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Combined Estimation of Shape and Pose for Statistical Analysis of Articulating Joints

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Abstract

Quantifying shape variations in articulated joints is of utmost interest to understand the underlying joint biomechanics and associated clinical symptoms. For joint comparisons and analysis, the relative positions of the bones can confound subsequent analysis. Clinicians design specific image acquisition protocols to neutralize the individual pose variations. However, recent studies have shown that even specific acquisition protocols fail to achieve consistent pose. The individual pose variations are largely attributed to the day-to-day functioning of the patient, such as gait during walk, as well as interactions between specific morphologies and joint alignment. This paper presents a novel two-step method to neutralize such patient-specific variations while simultaneously preserving the inherent relationship of the articulated joint. The resulting shape models are then used to discover clinically relevant shape variations in a population of hip joints.

Keywords

Statistical shape modeling; Articulated joints; Pose Alignment

1 Introduction

Statistical shape modeling of musculoskeletal structures enables a wide range of biomedical and clinical applications (e.g., [4, 8, 9, 16, 20, 22, 25, 26]). However, most studies are limited to isolated anatomies, and are rarely used to model articulated joints (e.g., hip and shoulder joints). Understanding the shape variations in articulated joints provides crucial insights into the associated biomechanics [23]. Further, these shape variations are often used to explain the clinically observed symptoms. For instance, the articulated relationship of femur and pelvis in the hip joint is particularly relevant in pathology that may lead to hip arthritis [3].

Statistical shape models aim to capture the subtle local variations (modulo of global geometric transformation) in a given anatomical population. For models that rely on explicit shape representation (i.e., correspondence models [10]), generalized Procrustes analysis (GPA) [19] is widely used to remove the similarity or rigid transformations before statistical analysis. However, the GPA method is not equipped to address variations in relative pose of distinct shapes, such as flexion and abduction, commonly observed in articulated joints.

Clinical 2 Authors Suppressed Due to Excessive Length protocols impose specific image acquisition guidelines in an attempt to mitigate such variations [24]. Results from [24] show that even a consistent acquisition protocol may not completely remove the influence of pose. Therefore, a pose neutralization step is necessary before quantitative analysis of articulated joints. For this purpose, Bossa and Olmos [6] perform GPA on independent components of the multi-object shape models. This approach is further adopted in [7], [14], and [15] for functional modeling of articulated joints. The independent alignment of components helps address the undesired subject-specific pose variations; although at the expense of preserving information about relative position, some of which is robust to patient/subject pose. This trade-off undermines the validity of biomechanics-based functional modeling, where distances or geometric relationships among shapes is important. In another attempt, Gorcowski *et al.* [18] use a two-step approach, where the first step involves a rigid alignment of the joint shape models followed by the final step of component-wise GPA. Even though the initial rigid alignment preserves the relative position of the joint segments, it fails to neutralize the subject-specific scaling. Further, the component-wise GPA nullifies the important aspect of first step.

Bindernagel *et al.* [5] and Kainmueller *et al.* [21] devise alignment schemes for specific human joints. In both cases, a two-step alignment is performed to neutralize the individual pose. First the joint shape models are rigidly aligned, then a rigid alignment of one of the components is performed. This method relies on the clinical assumptions, i.e. consistent articulation, that may not be generalizable in all cases. Further, it is unclear how the model will evolve for more than two components. Audenaert *et al.* [2] use partial least squares (PLS) regression to estimate the shape model of articulated joint from independent shape models of the involved components. The output joint shape model is assumed free from the subject-specific pose. However, Audenaert *et al.* did not assume any model for the pose related *error* or a validation mechanism to support the claim.

