Combined SPHARM-PDM and entropy-based particle systems shape analysis framework

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ABSTRACT

Description of purpose: The NA-MIC SPHARM-PDM Toolbox represents an automated set of tools for the computation of 3D structural statistical shape analysis. SPHARM-PDM solves the correspondence problem by defining a first order ellipsoid aligned, uniform spherical parameterization for each object with correspondence established at equivalently parameterized points. However, SPHARM correspondence has shown to be inadequate for some biological shapes that are not well described by a uniform spherical parameterization. Entropy-based particle systems compute correspondence by representing surfaces as discrete point sets that does not rely on any inherent parameterization. However, they are sensitive to initialization and have little ability to recover from initial errors. By combining both methodologies we compute reliable correspondences in topologically challenging biological shapes. *Data:* Diverse subcortical structures cohorts were used, obtained from MR brain images. *Method(s):* The SPHARM-PDM shape analysis toolbox was used to compute point based correspondent models that were then used as initializing particles for the entropy-based particle systems. The combined framework was implemented as a stand-alone Slicer3 module, which works as an end-to-end shape analysis module. *Results:* The combined SPHARM-PDM-Particle framework has demonstrated to improve correspondence in the example dataset over the conventional SPHARM-PDM toolbox. *Conclusions:* The work presented in this paper demonstrates a two-sided improvement for the scientific community, being able to 1) find good correspondences among spherically topological shapes, that can be used in many morphometry studies 2) offer an end-to-end solution that will facilitate the access to shape analysis framework to users without computer expertise.

Keywords: Spherical harmonic representation, entropy-based particle systems, statistical shape analysis, shape analysis framework, 3DSlicer

1. INTRODUCTION

Making a qualitative assessment of an anatomical structure is a trivial task for an experienced clinician but this qualitative expert knowledge is difficult to quantify, making it difficult or impossible to formulate accurate scientific conclusions and general-purpose theories of shape for applications in medicine. That is why shape analysis is a field that has become of increasing interest to the clinical research community due to its potential to precisely locate morphological changes between healthy and pathological structures, both cross-sectionally and longitudinally.

In order to accurately assess structural changes at specific locations, shape populations need to be represented by sampling each shape surface in a consistently ordered fashion so as to define homologous surface points across the each sample in the population. Needless to say, definition of correspondence among samples will influence directly the subsequent analysis. This manuscript presents a set of tools that compute shape correspondence by using a combined methodology: SPHARM[1] and entropy-based particle systems.[2]

- SPHARM-PDM toolbox presents an automated set of tools for the computation of shape analysis based in SPherical HArmonic Representation. SPHARM-PDM solves the correspondence problem by defining a spherical parameterization for each one of the objects in a shape population, assuming correspondence between equivalently parameterized points. However, biologically inspired shapes sometimes have not a clear parametric definition and in those cases the correspondence achieved by SPHARM is not optimal.

- Entropy-based particle systems[2] compute correspondence by representing surfaces as discrete point sets that does not rely in any inherent parameterization. This method uses methodology from the computer graphics field representing surfaces as dynamic set of particles across an ensemble of surfaces so that their positions optimize the information content of the system. However, they are sensitive to initialization and have little ability to recover from initial errors.

In this work, we combine the potential of SPHARM to compute a reliable set of correspondent points based in spherical parameterization and the potential of entropy-based particle systems to optimize correspondences in a shape population, regardless of any inherent parameterization. By combining both methodologies we compute reliable correspondences in topologically challenged biological shapes. Also, this work presents a end-to-end computing shape correspondence computing module included in 3D Slicer.[3] This software was developed at the Surgical Planning Laboratory (SPL, Brigham and Women's Hospital, Boston, MA, USA) and is an free open-source software application available on the internet.This comprehensive program intends to bridge the gaps between the experimental science made by computer scientists and the clinical research science, making it available to a bigger audience that does not need to have a big computer expertise or deep understanding of the underlying basic science to operate the tool.

2. DATA

Images were acquired on a Siemens head-only 3T scanner (Allegra, Siemens Medical System, Erlangen, Germany). Infants were scanned unsedated while asleep, fitted with ear protection and had their heads secured in a vacuum-fixation device at both 1 and 2 year follow up sessions. T1-weighted structural pulse sequences were a 3D magnetization prepared rapid gradient echo (MP-RAGE TR = 1820 msec, inversion time = 400 msec, echo time = 4.38 msec, flip angle = 7 degrees, n = 57). Proton density and T2-weighted images were obtained with a turbo spin echo sequence (TSE, TR = 6200 msec, TE1 = 20 msec, TE2 = 119 msec, flip angle 150 degrees). Spatial resolution was 1 X 1 X 1 mm voxel for T1-weighted images, 1.25 X 1.25 X 1.5 mm voxel with .5 mm interslice gap for proton density/T2-weight images. Due to the presence of unmyelinated white matter, it is necessary to perform the neonatal segmentations on T2-weighted scans to accurately segment the white matter, grey matter interface.

