Computed tomography landmark-based semi-automated mesh morphing and mapping techniques: Generation of patient specific models of the human pelvis without segmentation

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ABSTRACT

Current methods for the development of pelvic finite element (FE) models generally are based upon specimen specific computed tomography (CT) data. This approach has traditionally required segmentation of CT data sets, which is time consuming and necessitates high levels of user intervention due to the complex pelvic anatomy. The purpose of this research was to develop and assess CT landmark-based semi-automated mesh morphing and mapping techniques to aid the generation and mechanical analysis of specimen-specific FE models of the pelvis without the need for segmentation. A specimen-specific pelvic FE model (source) was created using traditional segmentation methods and morphed onto a CT scan of a different (target) pelvis using a landmark-based method. The morphed model was then refined through mesh mapping by moving the nodes to the bone boundary. A second target model was created using traditional segmentation techniques. CT intensity based material properties were assigned to the morphed/mapped model and to the traditionally segmented target models. Models were analyzed to evaluate their geometric concurrency and strain patterns. Strains generated in a double-leg stance configuration were compared to experimental strain gauge data generated from the same target cadaver pelvis. CT landmark-based morphing and mapping techniques were efficiently applied to create a geometrically multifaceted specimen-specific pelvic FE model, which was similar to the traditionally segmented target model and better replicated the experimental strain results ($R^2 = 0.873$). This study has shown that mesh morphing and mapping represents an efficient validated approach for pelvic FE model generation without the need for segmentation.

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1. Introduction

The human pelvis is a complex geometric structure, which transmits upper body loads to the lower limbs. Finite element (FE) analysis has been used to analyze load transfer through the pelvis (Anderson et al., 2005; Barker et al., 2005; Barratt et al., 2008; Dalstra et al., 1995; Dawson et al., 1999; García et al., 2000; Goel and Svensson 1977; Goel et al., 1978; Gupta et al., 2004; Hipp et al., 1989; Kaku et al., 2004; Leung et al., 2009; Li et al., 2007; Maurel et al., 2005; Neal and Kerckhoffs, 2009; Shim et al., 2007, 2008; Thompson et al., 2002). FE models of the pelvis have been created from specimen-specific computed tomography (CT) scans using a variety of model creation techniques, including manual segmentation, statistical shape model fitting and high order cubic Hermite

basis function based mesh generation (Anderson et al., 2005; Barratt et al., 2008; Leung et al., 2009; Seim et al., 2008; Shim et al., 2007, 2008; Thompson et al., 2002). However, generation of specimen-specific FE models of the pelvis has required a high level of user intervention and time investment at multiple stages (segmentation, surface generation, meshing and optimization). The pelvis has a complex geometry, regions of thick and thin bone, multifaceted curvatures, cavities, and articulations, limiting the ability of threshold based segmentation to capture its structure (Leung et al., 2009). Manual segmentation methods have been documented to be highly subjective in terms of structure identification, but low contrast in thin bone regions and articulations challenge automation of segmentation (Chen et al., 2011; Seim et al., 2008). Due to labour-intensive nature of generating pelvic FE models, many studies to date have utilized single specimen-specific models for analysis, limiting the impact of findings (Anderson et al., 2005; Dalstra et al., 1995; Goel and Svensson 1977; Goel et al., 1978; Li et al., 2007).

