Interpretability of Anatomical Variability Analysis of Abdominal Organs via Clusterization of Decomposition Modes

Mauricio Reyes, Miguel A. Gonzalez Ballester, Zhixi Li, Nina Kozic,
Ronald M. Summers, Marius George Linguraru

Abstract— **Extensive recent work has taken place on the construction of probabilistic atlases of anatomical organs, especially the brain, and their application in medical image analysis. These techniques are leading the way into similar studies of other organs and more comprehensively of groups of organs. In this paper we report results on the analysis of anatomical variability obtained from probabilistic atlases of abdominal organs. Two factor analysis techniques, namely principal component analysis (PCA) and principal factor analysis (PFA), were used to decompose and study shape variability within the abdomen. To assess and ease the interpretability of the resulting deformation modes, a clustering technique of the deformation vectors is proposed. The analysis of deformation fields obtained using these two factor analysis techniques showed strong correlation with anatomical landmarks and known mechanical deformations in the abdomen, allowing us to conclude that PFA is a complementary decomposition technique that offers easy-to-interpret additional information to PCA in a clinical setting. The analysis of organ anatomical variability will represent a potentially important research tool for abdominal diagnosis and modeling.**

I. INTRODUCTION

T HE analysis of shape variability of anatomical structures is of key importance in a number of clinical disciplines, as abnormality in shape is often related to disorders. Statistical shape analysis techniques have enjoyed a remarkable popularity within the medical image analysis community. Most existing statistical shape analysis methods rely on Principal Component Analysis (PCA) to build a compact model of principal modes of variation from a training set [1,2]. Examples in neurology include the study of brain asymmetry to verify its relation to schizophrenia [3], or the detection and quantification of atrophy as a correlate to multiple sclerosis. In cardiac applications, shape variability of the heart has also been integrated into a space and time-varying probabilistic atlas aimed to improve the

segmentation of 4D cardiac MR images [4]. In bone morphometry, shape variability information has been used, for example, to decrease the invasiveness of surgical procedures and increase their accuracy and safety [5], or in vertebral fracture quantification [6]. The deformations modes described by this type of model can be sometimes difficult to interpret or correlate with intuitive shape descriptions employed by clinical partners, and are normally combinations of several localized shears, twists, rotations, etc. In a previous work, another decomposition technique called Principal Factor Analysis (PFA) was used for morphological analysis of femur, corpus callosum, and vector-valued 3D deformations fields resulting from non-rigid registration of ventricles in MRI [7]. The obtained results showed the added value of PFA, offering a simpler analysis of shape variability by intuitively distinguishable factors. In this paper, the technique is further applied for the structural analysis of abdominal organs obtained under the development of an abdominal probabilistic atlas, which will serve as a tool for the scientific and medical community.

The homogeneity of the deformation field across the surface, for each mode of deformation, offers a degree of interpretability of shape variability decomposition. Thus, this study additionally introduces a technique to cluster a vector field describing a mode of deformation across a surface. The technique is based on the minimization of two-term energy: a first term based on the co-linearity among vector directions and a second term that considers the area gain when adding a candidate point to a cluster. The magnitude of the deformation at each point gives more weight to points having larger displacements.

II. METHODS

The methods can be subdivided into two major steps: models construction and analysis of anatomical variability. For the construction of the models, non-linear registrations from 30 manually segmented abdominal organs were used in conjunction with PCA and PFA for shape modeling. The analysis of variability is performed with a clustering technique applied on the deformation modes.

The models were constructed from a set of 10 abdominal CT scans of patients with no abnormalities: 5 male and 5 female with a mean age of 59.9 years. Data were collected

M. Reyes and N. Kozic are with the Institute of Surgical Technologies and Biomechanics, MEM Research Center, Univ. Bern, Switzerland (e-mail: mauricio.reyes@memcenter.unibe.ch).

M.A. Gonzalez Ballester is with Alma Systems, Barcelona, Spain.

Z. Li, R. M. Summers and M. G. Linguraru, are with the Diagnostic Radiology Department, Clinical Center, National Institutes of Health, Bethesda, MD 20892 USA (e-mail: lingurarum@mail.nih.gov).

using GE LightSpeed Ultra (GE Healthcare) and image resolution ranged from 0.54 x 0.54 x 1.0 mm³ to 0.77 x 0.77 x 1.00 mm³. The spleen, right kidney and pancreas were manually segmented. The implementation uses Visual C++ 8.0 (Microsoft), ITK 2.4 and Matlab 7.3 (Mathworks Inc.).