For all datasets, the segmentation used as input were performed using AutoSeg,[13] that is a tool allowing the segmentation of probabilistic sub-cortical structures and label maps, such as generic ROI maps and parcellation maps. The approach is a fully automatic segmentation via a deformable registration of an unbiased diffeomorphic atlas with probabilistic spatial priors. Postprocessing with 3D connectivity, morphological closing and minor manual editing provided simply connected 3D objects.

The validation dataset for our 3D Slicer SPHARM+Particle system shape correspondence pipeline consists of 20 segmented left hippocampus (H), 20 segmented left caudates (C) and 20 segmented left lateral ventricles (LV) (see figure 1).

3. METHODS

This section describes the SPHARM-PDM shape representation and the entropy-based particle systems. In summary, the input of the proposed shape analysis is a set of binary segmentations of a single type of subcortical structures (C, H and LV). These segmentations are first processed to fill any interior holes and a minimal smoothing operation. The processed binary segmentations are converted to surface meshes, and a spherical parametrization is computed for the surface meshes using a area-preserving, distortion minimizing spherical mapping. The SPHARM description is computed from the mesh and its spherical parametrization. The SPHARM description is then sampled into a triangulated surfaces (SPHARM-PDM) via icosahedron subdivision of the
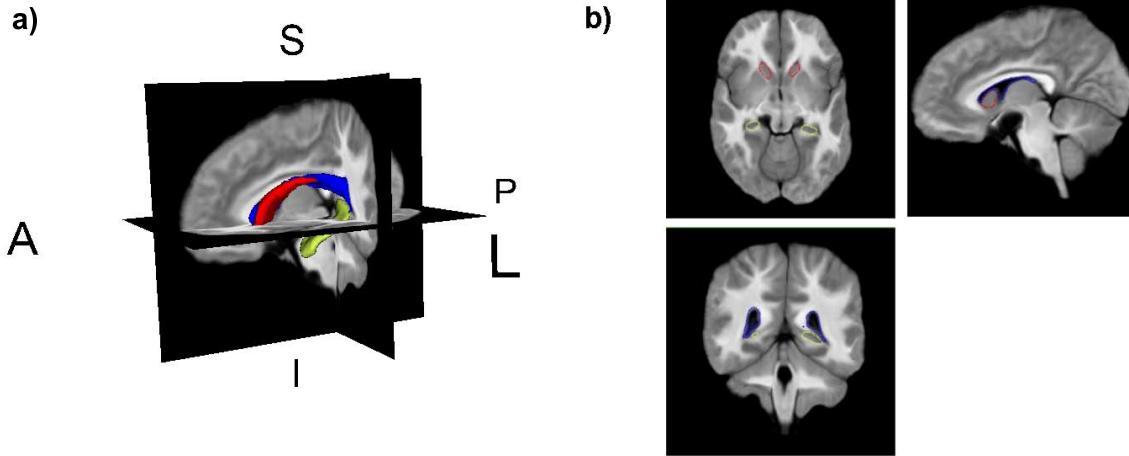
Figure 1. Pediatric subcortical structures segmented in 2yo scan. a) 3D rendering of C (in red), H (in yellow) and LV (in blue) displayed in axial-sagittal-coronal cross-sections of the brain for anatomical reference. b) Axial (top-left), sagittal (top-right) and coronal (bottom-left) cross-sections of the bran with C, H and LV slice intersections visible.

spherical parametrization. These SPHARM-PDM surfaces are all spatially aligned using rigid Procrustes alignment. SPHARM-PDM rigidly aligned surface meshes are converted to particle locations and particle files are created. These will be used as initialization as an input for entropy-based particle systems, that find correspondence by simultaneously maximizing both the geometric accuracy and the statistical simplicity of the model. The results obtained for three different types of subcortical structures (C, H and LV see Section 2) will be evaluated for SPHARM-only and SPHARM-Particles frameworks using generalization and specificity error metrics for model construction. Both SPHARM-PDM, particle-based entropy systems and validation error metrics will be described in detail in the next sections.

