Conformal initialization for shape analysis applications in SlicerSALT

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Abstract

Shape analysis is an important method used in neuroimaging research community due to its potential to precisely locate morphological changes between healthy and pathological structures. A popular shape analysis framework in the neuroimaging community is based on the encoding surface locations as spherical harmonics for a representation called SPHARM-PDM.[1] The SPHARM-PDM pipeline takes a set of brain segmentation of a single brain structure (for example, hippocampus) as input and converts them into a corresponding spherical harmonic description (SPHARM), which is then sampled into triangulated surface (SPHARM-PDM). At present, the SPHARM-PDM pipeline utilizes an area-preserving optimization of the spherical mapping based on an initial heat-equation based mapping of the surface mesh to the unit sphere. In the case of objects with complex shape, this initial spherical mapping suffers from a high degree of mapping distortion that cannot always be corrected by the following optimization procedure. Here we proposed the use of an alternative initialization based on a conformal flattening.[2] This method adopts a bijective angle preserving conformal flattening scheme to replace the heat equation mapping scheme as initialization for use in the SPHARM-PDM pipeline. After quantitative measures of shape calculated from various complex structures, we concluded that in most cases, the new pipeline produced dramatically better results than the old pipeline. The main contribution of this paper is a command line tool based on the Slicer Execution Model, which merges the conformal flattening into the SPHARM-PDM pipeline for use in the SALT shape analysis toolbox.

Keywords

Shape Analysis; Medical Image Analysis; Conformal Flattening Filter; Slicer SALT

1. INTRODUCTION

The Spherical Harmonic - Point Distribution Model (SPHARM-PDM) is a popular pipeline that computes point-based models using a parametric boundary description for the computing of Shape Analysis (Figure 1). Its objective is to bring populations of an anatomic object into correspondence and thus to allow statistical shape analysis.

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Starting with a binary label map, SPHARM-PDM generates parametric surfaces using a spherical harmonic decomposition scheme. SPHARM-PDM tests for spherical topology, and then generates a surface that can be mapped to a sphere using the method proposed by Brechbhler, et al.[3] The proposed method parametrizes the surface by defining a continuous, one-to-one mapping from the surface of the original object to the surface of a unit sphere. It formulates the parametrization as a constraint optimization problem and gets the practicable starting values by an initial mapping based on a heat equation model. Brechbhler performs the initialization parametrization considering two criteria:

1. Area preservation: Every object region must map to a region of proportional area in parameter space, with the constant of proportionality uniform across the surface

2. Minimal distortion: Every quadrilateral of the object should map to a spherical quadrilateral that has side length equals to the corresponding center angle (in radian) as the sphere has unit radius in parameter space

Brechbhler then calculates out system of nonlinear equations after establishing constraints for area preservation with half of the sum of the perimeters of all quadrilaterals being the objective function. Finally, the system of nonlinear equations is linearizing and solved via Newton-based optimization. Following this optimization, the framework computes the spherical harmonic coefficient representation of the surface coordinates, resamples these via an icosahedron subdivision of the spherical parameter spaces, and then resolves parameter and mesh space alignment issues. While the above approach provides appropriate and well performing surface representations for numerous biomedical objects, this is less the case specifically for complex or skinny objects. For such objects, the current heat equation model based initialization generate a SPHARM parametrization with a high degree of distortion that cannot always be corrected by the following optimization procedure.

In this paper, we propose the use of the conformal flattening ITK filter,[2] which was developed based on the paper by Sigurd Angenent, et al.,[4] to serve as the initial parametrization method in the SPHARM-PDM framework by replacing the current heat equation model based initialization. Specifically, we extended the command line tool called GenParaMesh used in the third step of the SPHARM-PDM shape analysis framework to improve the quality of the reconstructed 3D surface mesh. As expected, the SPHARM surface meshes derived from the conformal mapping initialization show significantly improved surface quality for complex structures such as the femur and the mandible. The parameter space optimization obtained via conformal mapping initialization also converges faster on all datasets than those with heat equation mapping initialization.