A. Model Construction

For the construction of the models, a random image from the database is set as reference J, and all other subject data, addressed as images I, are registered to the reference. For all subjects, the manual segmentation of ten abdominal organs was performed and masks of the organs were generated. Then each organ was registered individually to its corresponding mask in the reference set. Organ coordinates in each subject were normalized relative to the position of the xiphoid. Hence, we employed the non-linear registration algorithm based on B-splines [9] and normalized mutual information M [10], where $p(I,J)$ is the joint probability distribution of images I and J, and $p(I)$ and $p(J)$ their marginal distributions, as in Equation (1).

$$M(I \mid J) = \frac{p(I) + p(J)}{p(I,J)}. \tag{1}$$

The deformation of objects is governed by an underlying mesh of control points in a coarse to fine multiresolution approach. B-splines allow to locally controlling the deformation and a compromise between the similarities provided by the mutual information M and smoothing is searched. The resulting deformation fields between the reference image and the subject data are input in the analysis of anatomical variation. For more detail on the B-spline definition of the transformation, please refer to [10].

The physical coordinates of organs (image independent) were used, normalized by the xiphoid. Finally, organs were translated in the atlas to the location of the average normalized centroid.

Once point correspondences are established for every organ and for every sample dataset, anatomical variability is modeled through PCA and PFA. PCA is a projection model for factor analysis aiming to find a low-dimensional manifold in the space of the data, such that the distance between the data and its projection on the manifold is small [11]. PCA is the best, in the mean-square error sense, linear dimension reduction technique [2].

Unlike PCA, which is a projection model, PFA can be considered as a generative model in factor analysis. Generative models estimate the density function that is assumed to have generated the data, under constraints that restricts the set of possible models to those with a low intrinsic dimensionality. Whereas PFA models covariance between variables, PCA models the total variance in the data and as such it determines the factors that account for the total (unique and common) variance in the set of variables. Contrarily, PFA determines the least number of factors that can account for the common variance (correlation). For

more details and illustrative examples on PCA and PFA, please refer to [7, 11, 12].

B. Analysis of Anatomical Variability

The result from the generation of the statistical models using PCA and PFA is a point distribution model (PDM). The PDM is able to describe the shape variability of the structure as a surface or point cloud embedded in the 3D space. Let $P = \{p_1, p_2, \ldots, p_M\}$, $M \in N^*$, be a set of points that generate a surface in a domain $D \in R^3$. For each $p_i \in P$, $i = 1, \ldots, M$, a vector V_i is computed as

$$V_i = v_i^+ - v_i^-, \quad \text{with} \quad v_i^+ = \overline{m} + \alpha_j \Phi_j \quad \text{and}$$
$$v_i^- = \overline{m} - \alpha_j \Phi_j. \tag{2}$$

v_i^+ and v_i^- denote the generic PDM model generated from PCA, where $\overline{m}$ corresponds to the mean shape and α_j is a scaling value for the jth principal mode of the eigen-matrix ϕ_j. α_j is chosen according to the plausible range of values that generate valid shapes within the PDM training dataset (e.g. $\pm 3\sqrt{\lambda_j}$ for PCA).

The clusterization across the surface was initially inspired by the work presented in [8], which was conducted for vector field segmentation of moving objects in 2D image sequences. We extend this work to unstructured 3D displacement vector fields. The clusterization process can be seen as a minimization problem of the following functional over a region or domain $\Omega \subseteq D$

$$C = \arg\min_{\Omega} J(M(\Omega)), \tag{3}$$

where J is an energy with two components: a first component takes into account the colinearity between vectors within the domain Ω and the predominant vector direction V_Ω in Ω, weighted by the vector length in order to give more importance to regions having a stronger deformation; the second term acts as a maximal area constraint.

$$J(M(\Omega)) = \int_{\Omega} \left(\frac{\|V_\Omega \times V(m)\|}{\|V(m)\|} \right)^2 \frac{L_{max}}{\|V(m)\|} dm + \gamma \int_{D\setminus\Omega} dm, \tag{4}$$

where γ is a real value and $L_{max} = max_D\{|V(m)|\}$. The dominant vector direction V_Ω is found as the highest eigenvalue of the following matrix [7].

$$M(\Omega) = \int_{\Omega} V(m)V^t(m)dm, \tag{5}$$

The minimization of Equation (3) is done by a hierarchical scheme, where each pattern is first considered as a cluster and then iteratively visited and agglomerated according to the energy measure J, until all points on the

surface have been analyzed.

