	9	9	17	17	17	17	17	17	17	17	17	53
set of parameter	3	3	5(a)	3	3	3	3	3	4(a)	4(b)	5(a)	5(b)	3
no. of sample	6	13	13	6	8	10	12	13	13	13	13	13	13
bone1	1.66	1.79	1.88	1.88	1.85	1.76	1.74	1.85	1.75	1.84	1.77	1.77	1.39
bone2	1.47	1.58	1.47	1.48	1.44	1.34	1.44	1.39	1.37	1.37	1.46	1.42	1.56
bone3	1.66	1.84	1.74	1.46	1.56	1.70	1.67	1.71	1.72	1.71	1.68	1.31	1.58
bone4	1.74	2.14	1.75	1.88	1.97	2.10	2.20	2.22	2.25	0.28	1.88	2.03	2.31
bone5	1.48	1.29	1.26	1.54	1.27	1.35	1.26	1.23	1.31	1.26	1.25	1.25	1.68
bone6	1.92	1.73	1.80	1.69	1.86	1.82	1.70	1.66	1.58	1.69	1.74	1.72	1.61
bone7	0.96	0.54	0.43	0.89	0.64	0.70	0.51	0.55	0.68	0.51	0.47	0.69	0.76
bone8	2.08	1.47	1.52	1.93	1.37	1.37	1.45	1.41	1.35	1.46	1.41	1.33	1.37
bone9	2.00	1.77	1.87	2.53	2.18	1.45	1.46	1.43	1.42	1.53	1.59	1.49	1.57
bone10	2.74	1.97	1.98	2.40	2.23	1.98	1.94	1.92	1.97	1.97	2.03	2.13	1.89
bone11	2.57	2.23	2.05	2.43	2.29	2.28	2.05	1.98	1.96	1.89	1.79	1.81	1.94
bone12	2.54	1.99	1.64	2.27	2.10	2.01	1.75	1.73	1.65	1.69	1.68	1.87	1.92
bone13	3.72	1.66	1.62	3.27	2.98	2.85	2.41	1.63	1.62	1.70	1.73	1.56	1.78
Average	2.04	1.69	1.62	1.97	1.83	1.75	1.66	1.59	1.59	1.45	1.58	1.57	1.64

Tab. 1: Maximum deviation between the template model and the real bone.