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The development of robust methods for creating specimen-specific FE models that do not require initial segmentation would accelerate the generation of pelvic FE models. The concept of morphing a source mesh has been used successfully in musculoskeletal FE modeling to facilitate creation of multiple specimen-specific models (Allen et al., 2005; Bah et al., 2009; Baldwin et al., 2010; Chabanas et al., 2003; Couteau et al., 2000; Grosland et al., 2008; Hraiech et al., 2008; O'Reilly and Whyne 2008; Sigal et al., 2008; Tada et al., 2006). Morphing further allows soft tissue structures to follow skeletal changes. Manually assisted morphing and mapping techniques have been successfully implemented and validated in the creation of a specimen-specific pelvic FE model (Salo et al., 2012). A patient-specific CT scan was manually segmented to create a pelvic FE model. This FE model was then manually morphed and mapped onto a surface (target) also manually segmented from a different patient-specific CT scan to evaluate the ability of morphing and mapping techniques to generate a patient-specific FE model of the pelvis (Salo et al., 2012). The purpose of this study was to develop and evaluate the ability of landmark-based semi-automated mesh morphing and mapping algorithms to generate specimen-specific models of the pelvis directly from specimen-specific CT scans without the use of a target surface, eliminating the need for segmentation. It is hypothesized that this approach can yield pelvic FE models with equivalent performance to those created using traditional segmentation methods.

2. Materials and methods

2.1. Traditional FE generation of source and target models

Specimen-specific FE models were created using traditional methods via segmentation of a pelvic CT scan of a 58 year old male (source model) (Fig. 1a) (Leung et al., 2009) and a 56 year old female (target model) (CT scanning parameters: GE Lightspeed Plus CT scanner, 512×512 acquisition matrix, in-plane resolution 0.94×0.94 mm, slice thickness 3.2 mm, 99 slices). Models included the ilia, sacra, sacroiliac cartilage, symphysis pubis, acetabular cartilage, femurs and ligaments. The boundaries of each structure were triangulated and smoothed to create polygonal surfaces (Amira 3.3.1; Mercury Computer Systems Inc., Chelmsford, Massachusetts). The surface triangular element parameters (maximum angle, maximum edge length, aspect ratio and dihedral angle) were controlled to improve mesh quality and to avoid distorted, poor quality elements. Ligaments were modelled as two-noded non-compressible truss elements (Leung et al., 2009). The locations of the origins and insertions of the ligaments were identified on the CT scan. Truss elements were created in corresponding locations on the FE model. The traditionally segmented target model served as a standard for comparison to models generated using the morphing/mapping technique.