Most existing methods rely on alignment of independent components of the joint, and forgo shape relationships. For the purpose of statistical shape analysis, it is important to factor out the undesired similarity transformation among samples in the population. However, the relative pose may be disease-specific and therefore, needs to be preserved for a clinically relevant modeling. With this goal, we propose a two-step alignment scheme, which removes the similarity transformation and individual pose variations from a population of articulated joints. The proposed method does not rely on selected template shape from the population. Further, the method is not limited to a particular human joint and is generalizable to more than two components. A population of dysplastic hip joints, involving pelvis and femur bones, is used for the experiments. Next, we discuss the details of proposed method, followed by a brief description of dataset and comparative approaches, and conclude with a discussion of experimental results.

2 Method

Consider a shape population of articulated joints $S = \{S_1, S_2, \dots, S_N\}$, with K components i.e., $S_i = \{S_i^1, S_i^2, \dots, S_i^K\}$. The goal is to quantify statistical shape variations among the sample joints in S . Statistical shape analysis relies on a correspondence model to

consistently represent the sample shapes. Point-based models are a common choice for the purpose. In this section, we briefly discuss the method used to generate the point-based shape correspondence model, and describe the proposed two-step alignment scheme for a population of articulated joints.

2.1 Point-Based Shape Correspondence Model

Most existing methods optimize coordinate transformation between samples and a chosen template shape to generate the point-based correspondence models [2, 14]. Therefore, the resulting analysis often varies based on the choice of template. A recent study [17] shows that the nonparametric, entropy-based method [12] outperforms the pairwise and template-based approaches. Geometric features can be incorporated within the entropy framework to address the complex anatomies, such as the scapula and pelvis [1, 13]. Further, the correspondence model for multi-object complexes is produced by optimizing the statistics of combined shape [11]. For placing points on populations of shapes, we use the open-source implementation of this method, ShapeWorks [10].

2.2 Proposed Two-Step Alignment

It is imperative for statistical analysis to remove the global transformations (e.g., similarity or rigid) among samples in the shape population. Thus, GPA is used for analysis for the individual components across the population. In articulated joints, the statistical analysis aims for similar local anatomic variations in a simultaneous fashion across the components. However, it is important to neutralize the individual pose variations caused by flexion/extension, abduction/adduction, and internal/external rotation. In this regard, we propose the following two-step alignment:

1. *Global Alignment:* Consider each articulated joint S_i as a concatenated vector of all components $\{S_i^j\}_{j=1}^K$. GPA is performed on these joint shape vectors S_i , $i = 1, 2, \dots, N$ to estimate the similarity transformations T_i^g , $i = 1, 2, \dots, N$ resulting in aligned and size neutralized articulated joints $\hat{S}_i = T_i^g(S_i)$. The GPA is an iterative method to estimate the transformation T_i^g between the sample shape S_i and a template shape S_μ such that

$$T_i^g = \underset{T}{\operatorname{argmin}} D^2(T(S_i), S_\mu), \quad (1)$$

$$T^g(\mathbf{x}) = s\mathbf{R}\mathbf{x} + \mathbf{d}, \quad (2)$$

where D^2 is the squared distance between the template and Procrustes aligned shape vectors. The average shape after every iteration is used as the template shape for the next. Using mean shape as the template eliminates bias toward a particular sample. The iterative alignment is performed until convergence. The average of these aligned joints now can be used as a template for individual alignments.

2. *Local Alignment*: The globally aligned joints ($\hat{S}_i$) still contain individual pose from the acquisition time. To achieve a consistent pose across samples while preserving the relative position of involved components, we use the average shape $\hat{S}_\mu = \frac{1}{N} \sum_{i=1}^N \hat{S}_i$ as the fixed template and perform rigid alignment of independent components. The component-wise transformations are estimated as

$$T_{ij}^l = \underset{T}{\operatorname{argmin}} D^2(T(\hat{S}_i^j), \hat{S}_\mu^j), \quad (3)$$

$$T^l(\mathbf{x}) = \mathbf{R}\mathbf{x} + \mathbf{d}. \quad (4)$$

The relative scale between components of individual joint is crucial for modeling the biomechanics and combined shape variations. Thus, we preserve the size of independent components after the global alignment step.

