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Finite element modeling of the human kidney for probabilistic occupant models: Statistical shape analysis and mesh morphing

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ABSTRACT

Statistical shape analysis was conducted on 15 pairs (left and right) of human kidneys. It was shown that the left and right kidney were significantly different in size and shape. In addition, several common modes of kidney variation were identified using statistical shape analysis. Semi-automatic mesh morphing techniques have been developed to efficiently create subject specific meshes from a template mesh with a similar geometry. Subject specific meshes as well as probabilistic kidney meshes were created from a template mesh. Mesh quality remained about the same as the template mesh while only taking a fraction of the time to create the mesh from scratch or morph with manually identified landmarks. This technique can help enhance the quality of information gathered from experimental testing with subject specific meshes as well as help to more efficiently predict injury by creating models with the mean shape as well as models at the extremes for each principal component.

1. Introduction

Each year in the United States, there are roughly 35,000 fatalities associated with motor vehicle crashes (NHTSA, 2016). Abdominal organs in particular are commonly injured in crashes resulting in serious injuries or death (Cheynel et al., 2011). To prevent these deaths and serious injuries, many approaches have been taken such as better road design, active safety systems, and improved vehicle designs.

Human body models could help in improving the design of new vehicle and safety systems. Traditionally, post mortem human surrogates (PMHS) and anthropomorphic test devices (ATD) were used to investigate the human body's biomechanical and injury responses under the impact loadings (Crandall et al., 2011). These tests can provide a wealth of information, but they can be expensive and time consuming to conduct. Finite element analysis (FEA) offers a way to model the human body quickly and cheaply (Yang et al., 2006). Initial FE models consisted of one dimensional spring-mass-damper systems (Mentzer et al., 1992), but as computing power has increased, models have increased in complexity to three dimensional models consisting of explicitly modeled bones and organs. There are a couple challenges with using these FE models, however. The first challenge is related to model geometries. Human FE models as well as ATDs have been developed based on the internal and external geometries of subjects with statures and weights corresponding to 5th, 50th, and 95th percentile males and females (Davis et al., 2016; Schwartz et al., 2014; Vavalle et al., 2014a) or by simple scaling (Untaroiu et al., 2008). The human body, however, has considerable variation in the component geometries such as bones (Lu and Untaroiu, 2013) and abdominal organs (Hayes et al., 2013). Because of this variation, an organ of a percentile model developed based on a particular subject's geometry might be different that the corresponding percentile organ (Hayes et al., 2013). The second challenge is validation of these models based on test data recorded on PMHS with geometries usually different than the percentile models.

The first challenge can be addressed with statistical shape analysis (Dryden, 2016). Statistical shape analysis involves finding homologous landmarks between two shapes, and using these landmarks in a principal component analysis (PCA). If there is a large enough set of geometries, models can be made for the mean geometry as well as for extremes along each principal component. These principal components are mathematically derived, linearly independent modes of variation, and using them to create models allows a smaller set of FE models to represent a larger amount of the population. This statistical shape analysis has been used extensively in the study of anatomical variation and recently in the creation of probabilistic finite element models (Lu and Untaroiu, 2013; Lu and Untaroiu, 2014; Lu et al., 2013). With statistically defined geometries, it is still necessary to create meshes, which

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can be time consuming, particularly for irregular anatomical shapes.

For the second challenge, a template mesh can be morphed to the shape of the specific PMHS (or component) used in testing (Hwang et al., 2016; Klein et al., 2017; Sigal et al., 2008; Zhang et al., 2017). Mesh morphing involves changing the geometry of a template mesh to that of a target mesh while maintaining connectivity and mesh quality. While material properties are still variable, the morphed mesh will be more directly comparable to the PMHS. The mesh morphing procedure consists of two parts: finding correspondence between the template (original) and target geometries and morphing from the template mesh to the target. Previous studies into mesh morphing or parametric modeling have often relied on establishing correspondence through a relatively sparse set of manually or semi-automatically identified landmarks; often only on readily identifiable anatomical features (Beillas and Berthet, 2017; Beillas et al., 2016; Hwang et al., 2016; Jolivet et al., 2015; Klein et al., 2015; Vavalle et al., 2014a). In this study, an automated landmark sliding based approach that identifies homologous points between the template and target is proposed; allowing for landmarks to be established at any desired resolution.