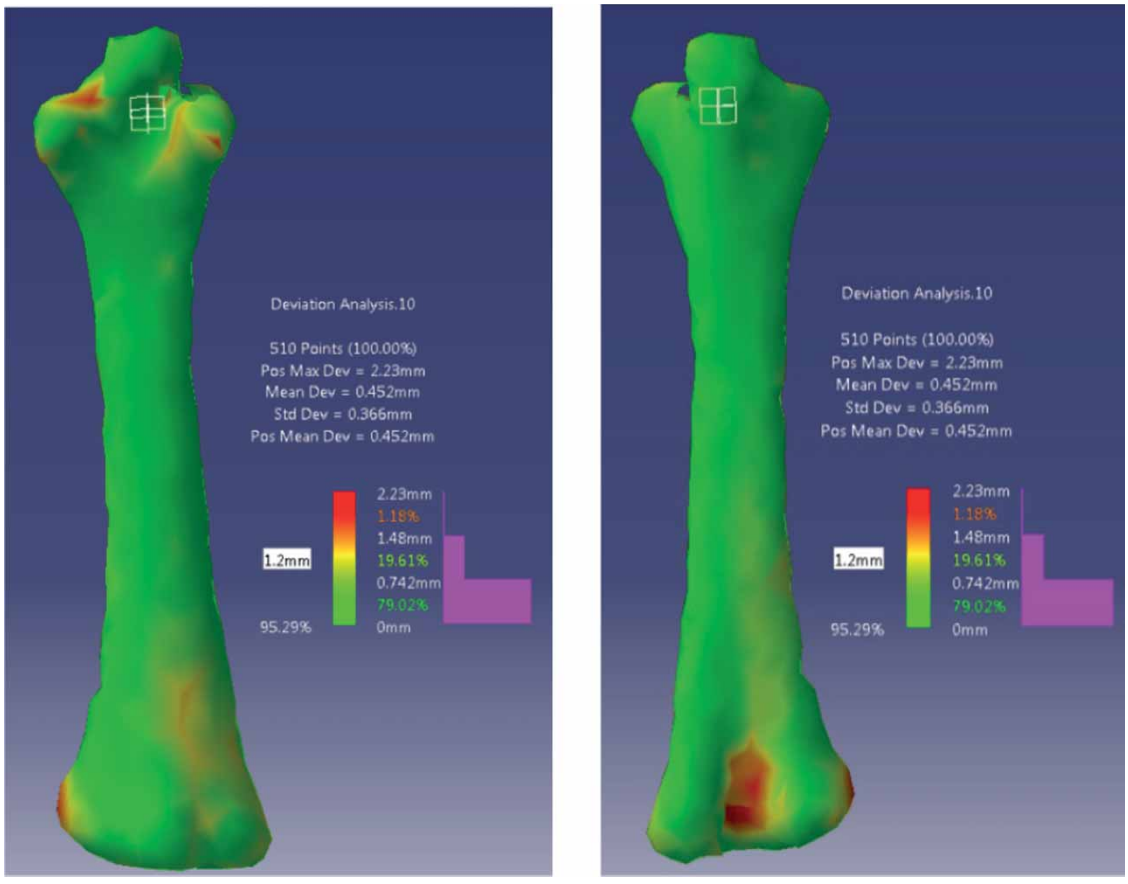

Fig. 4: The deviation analysis of bone number 10 (a) front view (b) back view.

4.1. Chicken Bone Models

It is useful to describe the series of experiments we performed in details. In order to test the robustness of the modeling, several different sample sizes were used to build the parameterization model: by using only the first six/eight/ten/twelve bones.

We also experimented to find out how many (and what type of) parameters are ideal. Obviously, a

Model number	1	2	3	4	5	6	7	8	9	10	11	12	13
bone1	0.90	0.92	0.91	0.90	0.90	0.90	0.90	0.92	0.92	0.94	0.88	0.87	0.84
bone2	0.79	0.72	0.76	0.80	0.78	0.76	0.75	0.72	0.69	0.73	0.71	0.77	0.67
bone3	0.88	0.91	0.90	0.87	0.86	0.91	0.93	0.93	0.88	0.92	0.93	0.78	0.91
bone4	0.78	0.83	0.81	0.70	0.71	0.85	0.85	0.83	0.86	0.77	0.71	0.81	0.83
bone5	0.73	0.86	0.86	0.69	0.76	0.84	0.86	0.86	0.87	0.85	0.84	0.84	0.91
bone6	0.82	0.82	0.84	0.74	0.81	0.78	0.74	0.79	0.79	0.80	0.82	0.74	0.79
bone7	0.63	0.35	0.35	0.59	0.44	0.45	0.36	0.36	0.47	0.38	0.38	0.48	0.43
bone8	1.36	1.01	1.02	1.35	0.96	0.99	1.03	1.02	0.87	0.99	0.99	0.89	0.95
bone9	1.40	0.79	0.76	1.32	1.23	0.84	0.80	0.75	0.76	0.74	0.71	0.77	1.02
bone10	1.33	0.94	0.88	1.34	1.20	0.94	0.92	0.90	0.89	0.88	0.89	0.87	0.81
bone11	1.08	0.89	0.94	1.12	1.06	1.03	0.87	0.86	0.87	0.95	0.90	0.81	0.74
bone12	1.35	0.97	0.93	1.26	1.19	1.09	1.00	0.99	0.91	0.85	0.89	1.04	1.00
bone13	1.75	0.98	0.94	1.97	1.87	1.59	1.38	0.92	0.88	0.88	0.89	0.88	0.85
Average	1.06	0.85	0.84	1.05	0.98	0.92	0.88	0.83	0.82	0.82	0.81	0.81	0.82

Tab. 2: 95% deviation between the template model and the real bone.