2. METHODS

Our framework for SPHARM-PDM combined with conformal ITK filter consists of five steps as shown in Figure 2. Here we focus on the description of the 3rd step that involved the generation of the surface mesh and its spherical parameter space mapping.

Instead of using the original heat equation mapping initialization, our framework utilizes the ITK conformal flattening filter to map the object surface to the unit sphere as an

initialization parametrization (Figure 2). With the area-preserving heat equation mapping initialization, the spherical representation of the surface mesh of the structure will have a large variation in size of triangles and has a poor uniformity of density of the size of triangles in the beginning. However, with angle-preserving conformal mapping initialization, the initial spherical representation of the surface mesh of the structure will reach a small variation in size of triangles and has significantly improved uniformity of density of the size of triangles. Therefore, it is expected that using conformal mapping initialization, the spherical representation will converge faster to the optimal state.

Here we briefly summarize how the ITK conformal flattening filter tool in the second step works as follows. Denote the genus zero surface to be flattened as Σ. As being proven in the appendix of [2], the mapping z, defined on S, satisfies the following:

$$\Delta z = \left(\frac{\partial}{\partial u} - i \frac{\partial}{\partial v} \right) \delta_p \quad (1)$$

where p is an arbitrary point on Σ. The function z maps Σ\{p} to the complex plane C. By standard sterographic projection, the complex plane is mapped to a sphere excluding the north pole. Our project adopts the conformal parametrized sphere as the new initialization parametrization.

We further renovate the tool by merging all three steps above into one step. With the new tool, researchers only need to set the conf flag on in the GenParaMesh command line tool in order to use conformal mapping based initialization parametrization.

3. MATERIALS

We apply the SPHARM-PDM pipeline tool with different iterations and with either heat equation mapping based initialization parametrization or conformal mapping based initialization parametrization and evaluate the quality of the surfaces after 0 to 500 iterations in steps of 50 iterations. Four different organ segmentations are used for testing and comparing the conformal mapping based initialization parametrization: the femur, the mandible, the condyle, and the molar. To evaluate the quality of the resulting SPHARM-DPM surfaces, we computed the Mean Absolute Distance (MAD) and the Coefficient of Variation of Cell Area (CVCA) between the reconstructed SPHARM surface meshes and the original surface meshes (software: MeshValMet[5] for MAD, MeshQuality for CVCA). The MAD represents a measure of reconstruction quality and the CVCA a measure of how well the goal of equal-area mapping was achieved. For both metrics, a lower value indicates a better performance.

3.1 The Femur Data Reference

The femur data were obtained from a collaboration with the University of Bern in 2004. The exact origin of the data is unfortunately unknown.

3.2   The Mandible & The Condyle Data Reference

The mandible and Condyle data was a subset of the data used in the study "3D superimposition and understanding temporomandibular joint arthritis".[6] In the original study, the Department of Orthodontics and Pediatric Dentistry at the University of Michigan acquired Cone beam CT scans from 69 subjects with long-term temporomandibular joint (TMJ) osteoarthritis (OA, mean age 39.1 15.7 years), 15 subjects at initial consult diagnosis of OA (mean age 44.9 14.8 years), and seven healthy controls (mean age 43 12.4 years).

3.3   The Molar Data Reference

The molar data used in my study is a subset of the data used in the study of "Algorithms to automatically quantify the geometric similarity of anatomical surfaces"[7] and "Group-wise shape correspondence of variable and complex objects",[8] and a detailed explanation of sample preparation can be found in "Relief index of second mandibular molars is a correlate of diet among prosimian primates and other euarchontan mammals".[9] In short, molds of actual tooth-rows were molded using a polyvinylsiloxane material (PresidentJet Plus) and cast in epoxy EpoTek 301. The second mandibular molar was trimmed from the tooth row and scanned with the Scanco CT-40 machine at Stony Brook University's Center for Biotechnology. Three-dimensional surfaces of each tooth were segmented from the resulting DICOM or TIFF stacks using Amira 5.1 or Avizo 6.0.

