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A Framework for Joint Image-and-Shape Analysis

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Abstract

Techniques in medical image analysis are many times used for the comparison or regression on the intensities of images. In general, the domain of the image is a given Cartesian grids. Shape analysis, on the other hand, studies the similarities and differences among spatial objects of arbitrary geometry and topology. Usually, there is no function defined on the domain of shapes. Recently, there has been a growing needs for defining and analyzing functions defined on the shape space, and a coupled analysis on both the shapes and the functions defined on them. Following this direction, in this work we present a coupled analysis for both images and shapes. As a result, the statistically significant discrepancies in both the image intensities as well as on the underlying shapes are detected. The method is applied on both brain images for the schizophrenia and heart images for atrial fibrillation patients.

1. DESCRIPTION OF PURPOSE

The analysis of the medical images many makes use of the image intensity, or higher order information applied to different subjects. Mathematically, the quantities being analyzed are functions defined on a rectangular region: $f_i : \Omega \subset \mathbb{R}^3 \rightarrow \mathbb{R}^d$ where Ω can be normalized and considered as $[0, 1]^3$. In this common domain, the image intensities or the derived quantities are compared.

For statistical shape analysis, being another actively studied field, the research interest is whether two (or more) groups of spatial objects have statistically significant differences.¹⁻⁵ It finds applications including biology,⁶ neuroscience,⁷ agriculture,⁸ and paleontology,⁹ to name a few. Usually, the targets being analyzed are objects distributed in space (e.g., surfaces of organs defining “shapes”), that is, subsets of $\mathbb{R}^3$, and there is often no function involved.

However, many research problems indicate that a joint image-and-shape analysis is needed for a better understanding of both the anatomical shapes as well as the “functional” signal derived or defined on them. For example, the thickness of the cortex is computed and

defined as a function on a common spherical surface and the comparison is carried out therein.¹⁰ In the present study, since we are performing volumetric analysis, the surface mapping techniques specific for 2D manifold are not sufficient for the current scenario. We therefore need a unified volumetric joint image-and-shape analysis.

2. METHOD

There are three major components/steps in the joint image-and-shape analysis. First, one builds the correspondence between shapes, i.e., the domains of the images. Then, the functions defined on the shapes are transformed to certain common domain. After that, statistical tests are performed.

2.1 Domain Correspondence

Since we need to establish the correspondences among volumes, rather than only among their surfaces, a volumetric registration technique is employed for building the correspondence. Mathematically, denote the shapes as $D_i \subset \mathbb{R}^3$; $i = 1, \dots, N$ and their respective group labels as $l_i \in \{0, 1\}$; $i = 1, \dots, N$. Furthermore, the “image” defined on each shape is a function $f_i : D_i \rightarrow \mathbb{R}$. The characteristic function of each shape gives their volumetric representations: $\chi_i : \mathbb{R}^3 \rightarrow \{0, 1\}$ where $\chi_i(\mathbf{x}) = 1$ if and only if $\mathbf{x} \in D_i$. In order to establish the correspondences among D_i 's, one feasible way is to deformably register the χ_i images. To that end, first, the linear discrepancies among them is removed by minimizing the L^2 distance among χ_i 's with respect to affine transformations. In particular, we opt to use an un-biased registration scheme: the mean shape χ is computed and all the shapes are registered to the mean shape. After registration, the mean shape is computed again, and the registration process repeats. In our work, the convergence of such a scheme can be achieved within less than 5 iterations and the resulting linearly registered shapes are denoted as $\tilde{D}_i$'s ($\tilde{\chi}_i$'s) and the linear transformations are denoted as A_i 's. As a result, $\tilde{D}_i = A_i \circ D_i$. It is noted that more advanced registration schemes could be used, such as,^{11–13} but we find the current scheme suffice for the shape analysis purpose here.

Next, in order to establish the non-linear correspondence among the shapes, a series of optimization problems are solved to obtain the transformation $u_i : \mathbb{R}^3 \rightarrow \mathbb{R}^3$:

$$u_i = \lim_{\sigma \rightarrow 0^+} \arg \min_{u: \mathbb{R}^3 \rightarrow \mathbb{R}^3} E_i^{(\sigma)}(u), \quad \text{with} \quad (1)$$

$$E_i^{(\sigma)}(u) := \int_{\mathbb{R}^3} (\chi(\mathbf{x}) - G_\sigma * \tilde{\chi}_i(u(\mathbf{x})))^2 + \sigma \cdot \|\nabla u(\mathbf{x})\|_F^2 d\mathbf{x}$$

In Equation (1), the G_σ is the Gaussian smoothing kernel with standard deviation σ and $*$ denotes convolution. $\chi(\mathbf{x})$ is the current mean shape of $G_\sigma * \chi_i$'s. The $\|\nabla u(\mathbf{x})\|_F$ is the Frobenius norm norm of the Jacobian matrix $\nabla u(\mathbf{x})$. The rationale of introducing such diminishing Gaussian filtering process on the characteristic functions is as follows: Without such a process, the interior of the shapes are all “flat” with value 1. Because of that, the transformation within the shape depends solely on the behavior of the regularizer. After introducing such a filtering scheme, the binary χ_i functions become smoothly varying with highest values around the center regions of the shape. As a result, the center of one shape will have a better matching with that of another. In the implementation of this sequential

optimization method, the optimized u at one σ is used as the initial value for a smaller σ . At convergence, when $\sigma \approx 0$, the regularizing term does not play a significant role and the matching in the interior of the shapes is maintained from when σ is relatively large.