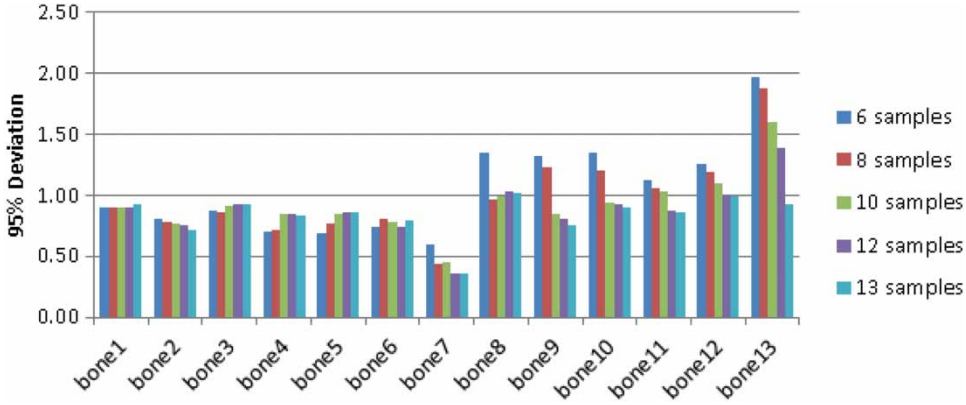

Fig. 5: 95% deviation between models with different number of samples.

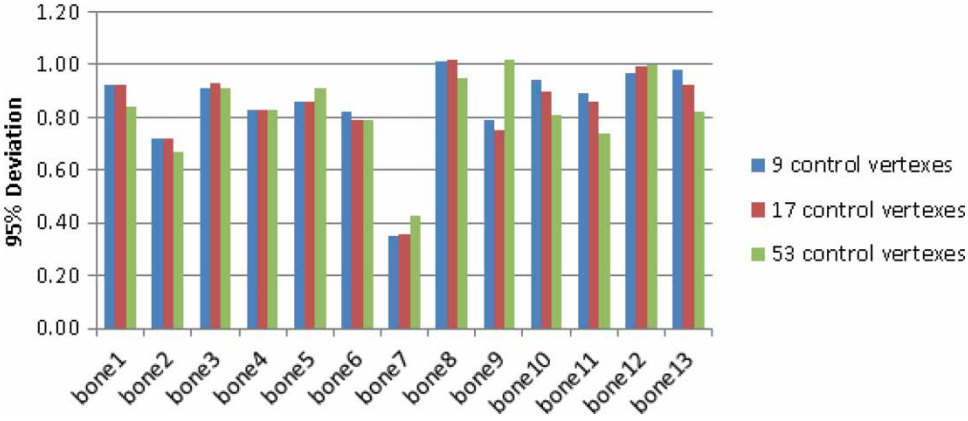

Fig. 6: 95% deviation between models with different number of control vertices.

single parameter (e.g. length) is likely to be poor, while a very large measured set, e.g. the entire mesh scan, would be very accurate but impractical. For the chicken bone, potential candidates that we considered included: length, head width, tail width, head height, tail height, head angle, tail angle, body angle and twist angle. We created different models using the following subsets of these measures:

3 parameters: length, head width, tail width

4 parameters: length, head width, tail width, body angle (called 4(a) below)

4 parameters: length, head width, tail width, twist angle (called 4(b) below)

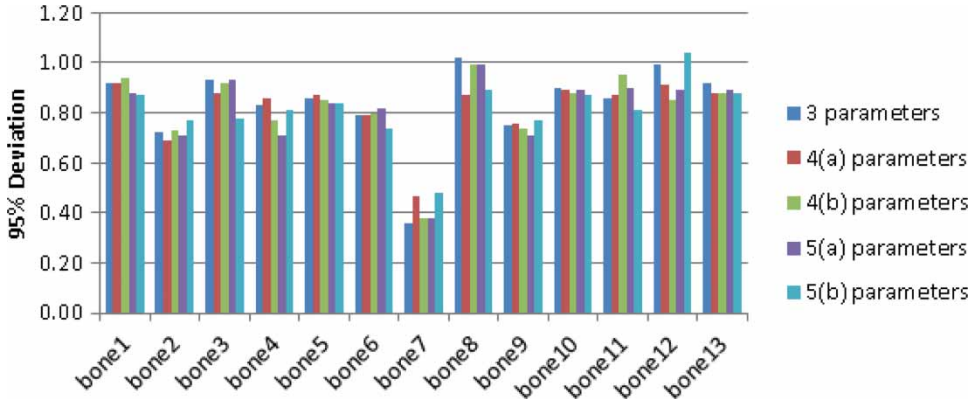

Fig. 7: 95% deviation between models with different sets of parameters.