3.1 SPHARM-PDM

In summary, the SPHARM description is a hierarchical, global, multi-scale boundary description that can represent objects of spherical topology, proposed initially by Brechbühler *et al.*[4] This SPHARM shape analysis approach was extended by Gerig *et al.*[5,6] to use the implied sampled surface (SPHARM- PDM, where PDM stands for Point Distribution Models). This shape analysis framework is based in spherical parameterization, that is computed via optimizing an equal area mapping of the 3D voxel mesh onto the sphere and minimizing angular distortions. The basis functions of the parameterized surface are spherical harmonics. Each individual SPHARM description is composed of a set of coefficients, weighting the basis functions. Kelemen *et al.*[7] demonstrated that SPHARM can be used to express shape deformations. Truncating the spherical harmonic series at different degrees results in object representations at different levels of detail. Based on a uniform icosahedron-subdivision of the spherical parameterization, we obtain a Point Distribution Model (PDM). Even though SPHARM-PDM shape correspondence framework has been applied in several studies on brain morphometry[8] and dentistry[9,10] successfully, if the biologically inspired shape has not a clear parametric definition the correspondence achieved by SPHARM might not be optimal. The correspondent PDMs will be used as initialization for the entropy-based particle systems (see figure 2), first developed by Cates *et al.*[2]

3.2 Entropy-based Particle Systems

This method constructs a point-based model of the samples that simultaneously maximizes both the geometric accuracy and the statistical simplicity of the model, by minimizing the ensemble entropy (how different are one shapes from the rest in the population) and the shape entropy (how well sampled is that individual model). The method has been extended by Oguz *et al.*,[11] including features related to geometry and functional information, in addition to just pure 3D information, into the optimization process. The main idea for the entropy based correspondence method is to construct a point-based sampling of the shape ensemble that simultaneously
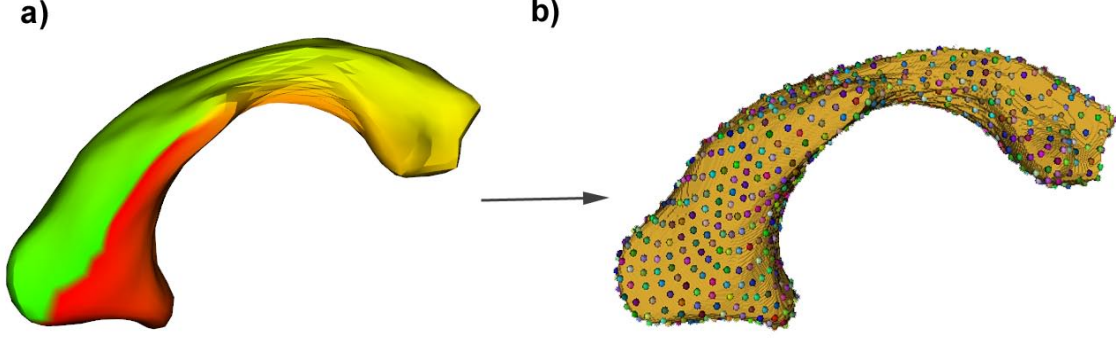
Figure 2. a) SPHARM representation of a neonatal LV, color coded using the spherical parameterization b) Particle set computed using the SPHARM representation triangulated mesh as initialization.

maximizes both the geometric accuracy and the statistical simplicity of the model. The inputs to the module are the SPHARM-PDM surfaces from which surface point samples, which also define the shape-to-shape correspondences, are modeled as sets of dynamic particles that are constrained to lie on a set of implicit surfaces. Sample positions are optimized by gradient descent on an energy function that balances the negative entropy of the distribution on each shape with the positive entropy of the ensemble of shapes. The outputs of the shape correspondence module are correspondent triangulated meshes and their equivalent set of 3D points, which can be used for shape morphometry statistics.

3.3 Validation metrics

In order to validate our SPHARM-Particles combined methodology we computed benchmark results for the three datasets used in the comparisons. Ideally, any model M computed using any shape correspondence framework should be:

- Able to represent any instance of the class.

- Only capable of representing legal instances of the class.

These two features are represented by *model generalization* and *model specificity*, respectively. The *generalization ability of a model $G(M)$* measures its capability to represent unseen instances of the object class. This is a fundamental property as it allows a model to learn the characteristics of an object class from a limited training set. If a model is overfit to the training set, it will be unable to generalize to unseen examples. The generalization ability of each model is measured using leave-one-out reconstruction. A model is built using all but one member of the training set and then fitted to the excluded example. The accuracy to which the model can describe the unseen example is measured. $G(M)$ is measured as a function of the number of shape parameters M used in the reconstruction. Its standard error $\sigma G(M)$ is derived from the sampling standard deviation σ and the training set size ns as: $\sigma G(M) = \frac{\sigma}{\sqrt{ns-1}}$.On the other hand, the *quantitative measure of specificity of a model $S(M)$* makes reference to the fact a model should only generate instances of the object class that are similar to those in the training set. It is useful to assess this qualitatively by generating a population of instances using the model and comparing them to the members of the training set. $S(M)$ is defined as the average distance of uniformly distributed, randomly generated objects in the model shape space to their nearest member in the training set. The standard error of $S(M)$ is given by: $\sigma S(M) = \frac{\sigma}{numberofrandomsamples}$ (N was chosen 10.000 in our experiments).