2.2. Alignment and morphing

Source mesh was roughly aligned with target CT scan based on three manually identified landmarks via an automated custom script (HyperMesh, AmiraDEV) (Fig. 1b) (Salo et al., 2012). A more extensive array of landmarks was then placed directly on the source and target CT scan based on the work of Boulay et al. (2006) (Fig. 1c, 476 landmarks). Optimization reduced the required number of landmarks by 31% (to 329 landmarks) for successful reconfiguration of the source model geometry onto the target CT scan (mean distance between the segmented and morphed model surfaces at the ilia < 1 mm). This landmark set forms an atlas, which can be transformed for application of this method to all subsequent pelvic CT data sets. Landmark placement in the pelvis has been reported to be precise to inter-user and intra-user variances of ± 5 mm (Khoury et al., 2008); however, the thin bone regions in the pelvis can be as thin as 2 mm. Therefore, landmark placement in these regions must be more accurate than their thicknesses. If the landmarks in this region are placed incorrectly, the following mapping step will not be performed correctly, alerting the operator of the landmark placement error. The operator can then correct the landmark and redo the morphing procedure. Based on the coordinates of these landmarks, each respective node on the source mesh was sequentially translated to the location of the temporary node on the target CT. Moving nodes in the source mesh were permitted motion with six degrees-of-freedom in order to reduce element distortion. Source mesh was automatically morphed onto target landmarks in an iterative manner. Eight additional landmarks were placed onto each femur to morph the femurs (Grassi et al., 2011).
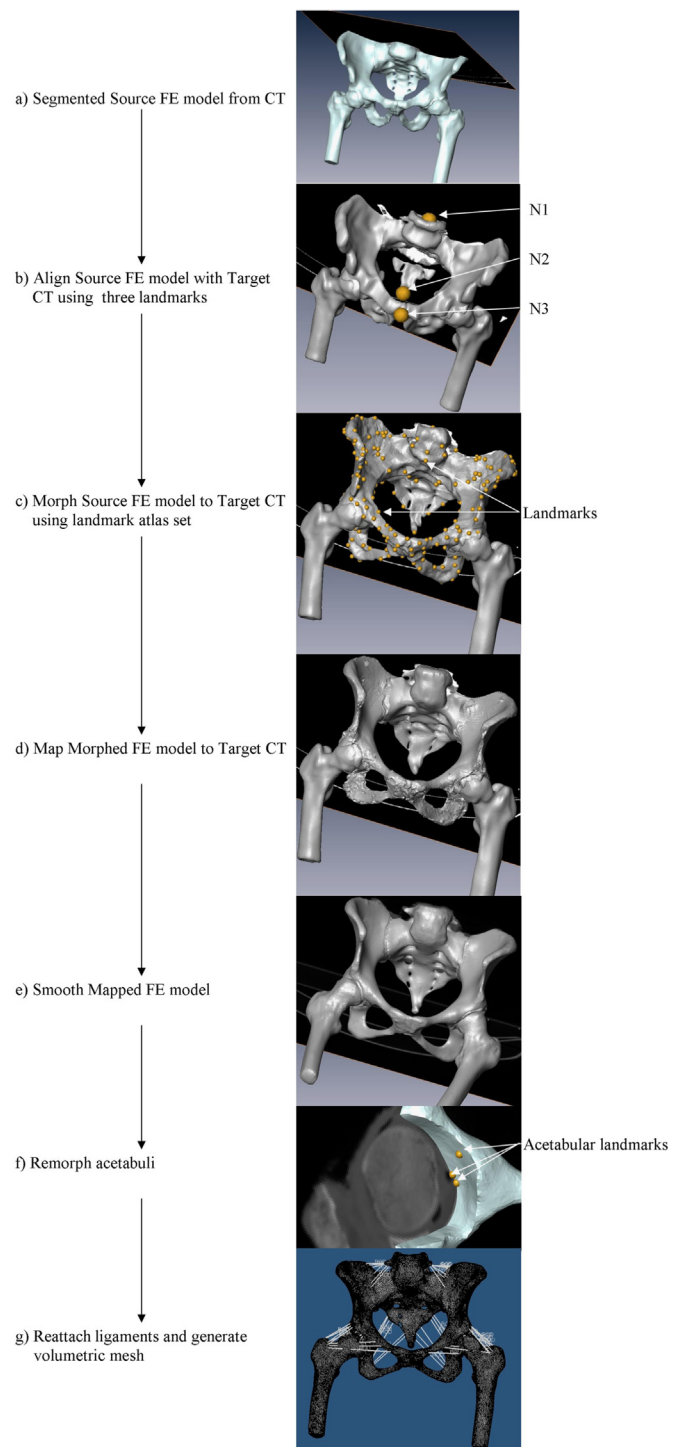

a) Segmented Source FE model from CT

b) Align Source FE model with Target CT using three landmarks — N1, N2, N3

c) Morph Source FE model to Target CT using landmark atlas set — Landmarks

d) Map Morphed FE model to Target CT

e) Smooth Mapped FE model

f) Remorph acetabuli — Acetabular landmarks

g) Reattach ligaments and generate volumetric mesh

Fig. 1. Pelvic mesh generation from specimen-specific CT using landmark based morphing/mapping procedure.

2.3. Mapping and smoothing

Morphed pelvic surface model was further refined through mesh mapping based on the work of Peleg et al. (2014) (Fig. 1d). Mapping was performed in three steps: (1) a Houndsfield Unit (HU) value was determined for each node based on the voxel in which the node was located; (2) a vector was calculated for each node from the normals of the elements attached directly to the node; (3) each surface node was translated in increments representing 1/2 the CT scan voxel dimension (0.47 mm in this case) along the direction of the vector until a predefined HU value was reached (based on the HU value of bone as determined by calibration of the CT scan). No movement was applied if the intensity criterion was not met within a