# of control facets	30			30			30			100		
# of control vertexes	17			17			17			52		
set of parameter	1			3			3			3		
no. of sample	8			8			10			8		
Deviation	max	95%	mean	max	95%	mean	max	95%	mean	max	95%	mean
bone1	3.94	1.60	0.59	3.88	1.60	0.57	3.84	1.60	0.56	3.59	1.40	0.49
bone2	4.26	2.20	0.91	2.87	1.90	0.65	3.10	1.90	0.67	2.56	1.50	0.57
bone3	3.73	2.00	0.79	3.47	1.70	0.65	3.48	1.80	0.68	3.05	1.70	0.58
bone4	5.12	2.80	1.21	1.11	0.60	0.20	1.47	1.10	0.49	0.91	0.50	0.18
bone5	3.27	2.00	0.74	3.03	1.90	0.71	3.54	1.90	0.75	3.31	1.90	0.66
bone6	3.82	2.10	0.83	3.29	1.70	0.68	3.37	1.80	0.69	3.15	1.50	0.61
bone7	5.25	2.20	0.91	3.85	1.80	0.70	4.66	1.80	0.75	3.33	1.50	0.60
bone8	3.94	1.70	0.61	3.98	1.70	0.64	3.97	1.60	0.61	4.35	1.60	0.57
bone9	4.43	3.10	1.42	3.70	2.70	1.15	3.05	2.00	0.81	4.03	2.70	1.14
bone10	4.72	3.30	1.51	3.84	2.50	1.09	3.25	1.80	0.71	4.17	2.80	1.15
Average	4.25	2.30	0.95	3.29	1.81	0.70	3.37	1.73	0.67	3.25	1.71	0.65

Tab. 3: Experimental results for pig bones: deviation between actual and predicted models.

5 parameters: length, head width, tail width, head angle, tail angle (5 (a))

5 parameters: length, head width, tail width, head height, tail height (5 (b)).

We also suspect that the number of control vertexes in the control mesh would cause some effect on the accuracy of the model. We have built a number of models using control meshes with 9, 17 or 53 control vertexes and compare their performance. We used the mesh model of bone 7 as the template. For each bone, we measured the parameter values and applied our mesh deformation model to obtain an instance of a bone, which was then compared against the actual mesh of the corresponding bone for error analysis. The data of the bones that were used as samples for constructing the model are shown in green highlighted cells below, and the template bone data is highlighted in yellow. The other bones were not used in constructing the model, and were used to validate the predictive accuracy of the model. The table below summarizes the maximum deviation test data. The error/deviation analysis was performed using a commercial CAD software, CATIA.

While some of the deviation values were somewhat large, the maximum deviation typically occurred in regions with poor scanned geometry (e.g. slightly occluded regions or sharp corners). Such regions are often not useful in constructing skeletal models, since there is no joint in this region. It is therefore more useful to test the accuracy on the model by ignoring these outliers, and looking at, say, the deviation at the 95-th percentile deviation between the predicted and actual bone model.

The following figures show the remaining experimental results.

4.2. Pig Bone Models

As above, a similar series of experiments was conducted for a set of ten pig femur bones. We were interested in testing mainly whether the approach worked for bones of different shapes, and also of different size. The main results of the experiments are summarized in the following table. For brevity, we do not show the various experimental variations, except to note that the experiments were made over different subsets of (with either one or three) parameters, and