4. TECHNOLOGY DISSEMINATION

The combined methodology (see figure 3) was implemented as a stand-alone 3D Slicer module, which works as an end-to-end shape correspondence module (figure 3 a)). This is a open-source free software, available in

NITRC (Neuroimaging Informatics Tools and Resources Clearinghouse.[12] In figure 3 b) is possible to see a daily downloads plot of the SPHARM-PDM Toolbox in NITRC, which shows the potential interest of the scientific community in shape correspondence. We expect to increase the download numbers after the addition off the new combined SPHARM-Particles combined methodology.
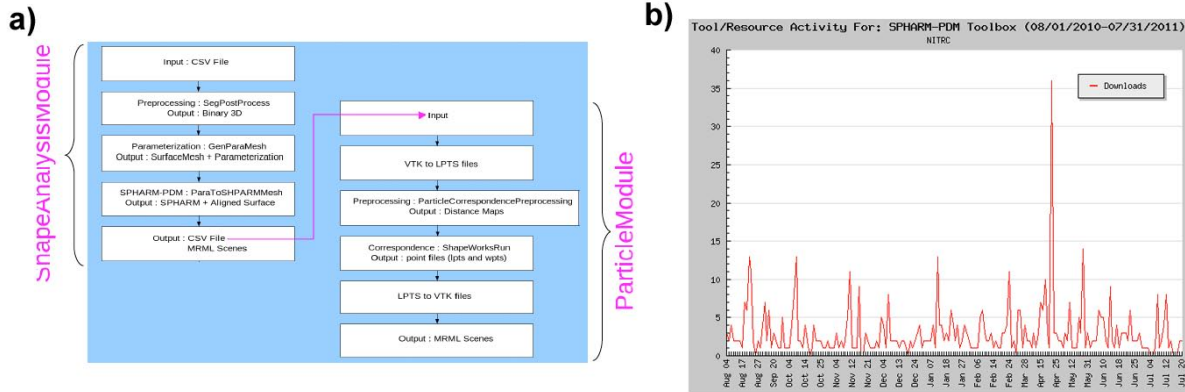

Figure 3. a) Proposed combined methodology overview b) Daily downloads of the SPHARM-PDM toolbox in NITRC.

5. RESULTS

In the following sections we present the results of the application of the proposed SPHARM-Particles correspondence framework compared with SPHARM-only correspondence methodology. Three different subcortical structure populations will be used: a left pediatric caudate population, a left pediatric hippocampus population and a left lateral ventricle population of 20 subjects each. In this document, we focus only on the accuracy of model building and correspondence, not in the application of these models to respond clinical questions.

In Figure 4 errors graphs of generalization ($G(M)$, a), c), and e)) and specificity ($S(M)$, b), d) and f)) are shown for caudate, hippocampus and ventricle studies. In all datasets both $G(M)$ and $S(M)$ presented lower error values in the combined SPHARM+Particles proposed methodology, demonstrating that this framework computes correspondence that best represent the sample populations. The lateral ventricle dataset has higher error values, probably due to its complicated geometry.

6. CONCLUSIONS

In this paper, we have presented a SPHARM-PDM and particle-based entropy system methodology compared with SPHARM-PDM toolbox in three populations of pediatric subcortical structures. We have analyzed both frameworks by analyzing properties of the model implied by the correspondences, in regard to generalization and specificity. Our combined method has demonstrated to improve correspondence in the different example datasets, while SPHARM-PDM toolbox only was not finding good correspondences.

The proposed framework is disseminated in easy, streamlined 3D Slicer modules, trying to bridge the gap existing between basic and applied science: basic biomedical research science has the trend to evolve thanks to promotions and grants based largely on the papers scientists have published in top journals, not on how much they have advanced medicine. On the other hand, many clinicians who treat patients in the faculty practice clinics have little time or inclination to keep up with an increasingly complex basic literature. 3D Slicer is a big initiative for translational research solutions, developed under the auspices of the National Alliance for Medical Image Computing (NAMIC). NAMIC also shares the recognition that modern healthcare demands improved technologies based in imaging to ease suffering and prolong productive life and improve current clinical practices. Therefore using 3D Slicer as dissemination technology seemed the most suitable approach.

