Comparing Methods for Modeling Shapes of the Tibia and Femur in Osteoarthritis

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INTRODUCTION: Shape models (SMs) derived from MRI segmentations of the tibia and femur are frequently used to quantify 3D bone shapes in structural analyses of knee osteoarthritis (KOA). Bone shape has been shown to be associated with pain and progression, to be predictive of the onset of radiographic KOA, and to be a potential contributing factor to post-traumatic OA development after anterior cruciate ligament injury [1,2]. These shape data are nearly all generated from SMs based on principal component analysis (PCA), a linear method that can be conceptualized as fitting an n-dimensional ellipsoid to the data distribution [3]. However, there is no reason to assume that the distribution of bone shapes in KOA, characterized by heterogeneous osteophyte formations, would be well represented by such a model. The purpose of this study was to the investigate alternative, nonlinear methods (kernel PCA and relative warp analysis) for generating SMs of KOA and to compare them using well-established criteria (compactness, specificity, and generalizability).

METHODS: Segmentations of the tibia and femur from 100 subjects, 20 from each Kellgren-Lawrence (KL) grade, were obtained from the publicly available OAI ZIB dataset, reconstructed using a marching cubes algorithm, and smoothed using improved Laplacian smoothing [4]. A subject from the KL0 group (no indication of OA) was chosen at random to use as a template and the tibia and femur reconstructions of all other subjects were aligned to those templates using the iterative closest point algorithm. To ensure point correspondence across subjects, the template surface models were then deformably registered to all others using the coherent point drift method. Next, a generalized Procrustes analysis was used to remove size variations between subjects, and three SMs were created from the resulting surface distributions. In addition to a linear PCA-based model, kernel PCA (KPCA) and relative warp analysis (RWA) were used to generate SMs of the tibia and femur separately. KPCA uses the kernel trick to project data into a nonlinear feature space where a PCA is performed. By projecting the data into this (generally higher dimensional) feature space, it is possible to transform a complex distribution into a linearly separable one [5]. An exponential kernel was chosen for this analysis. In contrast to PCA and KPCA which organize model components by data variance, RWA uses the variation in weights of fitted interpolating functions, thin plate splines. This weighted combination of thin plate splines represents a smooth interpolant from one surface to another and minimizes the "bending energy" of the transformation [6]. Each of the SM methods resulted in sets of 100 feature vectors for the femur and tibia that represented the major modes of variability in bone shapes. These models were then compared using three metrics: compactness, specificity, and generalizability [7]. Since RWA analyzes a different variance than PCA and KPCA, model compactness was compared using the cumulative relative variability of features ordered by their proportions of variance explained. Specificity was assessed by computing the sum of squared errors (SSE) between model instances generated by randomly sampling parameters in the range of the dataset and the subject that was closest to that model instance. A total of 10,000 instances were generated for each SM and bone. Generalizability of the SMs were evaluated using a leave-one-out approach where the SSE between a model created using all but one subject and the model's reconstruction of that subject was computed for each subject.

RESULTS: PCA created the most compact SMs for both the tibia and femur followed closely by KPCA (Figure 1); however, KPCA was the most specific SM method, followed by RWA (Figure 2). Interestingly, the specificity of the femur PCA model was greater (lower average SSE) that than of the tibia while specificity was similar between bones for KPCA and RWA. Linear PCA also resulted in the most general bone SMs, fitting the left out subject surfaces almost exactly while RWA was the least (largest average SSE) general SM method (Figure 3).

DISCUSSION: Although, in the current study, PCA was found to be the most general SM method, this could be misleading. In KPCA, there is no exact solution for projecting data out of feature space. This "preimage" problem means that any reconstruction in the original space is only an approximation of the, likely more accurate, reconstruction in feature space. KPCA being the most specific SM method also indicates advantages for the nonlinear feature space in terms of continuity, which could enhance the discriminatory capability of shape-based biomarkers for KOA. Additionally, the lower specificity of the PCA-based tibia SM compared to the femur may help to explain the diminished predictive ability of tibia shape features in previous literature [1]. The results of this study suggest that KPCA may be the optimal method for modeling bone shapes in KOA; however, these findings will need to be confirmed in larger datasets.

SIGNIFICANCE/CLINICAL RELEVANCE: Improved characterization of bone shape in KOA could lead to a better understanding of the disease and help to develop targeted treatments.

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Figure 1. Compactness of the femur SMs represented by cumulative relative variance for PCA (solid line), KPCA (dashed line), and RWA (dotted line).

Figure 2. Specificity represented by average and standard deviation of model SSEs (lower is better) for the femur (black squares) and tibia (white squares) SMs.

Figure 3. Generalizability represented by the average and standard deviation of model SSEs (lower is better) for the femur (black squares) and tibia (white squares) SMs.