III. RESULTS

Figures 1 to 3 show the shape models obtained for PCA (upper row) and PFA (lower row) for the spleen, right kidney and the pancreas. From the PDM, shapes are represented as blue and red colored cloud of points representing positive and negative values, respectively, of the model parameters spanning plausible shapes (e.g. $\pm 3\sqrt{\lambda_j}$ for PCA). As it can be observed from Figure 1, the interpretation of the deformations is not evident. Hence, the clustering method permits further evaluation of results.

Figures 4 shows clustering results for the first three modes of variation obtained from PCA and PFA for the spleen. Similarly, figure 5 illustrates the results obtained for the predominant mode of anatomical variability of the right kidney and pancreas. Each clustering image is a set of points in space with random colors representing each cluster. The number of clusters reflects the degree of homogeneity of the deformations fields per principal mode.

PCA

PFA

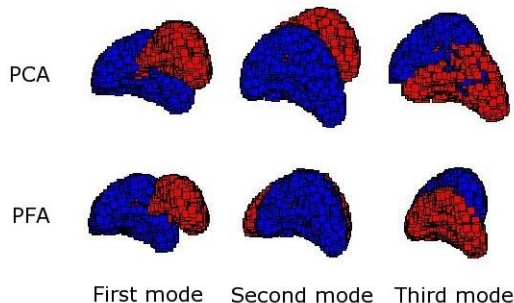First mode   Second mode   Third mode

Fig. 1: First three main modes of deformation of the spleen using PCA (upper row), and PFA (lower row). Blue and red shapes represent positive and negative values, respectively, of the model parameters. Holes in the image are caused by the anisotropy of image resolution and are created from the deformation of the point space.
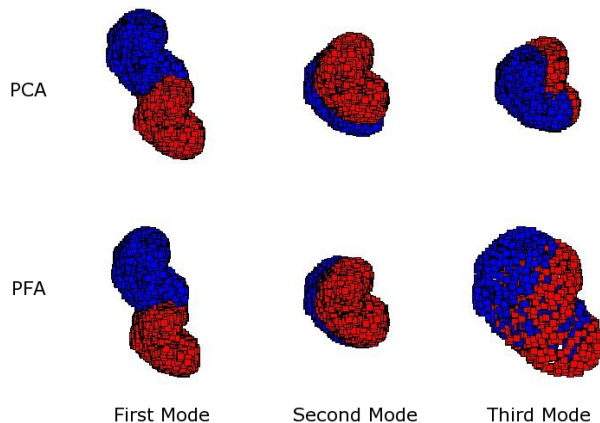

PCA

PFA

First Mode   Second Mode   Third Mode

Fig. 2: First three main modes of deformation of the right kidney using PCA (upper row), and PFA (lower row). Blue and red shapes represent positive and negative values, respectively, of the model parameters.

PCA
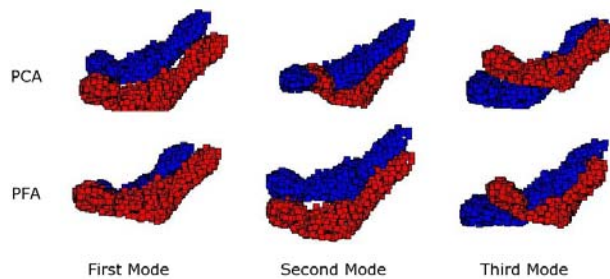
PFA

First Mode   Second Mode   Third Mode

Fig. 3: First three main modes of deformation of the pancreas using PCA (upper row), and PFA (lower row). Blue and red shapes represent positive and negative values, respectively, of the model parameters.
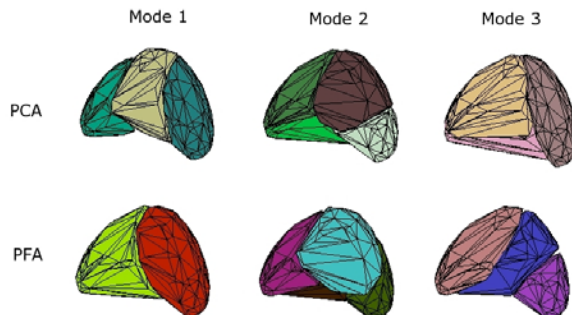

Mode 1   Mode 2   Mode 3

PCA

PFA

Fig. 4: Clusterization results for the first three modes of anatomical variability of the spleen using PCA (upper row) and PFA (lower row). Clusters colors are random.