4.   RESULTS

Figure 3 shows a representative 3D view of (1) the femur, (2) the molar, (3) the condyle and (4) the mandible at different stages of the SPHARM-PDM pipeline. Obviously, the initial parametrized spheres with (c) conformal mapping based initialization parametrization are always better in quality than those with (d) heat equation mapping based initialization parametrization. The reconstructed SPHARM surface meshes of (2) the molar, (3) the condyle and (4) the mandible achieve similar quality using both initializations given 500 iterations except (1) the femur, where the surface reconstruction completely failed with heat equation mapping based initialization parametrization, but succeeded with conformal mapping based initialization parametrization.

Figure 4 and Figure 5 show the quantitative evaluation at different iterations. The blanks in the charts were caused by failure of the analysis software. The conformal mapping based parametrization shows clearly improved reconstruction quality of (1) the femur and (4) the mandible, while (2) the molar and (3) the condyle showed minimal differences between the two initialization methods. Furthermore, the optimization process with conformal mapping based initialization was significantly sped up for all four structures, having reached near optimal value with 50 iterations.

5.   CONCLUSSIONS

Our proposed method to employ conformal mapping initialization parametrization for shape analysis significantly reduces the iteration number to reach best reconstruction quality of all four structures tested and significantly improves the reconstruction quality of the femur and the mandible structures while maintaining similar reconstruction quality for the molar and

the condyle structures. Complete reconstruction failures were eliminated in our experimental data. It is noteworthy that further work is necessary for other complex and skinny objects such as small lateral ventricles.

