Empowering Anatomical Shape Analysis with Medial Curves and 1-D Group-Wise Registration

Abstract No:

5943

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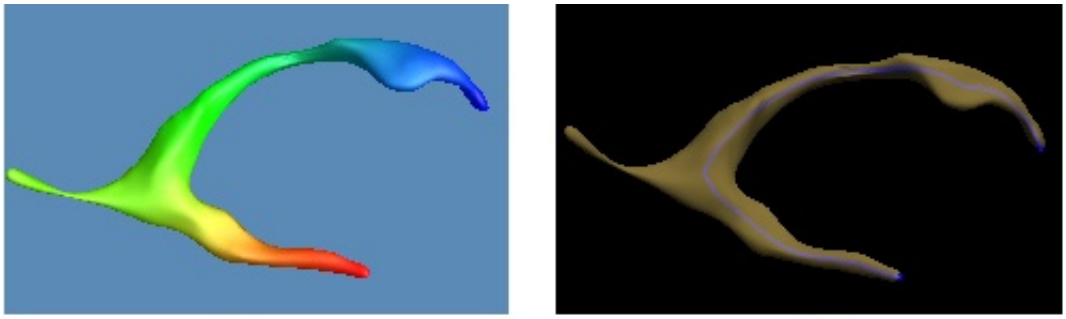
Introduction:

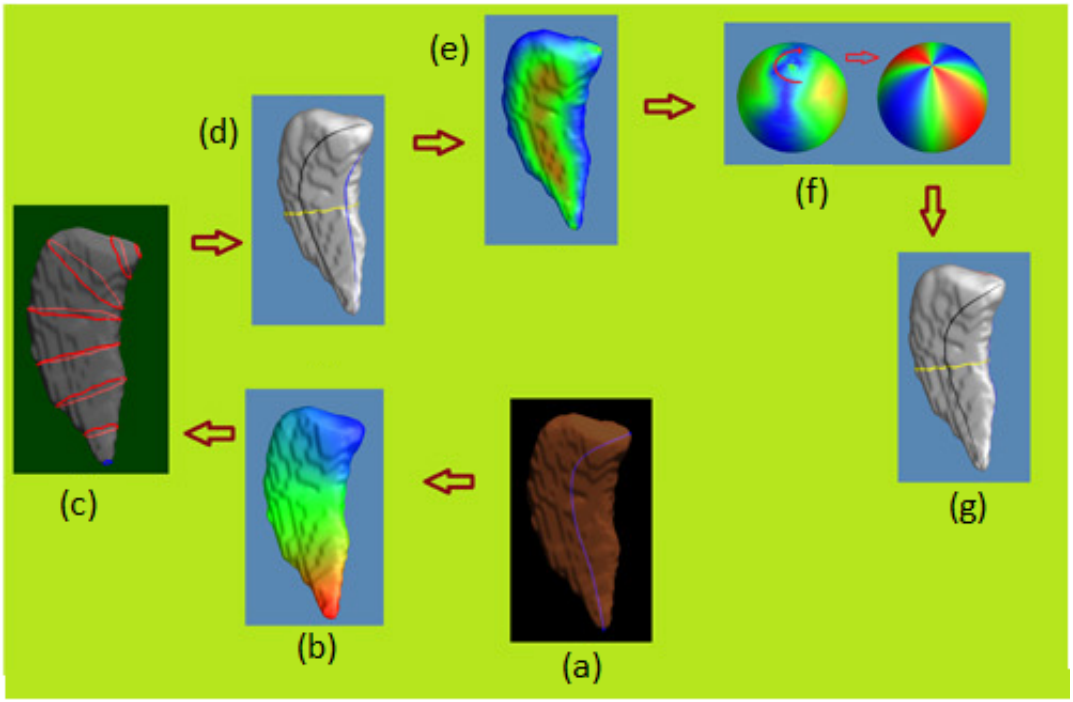
We developed a method for subcortical shape analysis, and showed it increases the power to detect disease-related differences in ventricular and caudate anatomy in studies of mild cognitive impairment versus controls, and HIV+ patients versus controls.
Local subcortical shape analysis involves three related problems: shape modeling, registration, and statistical analysis. Ideally these problems should be solved simultaneously, but current approaches couple at best two of the three steps [1,2]. We present a framework to solve all three problems simultaneously by reducing group wise shape registration to a one-dimensional problem. We use a novel framework for medial curve computation that enables a larger family of shapes to admit a single-curve skeletonization than was previously possible. As computational complexity is reduced, we can register hundreds of anatomical shapes in a few minutes. We validate our results on models of the caudate nucleus and lateral ventricles, and show improvements relative to a well-known spherical harmonic method.

