A Novel Parameterization-Invariant Riemannian Framework for Comparing Shapes of 3D Anatomical Structures

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Introduction:

Our goal in this paper is to introduce a fundamental framework for shape analysis of 3D rigid objects by considering them as (continuous) 2D closed surfaces in R^3. This tool is particularly important in analyzing MRI images of brains since, in order to study shapes of anatomical structures, such as those shown in Fig. 1, one can naturally view them as parameterized surfaces. Shape analysis is concerned with comparing, matching, and deforming objects in a manner that is invariant to their rigid motions and global scale. A computer implementation, however, requires that we discretize a surface and this is done by approximating it with a polygonated mesh: a finite set of points on a surface connected only to their neighbors through edges (other approaches include [3], [4]). Since these meshes are somewhat arbitrary, depending on the data collection and pre-processing, the quantifications and comparisons of shapes should also be independent of the meshes used. More formally, one can view a mesh as a (discrete sampling of a) particular parameterization on the surface, and we desire a shape metric that is *invariant* to the action of the re-parameterization group on the space of surfaces. Our approach is to represent the anatomical surface with a special function such that, under the standard L^2 (Euclidean) metric, a re-parameterization of two surfaces preserves distances between them.

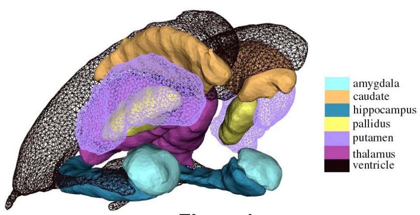

Figure1

Methodology:

Let a function f: $S^2 \rightarrow R^3$ denote a parameterized anatomical surface. Let Γ denote the set of all re-parameterization functions (these are actually all diffeomorphisms from the 2-sphere to itself). Then, for any $\gamma \in \Gamma$, the re-parameterized surface is given by $f \circ \gamma$, i.e. f composed with γ. It can be shown that under the standard L^2 (Euclidean) metric, the distances between the re-parameterized surfaces are not preserved, i.e. $\|f_1 - f_2\|$ is not equal to $\|f_1 \circ \gamma - f_2 \circ \gamma\|$ unless γ is identity. That means, any shape comparison with this choice is intimately dependent upon the particular meshes being used. To remedy this situation, we represent a surface f by another function q that is defined as $q(s) = \kappa(s)^{1/2} f(s)$, where $\kappa(s)$ is the area multiplication factor of the surface at the point s. The re-parameterization of a surface changes its q function to $(q, \gamma) = q(\gamma(s))\sqrt{J_\gamma(s)}$, where J_γ is the Jacobian of γ. It can be shown that for this representation, the distances remain unchanged after re-parameterization. That is, $\|q_1 - q_2\| = \|(q_1, \gamma) - (q_2, \gamma)\|$ for all γ. This leads to a new definition of a Riemannian distance between any two surfaces as follows: $d(f_1,f_2) = \inf_\gamma \|q_1 - (q_2, \gamma)\|$. This definition satisfies all three properties of being a distance: symmetry, non-negativity and discernability, and the triangle inequality. In particular, the distance between any two surfaces is zero if one is simply a rotation, scaling, translation, and/or a re-parameterization of the other. The actual computation of the distance involves an optimization over the manifold Γ, and is performed in our framework using a gradient approach. We pre-compute a finite number of basis elements of the space Γ at identity, and use them to approximate the gradient of the cost function iteratively. The update on γ is performed using the group structure of Γ. This framework is an extension of previous work in shape analysis of curves [1]. For further details please refer to [2].

Results:

In Figure 2, we present an example of this matching with the left putamens of two subjects. The algorithm results in optimal re-parameterization, using the gradient-based optimization over Γ, of the second putamen (i.e. deforming the corresponding mesh) to match it best with the first putamen. The resulting distance between the two surfaces is 0.0218. The figure shows surface 1, surface 2 before re-parameterization and surface 2 after re-parameterization using the gradient method. Since the changes in the mesh are hard to discern, we display the deformation of the mesh on the second surface (bright spots denote larger deformation), and the resulting decrease in the cost function.

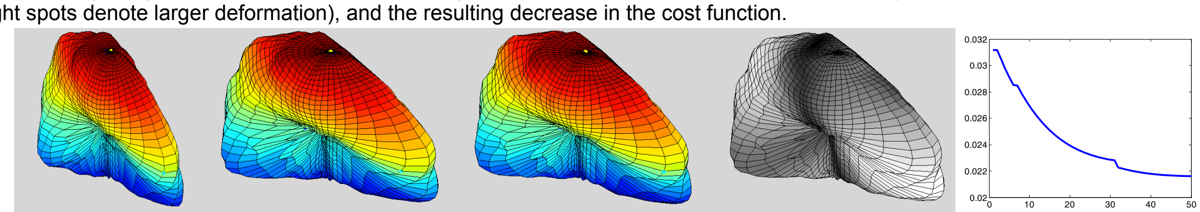

Figure 2:(a) Subject 1 (b) Subject 2 (before) (c) Subject 2 (after)(d) Mesh deformation field (magnitude)(e) Cost function

In the next experiment, we computed the distances between left putamens of 10 subjects. These datasets were selected from the Detroit Prenatal Alcohol and Cocaine Exposure Cohort of young adults, in which subjects 1, 3, 4, 6, and 10 were exposed prenatally to alcohol at moderate-to-heavy levels, and the remaining were not prenatally exposed to alcohol or illicit drugs. Figure 3 shows the result of clustering subjects using the Riemannian distance proposed here. The left panel shows a dendrogram clustering of the 10 subjects while the right panel shows the subjects as points in two-dimensional MDS space (color coded). The results show that exposed subjects are mostly clustered together away from the non-exposed subjects. The only exceptions were subjects 8 and 10 who are clustered away from the remaining subjects.

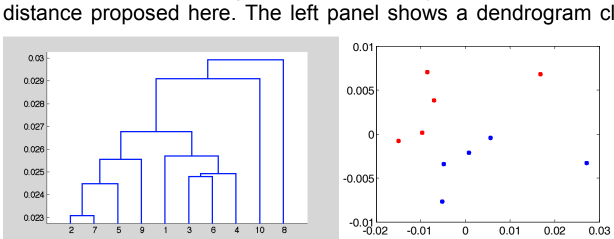

Figure 3:(a) Dendrogram (b) MDS display (exposed --red, non-exposed --blue)

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References: [1] E. Klassen et al., Analysis of Planar Shapes Using Geodesic Paths on Shape Spaces, IEEE PAMI 26(3), 372-383, 2004. [2] S. Kurtek, E. Klassen, and A. Srivastava, A Riemannian Framework for Shape Analysis of 3D Objects, FSU Tech Report. 2009. [3] X. Gu and B. C. Vemuri. Matching 3d shapes using 2d conformal, representations, *MICCAI, Volume, 3216*, pages 771–780, 2004. [4] S. Bouix et al., Hippocampal shape analysis using medial surfaces. *NEUROIMAGE*, 25:1077–1089, 2001.