It is important to note that, if image acquisition protocols are enough to ensure a consistent relative position among the joints, the second step of Local Alignment should yield identity transformations. Similarly for the isolated anatomies, this method will be effectively reduced to only one step of global alignment. After the proposed alignment, each component in the joint shape vector $\tilde{S}_i$ is computed as

$$\tilde{S}_i^j = T_{ij}^l \circ T_i^g(S_i^j).$$

3 Experimental Setup

We used a dataset of 84 presurgery femur-pelvis pairs from 48 female patients with dysplasia¹. The presence of dysplasia was confirmed based on the measurement of the lateral center edge angle (LCEA) acquired from a single anteroposterior radiograph. The age of the subjects ranged from 16 to 58 years, with a mean and standard deviation of 37.74 and 10.23 years, respectively. The CT acquisition protocol for patients with hip dysplasia specifies that they be in a supine position, legs straight with knee and toes pointing upward. The CT image resolution ranged from $(0.76 - 0.84) \times (0.76 - 0.84) \times (1 - 1.25) \text{ mm}^3$. The bones were segmented from CT images using Amira software (Visage Imaging, San Diego, CA, USA). The binary segmentations were then resampled to a consistent resolution of $0.5 \times 0.5 \times 0.5 \text{ mm}^3$. The shape models with 2048 and 4096 correspondences on pelvis and femur, respectively were optimized using geometric features in ShapeWorks.

Since the data was acquired using a consistent clinical protocol, we consider the shape model resulting from the global alignment step as a candidate model for comparison, this model was referred to as Global. As done in most existing methods, we generated comparative models using component-wise Procrustes alignment with the mean shape as the template. Two models (LocalSim and LocalRigid) were generated, where LocalSim

¹Thanks to Dr. Tokunaga and Keisuke Uemura for data collection and providing this dataset.

considers similarity transformation (described in eq(2)) and LocalRigid uses rigid transformation (described in eq(4)). We used the mean shape and eigen analysis of joint shape vectors (S_j) to investigate the resulting statistical models.

4 Results and Discussion

Existing studies are often influenced by the choice of template for alignment. We chose to use mean shape as the template to eliminate sample bias. Therefore, as shown in Figure 1, the mean shapes from four resulting models look nearly identical. A template free correspondence model generation also contributed to the consistent mean shapes. Further analysis of eigen spectrum and statistical modes of variation highlights the drawbacks in the local alignment and single step global alignment schemes. Since the articulated joint is disintegrated in both local alignment methods, we expect to see unnatural collision between the two components when we visualize the statistical modes of variation. As mentioned earlier, the global alignment is expected to fail to remove the rotation based pose variations. Next, we analyze the resulting eigen spectrum from the four methods.

LocalRigid:

Often in musculoskeletal shape analysis, scale is considered as a desired shape variation. Therefore, only rigid transformations are removed for the purpose of statistical modeling, and as is done when modeling joints [5, 21]. Figure 2(a) shows the variance plot for the resulting statistical model. The top two dominant modes represent more than 90% of the underlying variation. As would be expected, Figure 2(b) indicates that the primary mode is occupied by the change in size of the bones. The unnatural collisions within the joint renders this method unusable for pose estimation. Further, Figure 2(c) shows the collision between the femur and pelvis as the shape variation progresses beyond mean towards the second eigen direction.

LocalSim:

Next, we consider the LocalSim model, which neutralizes the scaling among samples in addition to the rigid alignment. With the scale variations removed, the resulting shape model contains local anatomic variations. The variance plot in Figure 3(a) shows that 24 eigen modes capture the 90% of underlying variation. Figures 3(b) and 3(c) showcase reconstructed hip joints along the first two eigen modes. In both modes, collisions occurred when the femur and pelvis shapes deviate from the mean shape. Further, decoupling of the segments compromises the combined statistical variations among the joint, as the shapes vary along the eigen directions. Therefore, it is essential to preserve the relationship between components in a joint model for the purpose of analyzing the morphometrics of these tissue structures and for making conjectures as to how abnormal joint shape and orientation are contributing to symptoms and mechanical damage.. The next model attempts to preserve this relationship by considering the entire joint as a single entity during alignment.