In conclusion, the work presented in this paper demonstrates a two-sided improvement for the scientific community, being able to 1) find good correspondences among any population of shapes, that can be used
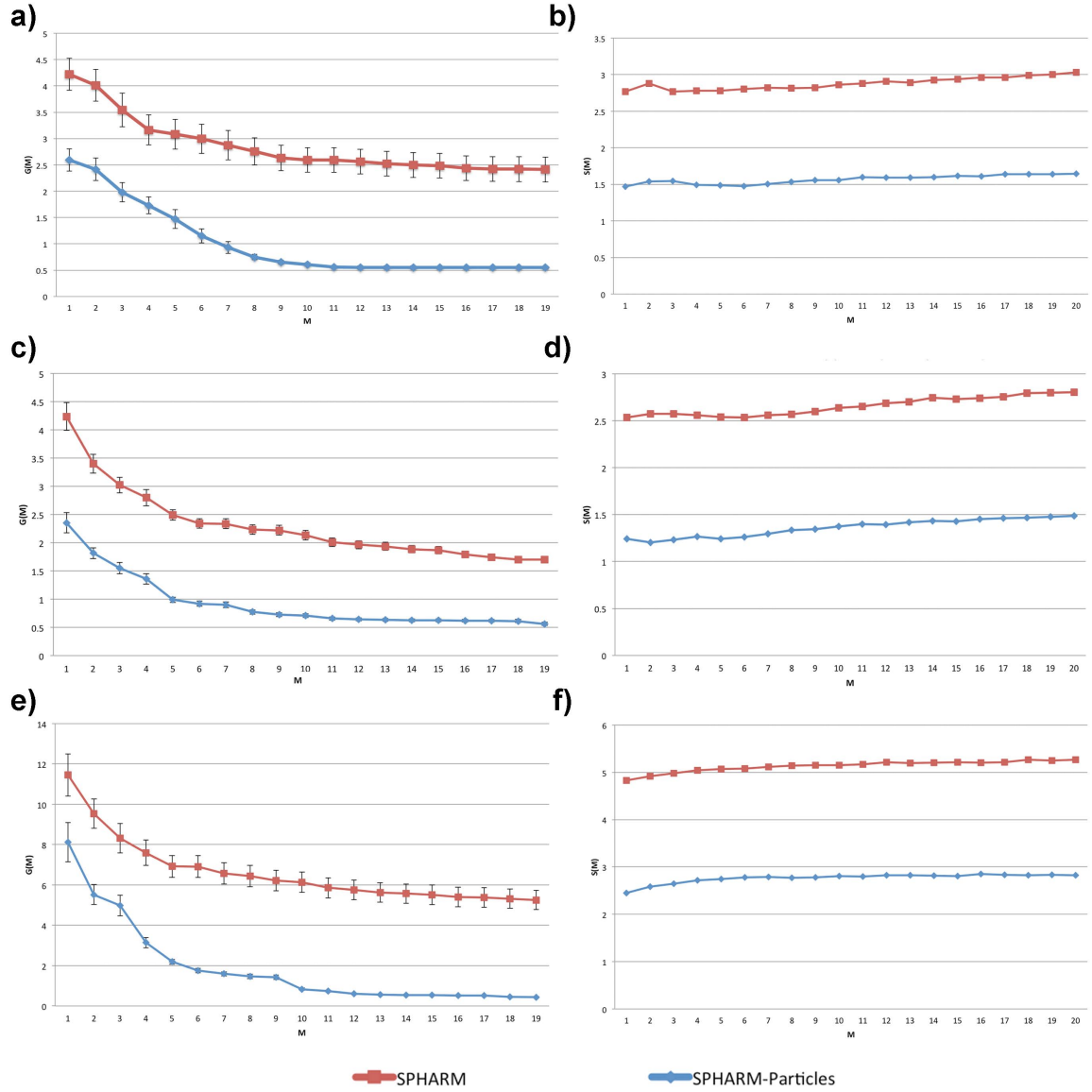
Figure 4. Table with errors graphs of generalization $(G(M))$ and specificity $(S(M))$ for caudate (a) and b)), hippocampus (c) and d)) and lateral ventricle (e) and f)). To avoid redundance, only left structures were used. SPHARM-only methodology shows clearly worse results than the SPHARM-Particle combined methodology for all studied datasets.

in many morphometry studies 2) offer a end-to-end solution that facilitates access of complicated computer processing methodologies to clinical users without needing extensive computer expertise or knowledge of the underlying basic science.

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