Methods:

We assume that our shapes of interest can be described with a single curve skeleton, and choose medial thickness as a local shape descriptor, commonly used in neuroimaging [3]. To compute the medial curve, we introduce a novel variational framework in which the medial curve is defined as a global minimum of a weighted Hausdorff distance. The weights decrease continuously as the vector from the surface to the curve becomes less normal to the curve, and vanish when the line of sight to the surface passes outside the shape. Compared to existing methods [4, 5, 6], this framework enforces the intuitive 1-curve topology, and allows a large class of shapes to admit such a skeletonization. This is critical for consistent shape registration.
The medial curve c(t) induces two feature functions, the thickness and the global orientation function (GOF), $G(p) = \arg\min \{t \in [0,1]\} ||c(t) - p||$. We modify a fast spherical mapping [7] to use these functions to register surfaces by minimizing the L2 difference between scalar maps.
To reduce variance in medial thickness, we compute the 1-D profile of each shape's thickness, mapping each cross-section's average thickness to the curve. To enable approximate group wise registration, we adjust each shape's GOF by simultaneously registering all curves in a given study to reduce group variance in thickness at each curve point. This results in descriptor-aware registration of all shapes. As the GOF primarily drives the shape registration, statistical comparisons are more sensitive. Thus the group-wise curve registration couples all three aspects of shape analysis.



A medial curve of a lateral ventricle (b) and the resulting GOF (a)



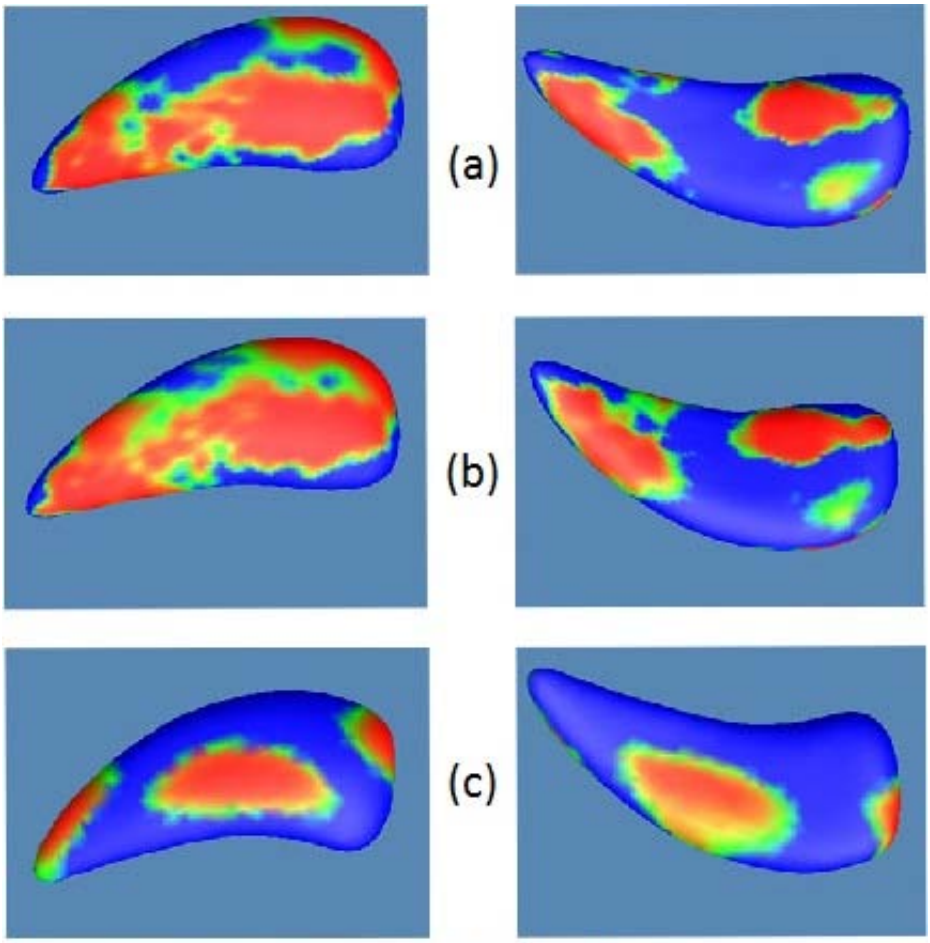
A flow-chart for curve-based spherical parameterization. *(a)* initial curve; *(b)* smoothed GOF; *(c)* level set curves of the GOF; *(d)* smooth spherical parameterization. *(e)* normalized thickness map; *(f)* correlating normalized thickness map with the ideal thickness map on the sphere; *(g)* resulting final parameterization