At convergence, the transformations u_i 's are recorded. As a result, the point-wise correspondence T_i between D_i and D_j is $T_j^i = A_j^{-1} \circ u_j^{-1} \circ u_i \circ A_i$ satisfying $T_j^i D_i = D_j$. Moreover, we denote the transformation $S_i := u_i \circ A_i$ as the mapping from the shape D_i to the final non-linear mean shape D .

2.2 Image Mapping

Once the T_j^i 's (S_i 's) have been computed, the image defined on the shapes can be mapped to a common domain for statistical analysis. We define new functions g_i to be the pullback of f_i by S_i^{-1} . As a result, g_i 's will be defined on the common domain D , and this enables the statistical analysis of f_i 's.

Depending on the physical meaning of the f_i functions, the transformations of f_i 's may be carried out in the mass transportation sense. Specifically, the functions g_i can also be defined as the pullback of f_i by $\det(J_i) S_i^{-1}$, where J_i is the Jacobian of S_i . Intuitively, when transferring a function to a larger region, the function value will decrease due to the “diluting” effect of the transformation.

2.3 Joint image-and-shape statistical analysis

The discrepancies among the shapes may be characterized by the S_i transformations. That is, following the tensor based morphometry scheme, $\det(J_i(x))$ depicts the deviation from the mean shape D towards the shape D_i at the point $x \in D$.¹⁴ Combined with g_i , a two dimensional feature function $h_i : D \rightarrow \mathbb{R}^2$ is defined for each image-and-shape as $h_i : x \mapsto (\det(J_i(x)), \gamma g_i(x))^\top$, where γ is a constant factor to balance the magnitude difference between the shape and the image. In order to perform the statistical analysis, following,¹⁵ the Hotelling T^2 metric is computed and the permutation test is performed. After that, the multiple comparison is corrected with the false discovery rate method. Finally, the p-value map defined on the mean shape is constructed.

3. EXPERIMENTS AND RESULTS

3.1 Left atrium fibrillation

Radio-frequency ablation can be an effective treatment for left atrial fibrillation (AFib). However, the relative high AFib recurrence rate after the ablation is a concern in clinical practice.¹⁶ Before and during the ablation treatment, it would be helpful for the doctors if a computational prediction of the AFib recurrence rate can be made. In this study, the shape of the left atrium and the late gadolinium-enhanced MR signal are analyzed jointly. Since the enhanced MR signal is considered to be related with the fibrosis in the left atrial wall, such analysis may be able to detect the correlation between the AFib recurrence rate with the fibrosis distributed in the left atrial wall. Such correlation between the cure/recurrence ratio

with the distribution of the fibrosis would provide insight on the disease assessment and treatment planning.

The proposed method is applied on the pre-ablation DEC-MR images of 50 AFib patients and segmentation of the left atrium is performed by experts in the Comprehensive Arrhythmia Research and Management Center at the University of Utah.¹⁷ 31 of them are cured while the other 19 suffered AFib recurrence. The analysis gives the p-value map distributed in the left atrial wall, as shown in Figure 1. The epicardial surface of the left atrium is shown in the half-transparent gray color and the p-value map is shown in color. p-values larger than 0.05 are not shown whereas the significantly different regions are displayed. From the figure we see that greatest differences are around the vein regions. However, it is known that the segmentation around the vein region has a relative large intra- and inter-rater variation. As a result, it is our on-going research to determine whether the statistical difference captured here is caused by such segmentation variation.

3.2 Striatum analysis for schizophrenia

The shape of the striatum, in particular the caudate nucleus, is considered to be related to the schizophrenia.¹⁸ In this study, we further incorporate the T1-MR image information within the striatum into the analysis. Specifically, 27 healthy subjects and 27 schizophrenia patients collected at the Brigham and Women's Hospital are studied. The p-value map is shown in Figure 2. Interestingly, the significant different regions are found to be in the *interior* region of the right caudate, this demonstrates the benefit of performing *volumetric* analysis over the surface only analysis.

4. CONCLUSION AND FUTURE RESEARCH DIRECTIONS

In this work we proposed a general framework for performing joint shape and image-on-shape analysis. Incorporating both pieces of information would provide better discriminating and prediction power between different groups. The method is applied on heart and brain imagery. Future directions include investigating different shape correspondence techniques. Also, we will extend the method to handling vector valued image-on-shape information, such as diffusion tensor imaging.

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Figure 1. p-value map of the image-and-shape joint analysis for the left atrium wall between AFib curred and recurrent patients. Shown in (a) anterior (b) posterior (c) left, and (d) superior views.

Figure 2. p-value map of the image-and-shape joint analysis for the striatum between healthy and schizophrenia patients. Shown in (a) superior (b) posterior (c) right, and (d) left views.