Global:

Here, we analyze the shape model after the first step of global alignment in the proposed two-step method. Figure 4(a) shows a much more compact variance plot compared to the

LocalSim (Figure 3(a)), with first six modes responsible for more than 90% of the population-wide statistics. This more compact variance plot indicates larger transformations compared to the targeted subtle anatomic variations. Figures 4(b)–4(d) validate this hypothesis, as we observe the articulated rotations clinically described as flexion/extension, abduction/adduction, and medial rotation. It is important to note that the order of these rotations in the eigen spectrum closely matches with the possible range of movement in hip joint. This crucial finding further highlights the need of pose neutralization at the level of shape modeling, regardless of a consistent image acquisition protocol.

Proposed:

Using the average joint shape from global alignment as the template helps to preserve the relative position within the joint. Thus, we do not observe any unnatural shape variation as the femur and pelvis jointly vary along the eigen modes. A total of 18 modes represent the 90% of shape variations; Figure 5(a) shows the cumulative variance plot. The first eigen mode in Figure 5(b) shows the importance of relative size of components in the joint. The shape variation jointly captures the twist along femoral shaft in conjunction with the simultaneous change in the size of the pelvis and femoral head shapes. This combined behaviour results in variable femoral head coverage, a clinically relevant feature to diagnose dysplasia [24]. Second mode in Figure 5(c) captures the synchronized twisting of the femur and pelvis, with femur twist along the shaft and acetabulum being the center of twist in pelvis. Clinicians expect such variations and often attribute the variation in coverage to this combined shape variation. Figure 5(d) shows some more subtle twist as the two shape vary along the third eigen mode.

5 Conclusion

This paper addresses a crucial problem of pose neutralization in the analysis of articulated joints. Using a point-based statistical shape model, and the proposed two-step alignment we are able to discover the clinically relevant shape variations in a population of patients with hip dysplasia. The described approach has the potential to influence clinical diagnostics and clinical decision making by quantifying variation in both the shape of a joint and its orientation in space. Comparisons between the various models described herein demonstrates the limitations of prior methods to address pose variations. Further, the statistical modes of shape variation show that clinical practices of a consistent acquisition fail to remove individual rotations. The proposed method is not limited to the hip anatomy and is applicable to other joints that may have two or more segments.

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Fig. 1.
Comparing mean shapes from the four models: (a) LocalRigid, (b) LocalSim, (c) Global, and (d) Proposed.

Fig. 2.

LocalRigid: (a) Variance plot, (b) first eigen mode - yellow represents mean shape, blue and red are reconstructions for mean plus and minus two standard deviations, respectively, in the eigen direction, and (c) reconstructed shape representing the mean plus two standard deviations in second eigen direction.

Fig. 3.

LocalSim: (a) Variance plot, (b) reconstructed shape representing the mean minus two standard deviations in first eigen direction, and (c) reconstructed shape for the mean minus two standard deviations in second eigen direction.

Fig. 4. Global: (a) Variance plot, (b) first eigen mode representing the flexion and extension in hip joint, (c) second eigen mode representing the abduction and adduction, and (d) fourth eigen mode representing the internal and external rotation. (b-d) Yellow represents mean shape, blue and red are reconstructions for mean plus and minus two standard deviations in the respective eigen directions.

Fig. 5.

Proposed method: (a) Variance plot, (b) first eigen mode, (c) second eigen mode, and (d) third eigen mode. (b-d) Yellow represents mean shape, blue and red are reconstructions for mean plus and minus two standard deviations in the respective eigen directions.