1-D group registration is done between steps (a) and (b)

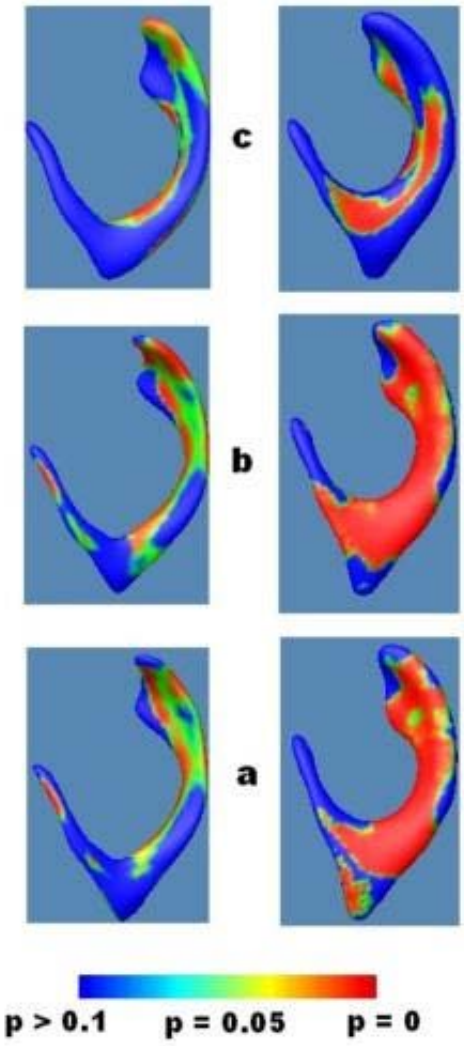
Results:

Two datasets of left lateral ventricles were analyzed: the ADNI baseline MRI dataset consisting of 391 subjects with mild cognitive impairment (MCI), and 229 age-matched controls; and a dataset of 11 HIV subjects and 8 age-matched controls [8]. Also, the ADNI baseline left caudate data was used (199 AD/227 NC). We compared 3 analysis methods: SPHARM-PDM [9], and our Medial-Spherical Analysis (MSA) with and without group wise registration. Group-MSA took several minutes to compute even for the ADNI cohort. 100000 permutations were used to assess overall group

difference for each method. The ADNI cohort showed overall differences of p=0.0068, 0.00046 and 0.00029 for SPHARM-PDM, MSA and group-MSA, respectively. The HIV cohort showed p=0.0149, 0.01039 and 0.00988. The caudate results were p = 0.027, 0.0014, 0.00065. Group-wise registration was performed blind to diagnosis.



Caudate p-maps for AD-NC difference based on (a) group-MSA, (b) MSA, and (c) SPHARM



Ventricular p-maps for MCI-NC (right column) and HIV-NC (left column) differences based on (a) group-MSA, (b) MSA, and (c) SPHARM-PDM

Conclusions:

Our novel method for subcortical shape analysis combines registration, description and statistical comparison. Compared to related methods, our method gave greater effect sizes for distinguishing mild cognitive impairment from healthy controls, and HIV+ patients from controls. The highly efficient method registers hundreds of shapes in minutes, and can robustly handle complex, branching and noisy shapes such as lateral ventricles.

Modeling and Analysis Methods:

Image Registration and Computational Anatomy

Abstract Information

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