A combined process of automatic statistical shape analysis with mesh morphing was utilized to investigate the human kidney. The kidney was chosen because it demonstrates applicability of this process to a complex shape that also has sparse, manually identifiable landmarks. Additionally, differences between the left and right kidney could be examined. This study utilized a data set consisting of 15 pairs of kidneys taken from two studies on the morphology of the abdominal organs in a vehicle occupant posture (Beillas et al., 2009; Hayes et al., 2013). The mesh morphing procedure was used to create meshes for each kidney in the data set as well as for geometries created by the statistical shape analysis resulting in both subject specific and probabilistic models. Previous probabilistic mesh models (Gayzik et al., 2006; Shi et al., 2014b; Wang et al., 2016) have involved extensive manual work to identify landmarks, so this method allows for much faster creation of new models.

2. Methods

2.1. Registration

The data set (Table 1) used for this study contains 15 sets of kidneys that were segmented from MRI scans taken in a seated posture (Beillas et al., 2009; Hayes et al., 2013). The "Beillas" MRIs were taken with a seat 25° from vertical with a resolution of 1.56 mm and slice thickness of 5 mm; the kidneys were then segmented with a custom toolbox (Beillas et al., 2009). The "Hayes" MRIs were taken with a seat 23° from vertical with a resolution of 2.1 mm and slice thickness of 2 mm and the kidneys were segmented manually in Mimics (v. 14, Materialise, Leuven, Belgium) (Hayes et al., 2013). While the data sets from these studies were collected with slightly different methods, they were chosen because they represent the only investigations of organ shape while seated in an occupant posture. Each shape instance in the data set consists of a surface mesh made of about 8000 nodes and elements about 1–1.5 mm on each side. The first part of the statistical shape analysis process was to find homologous landmarks across each shape instance. This landmark identification was a multi-part procedure completed in MATLAB (Mathworks, Natick, MA) (Lu and Untaroiu, 2013; Lu and Untaroiu, 2014; Lu et al., 2013; Yates et al., 2016). The first step was to find the normal and two orthogonal tangent vectors for each point. This process was done by finding the set of points adjacent to the point of interest and then performing a singular value decomposition on that set of points. Next, one kidney was chosen as a template due to its classical "bean" shape. This template kidney was then centered and overlaid with a cubic grid with gridlines spaced every 5 mm. The point nearest to the center of each cube was selected as a landmark for a total of 701 landmarks. Each target shape instance was then aligned to the template through an iterative closest point registration (ICPR) algorithm (Fitzgibbon, 2003). Since the template kidney was a right kidney, all left kidneys were first reflected to obtain their mirror images.

2.2. Correspondence

Next, target landmarks were determined through an automated two-part process. First the closest point to the template landmark in an n∗6 matrix was selected as the target landmark, where each row consists of $[x, y, z, \lambda[i, j, k]]$ were x, y, and z are the coordinates and i, j, and k are the surface normal with λ as a scaling parameter (van de Giessen et al., 2009; Yates et al., 2016). Next, the positions of these landmarks were refined through iterative landmark sliding as described further in our previous publication (Yates et al., 2016). Briefly, this process balances two types of error, shape deformation error and shape representation error (Dalal et al., 2007; Dalal and Wang, 2012). The deformation error is defined as the thin plate spline bending energy from the template landmarks to the target landmark locations. Shape representation error is defined as how well the target landmarks represent the target shape, but since that is computationally expensive to calculate, the fit error between the landmarks of template and target is used as an approximation. For each landmark, a search space is defined as an area on the plane tangent to the target surface, and a trust region reflective

Table 1
Data set subject anthropometry/demographics.

ID	Sex	Height (m)	Weight (kg)	Age (yr)	Left kidney volume (cc)	Right kidney volume (cc)	Data source
f01	Female	1.74	68	41	162	150	"Beillas"
f02	Female	1.72	64	42	165	137	"Beillas"
f03	Female	1.62	53	34	120	134	"Beillas"
f04	Female	1.5	48	24	129	107	"Hayes"
f05	Female	1.62	60.8	31	180	156	"Hayes"
f06	Female	1.67	91.7	33	157	132	"Hayes"
m01	Male	1.75	70	29	138	118	"Beillas"
m02	Male	1.91	88	32	177	176	"Beillas"
m03	Male	1.75	70	29	156	134	"Beillas"
m04	Male	1.69	60	26	141	150	"Beillas"
m05	Male	1.81	80	26	148	141	"Beillas"
m06	Male	1.83	82	37	153	162	"Beillas"
m07	Male	1.6	56.2	27	120	126	"Hayes"
m08	Male	1.75	78.6	26	137	124	"Hayes"
m09	Male	1.9	102.1	26	230	225	"Hayes"

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