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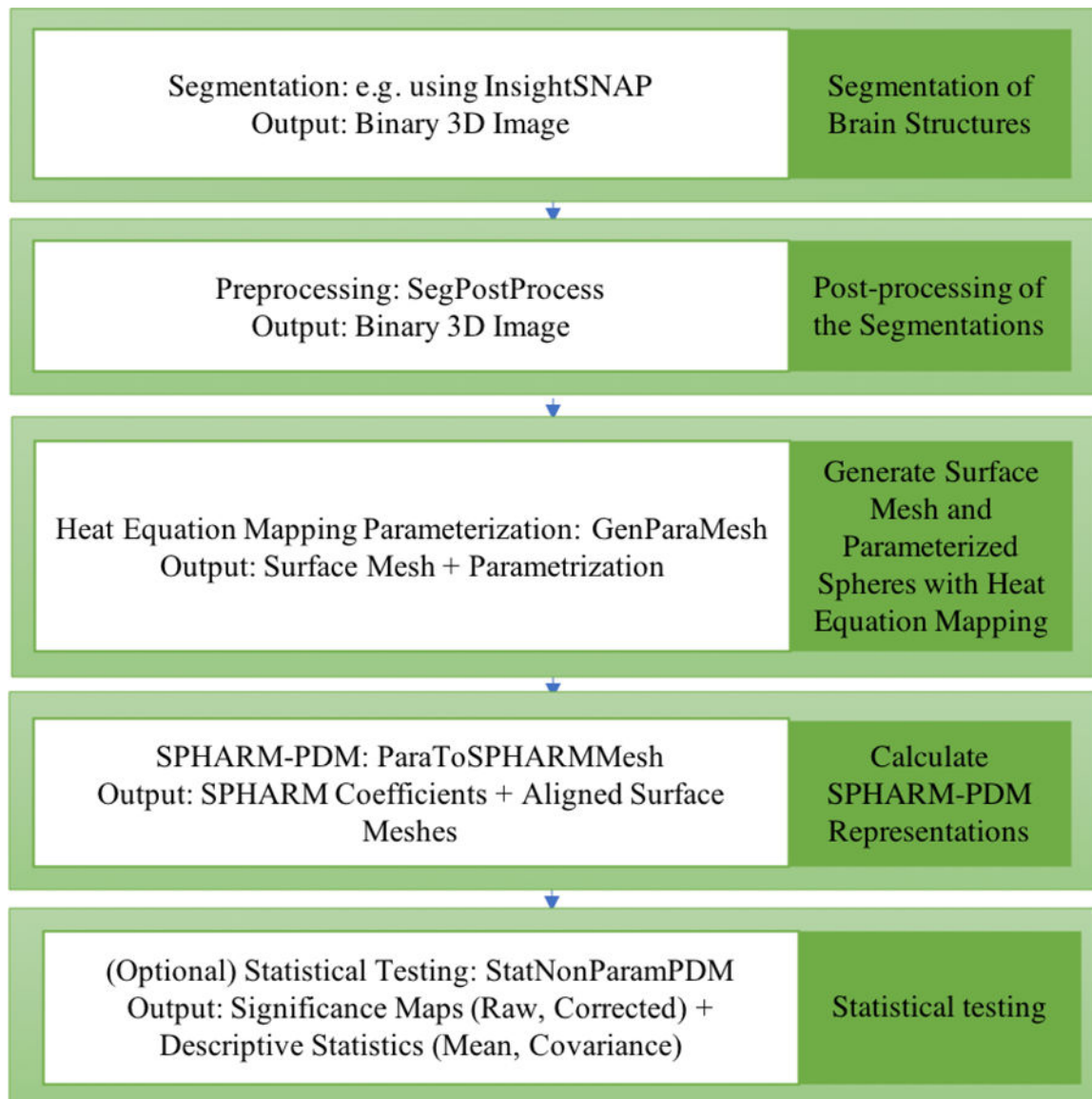
Figure 1.
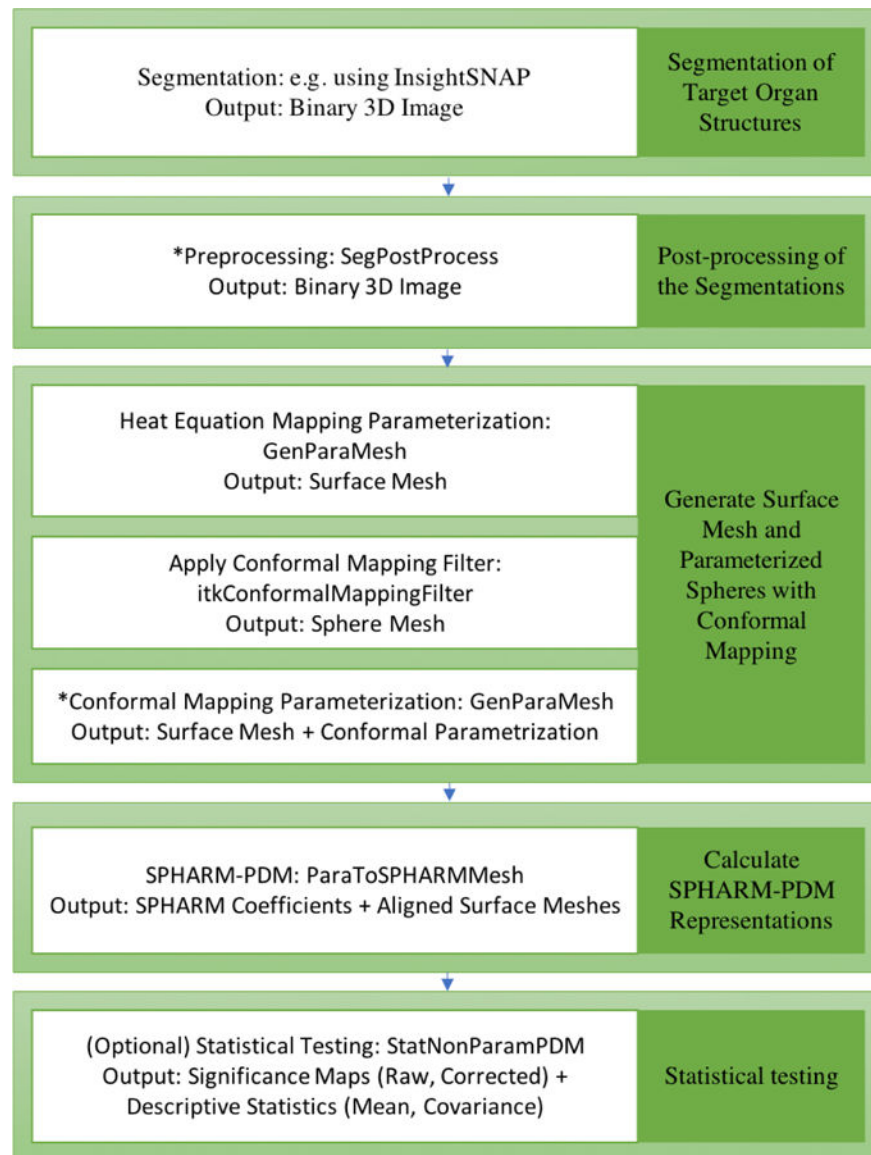The original SPHARM-PDM shape analysis pipeline

