



Predicting cartilage morphology from bone using a statistical shape model

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Background

Patient-specific computational models of the knee offer the potential to improve the diagnosis and treatment of disorders such as patellofemoral pain and osteoarthritis. The first step in creating a patient-specific model of the knee is to segment medical imaging data to accurately reconstruct the geometry of the bone and cartilage. Segmentation of cartilage currently requires high resolution, volumetric MRI and a trained expert to produce an accurate result. This process is both time-consuming and expensive, and is one of the rate-limiting steps preventing the uptake of computational models in a clinical setting.

By exploiting the relationship between the bone and cartilage morphology, we present a novel method for predicting cartilage morphology from bone data. This will enable the rapid generation of cartilage morphology using sparse imaging data, such as plain film x-ray.

Method MRI data (n=35) was segmented in Stradwin. Segmented data (n=35) split into training set (n=30) and test set (n=5). MRI (n=35) Training set femurs and FOV normalised bones tibias were normalized to Segmented bones correct for variable field of view (FOV) in MAPClient and MeshLab. Radial basis function fitting and rigid alignment was used to introduce correspondence and align the training set. Normalised FOV Aligned training set (n=30) MR Image FOV Principle Component Analysis (PCA) was used to generate a statistical Segmented bones shape model (SSM) of the bones and cartilage. The SSM was fitted to the segmented bones of the test set to predict cartilage morphology.

Figure 1: Overview of the workflow for generating an SSM and for predicting cartilage morphology from bone.

Knee SSM showing

mean, $+2 \sigma$ and -2σ

Fitted SSM

Results & Discussion

The mean error in the predicted cartilage meshes was largest in the medial tibial (0.89 \pm 0.127 mm) and smallest in the lateral tibia (0.71 \pm 0.095 mm) (Table 1).

The highest errors were distributed near the boundaries of the cartilage: up to 6.82 mm error when predicting the femoral cartilage in the test data.

Table 1: Average errors and DICE scores between predicted and manually segmented cartilage morphologies across test set (n=5).

Cartilage	Max	RMS	Mean	DICE
	error	error	error	score
Femoral	6.82	0.97	0.76	0.72
Patellar	3.61	0.89	0.72	0.78
Lateral tibial	4.14	0.90	0.71	0.78
Medial tibial	3.76	1.01	0.89	0.73

Cartilage predictions were best near the load bearing areas and worst at the boundaries (Figure 2).

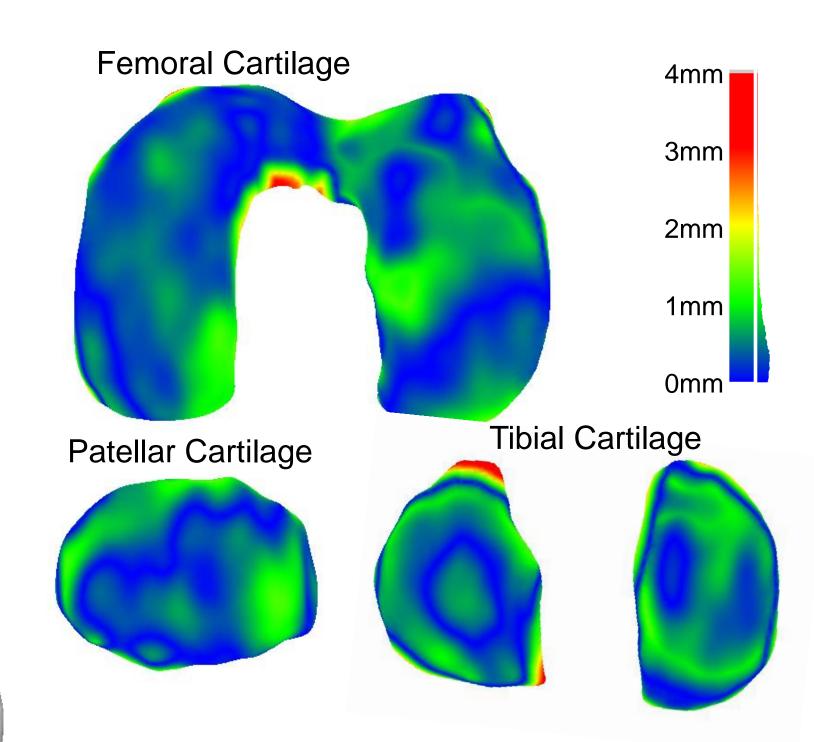


Figure 2: Absolute error distribution between predicted and manually segmented cartilage for example subject.

Summary

The method shows promise for predicting patient-specific cartilage from sparse data, and performed reasonably despite a small training set of n=30. Further training is expected to improve the performance of this method.

References

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- 2. Zhang J et al. (2014). *Biomed Sim.* **8789**, 182-192.

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