As expected, the clusters of deformations are related to the anatomical and mechanical constraints in the abdomen. The clusters of modes of deformation might be explained by abdominal ligaments that join the spleen, liver and, stomach, or the presence of large blood vessels and contact with neighboring organs. For example, in Figure 4, the clusters of the PFA first mode of the spleen separate at the entry of the splenic vein, and the second mode clusters of both PCA and PFA reflect the positions of the gastric, colic and kidney impressions and the biomechanical deformation associated with them. Similarly, the analysis of the kidney modes of variation in Figure 5(a) emphasizes the superior pole located against the liver, and the inferior pole with the abdominal muscles impression, with an anterior-posterior separation at the location of the renal pelvis and blood vessels. In Figure 5(b) there is a clear correlation between the clusters of the first mode and the anatomical boundaries between the head, body and tail of the pancreas; the head is the best-anchored part of the organ and the tail the most mobile.
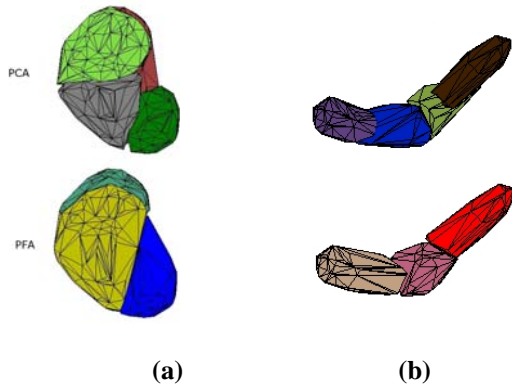
(a)   **(b)**

Fig. 5: Clusterization results for the first mode of anatomical variability of (a) the right kidney and (b) the pancreas, using PCA (upper row) and PFA (lower row). Clusters colors are random.

The anatomical variability analysis is correlated with key anatomical landmarks of the studied organs, which can be input as physical and biomechanical constraints in the analysis of the abdomen. Table 1 presents the relative size of the clusters in the first three modes of variation. PFA generally shows fewer clusters of the deformation modes than PCA, which may potentially make the interpretation of complex results easier in clinical applications of this method.

TABLE 1: NUMBER OF CLUSTERS FOR PCA AND PFA DECOMPOSITIONS OF THE PANCREAS, SPLEEN, AND THE RIGHT KIDNEY. BOLD NUMBERS INDICATE WHERE PFA YIELDS FEWER CLUSTERS THAN PCA.

	Mode 1		Mode 2		Mode 3	
	PCA	PFA	PCA	PFA	PCA	PFA
Spleen	3	**2**	4	4	3	3
Kidney	4	**3**	3	3	4	**3**
Pancreas	4	**3**	3	3	3	3

IV. DISCUSSION

The paper introduces an anatomical variability study of abdominal organs to assist with the statistical and structural analysis of the abdomen. Previous results on an alternative shape analysis technique called principal factor analysis (PFA) [7] were further investigated for abdominal organs, and a comparison in terms of interpretability of the decompositions with PCA was established through a quantitative method based on clustering of deformation modes. We contend that shape variability decomposition is easier to interpret using clusters of more regular or homogeneous patterns of the shape deformation across the surface. The analysis of deformation fields showed a strong correlation with anatomical landmarks and known mechanical deformations in the abdomen, which are better explained by PFA. In this sense, further work includes the evaluation of the correspondences establishing [13]. Clinical applications of the proposed technique include, for instance, the development of registration techniques based on uncertainty and sensitive to the organ shape and rigidity. The ability to characterize shape deformation in terms of its preferred direction and the region of interest where this deformation is predominant could greatly aid in the

segmentation of soft tissue from incomplete data. The examples shown in this paper include a more rigid abdominal organ, the kidney, a soft organ, the spleen, and the pancreas, an organ with a fixed head and a movable tail. The analysis of other abdominal organs will be presented in future work.

The results of the anatomical variability analysis are preliminary and focus on the identification and interpretation of deformation modes to better understand the modeling and biomechanical characteristics of abdominal organs and soft tissue in general. They will be expanded to the analysis of the abdomen deformation, beyond organ-based analysis. Nevertheless, the results in this paper give an overview of the wide range of potential analyses that can be extracted from the analysis of probabilistic data using statistical shape modeling. Finally, it can be concluded that using a reduced number of clusters of deformation fields allows for an easier to interpret analysis of anatomical variability, traditionally very difficult on a vector or scalar space.

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