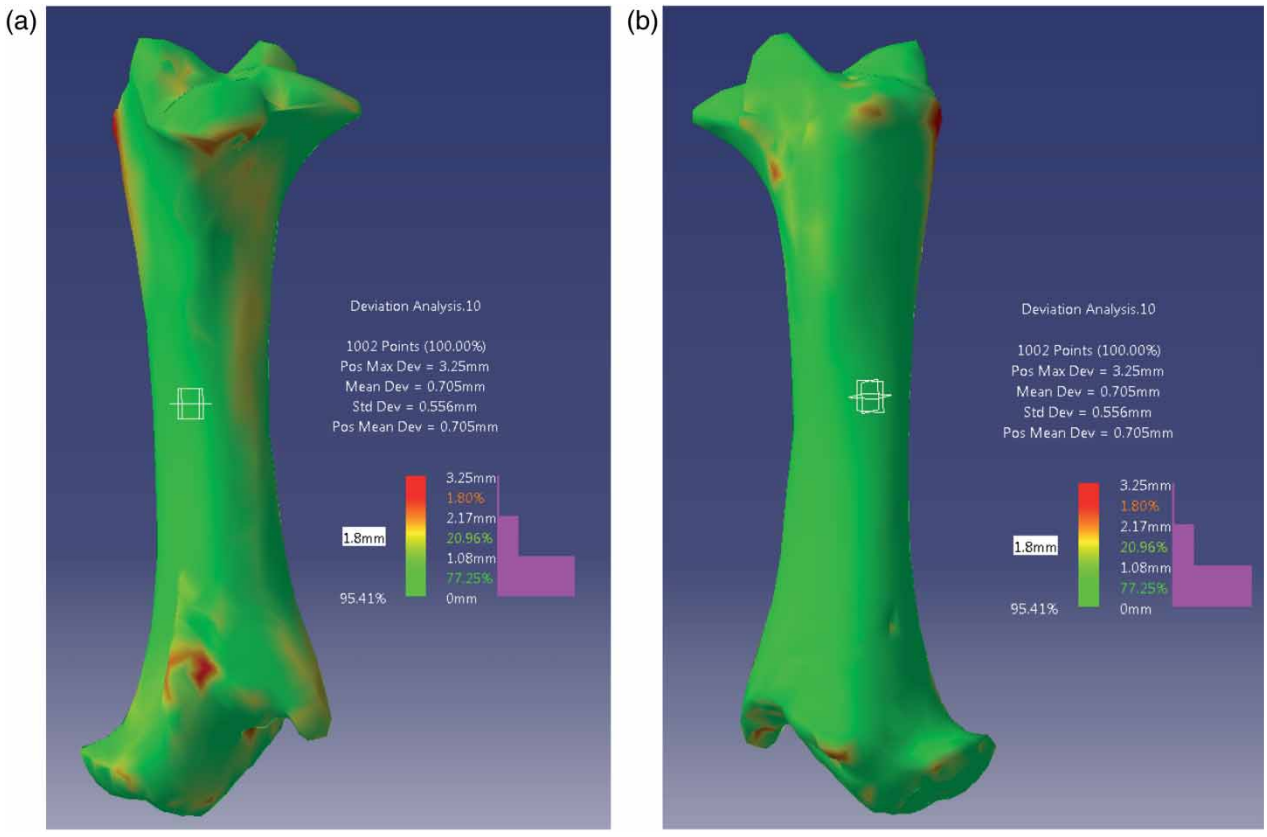

Fig. 8: The deviation analysis of bone number 10 (a) front view (b) back view.

with control meshes containing either 52, or as few as 17 vertices.

5. DISCUSSION AND CONCLUSIONS

We first make a few observations about our proposed methodology. We see a slight deviation between the predicted model and the actual model of the template bone. This is due to the use of the regression model; even if we select a template model bone as one with a somewhat unusual shape, the effect of this irregularity is reduced due to our approach, as this effect is dampened due to the other samples.

In the deviation analysis images, the red areas (which indicate the max deviation), are usually located at the corner or hole of the bone. This may due to the problem of scanning. Some holes or corners cannot be easily scanned. Therefore we recommend using the 95-th percentile deviation point as a more robust measure for the predictive inaccuracy. No obvious trend was found for using different number of control vertices, and in fact the models with fairly sparse control meshes perform quite well. There is a significant decrease in error when we move from one parameter to three parameters. But beyond 4 or 5 parameters, the accuracy does not really change significantly. This is also reassuring, since it indicates that relatively few measurements obtained, e.g., from external measurements on the body can be fairly useful in generating accurate predicted models. However, the accuracy does depend on which parameter(s) are used in the model. This indicates that some domain expertise may be required to create concise but robust models. Finally, the results for pig and chicken bones are fairly consistent, which is also reassuring since the bones in a typical human foot, e.g., vary quite a lot in size and shape.

We conclude by noting that we have presented a new approach to create parametric models of complex shapes, such as those of bones in human/animal skeletons. We believe that the approach is accurate enough for some applications where models of skeletons need to be generated based on a few parametric measurements; the accuracy can be further improved by experimenting with more sophisticated versions of the FFD model and regression algorithm in the future. However, we still need to extend our work in several ways before we can comment on its applicability to our original motivation. In particular, how to estimate the parameter values for each bone in a foot skeleton based on, say, only a scan of the external shape of a foot is a challenging problem.

ACKNOWLEDGEMENTS

Part of this research was funded by UGC GRF grants # HKUST 614205 and HKUST 614407.

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