Figure 2.
SPHARM-PDM shape analysis framework utilizing conformal flattening filter as the initial parametrization method

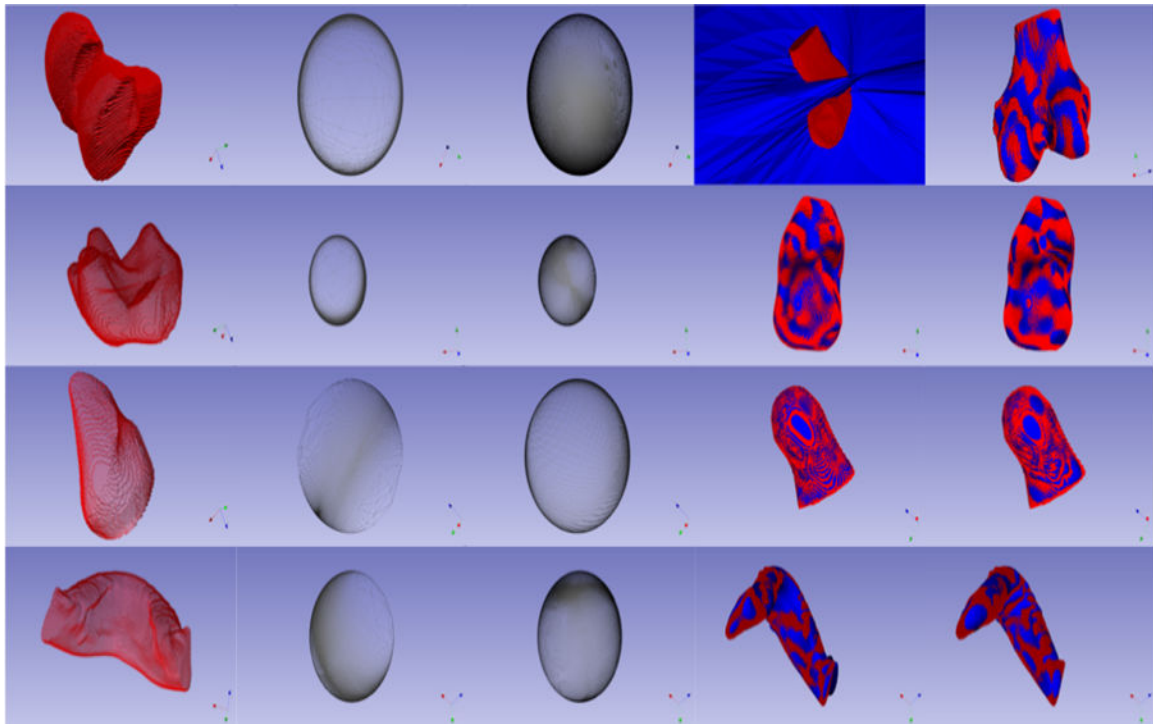*: The output of the Preprocessing step is used as input in Conformal Mapping Parametrization step

Figure 3.
From top to bottom: 3D view of the structures of (1) the femur, (2) the molar, (3) the condyle and (4) the mandible at different stages of SPHARM-PDM pipeline. From left to right: (a) the original segmentation; initial parametrized sphere with (b) heat equation mapping or (c) conformal mapping based initialization parametrization; surface mesh overlay of the original surface mesh (red) and the SPHARM surface mesh with (d) heat equation mapping or (e) conformal mapping based initialization with iteration 500 (blue)
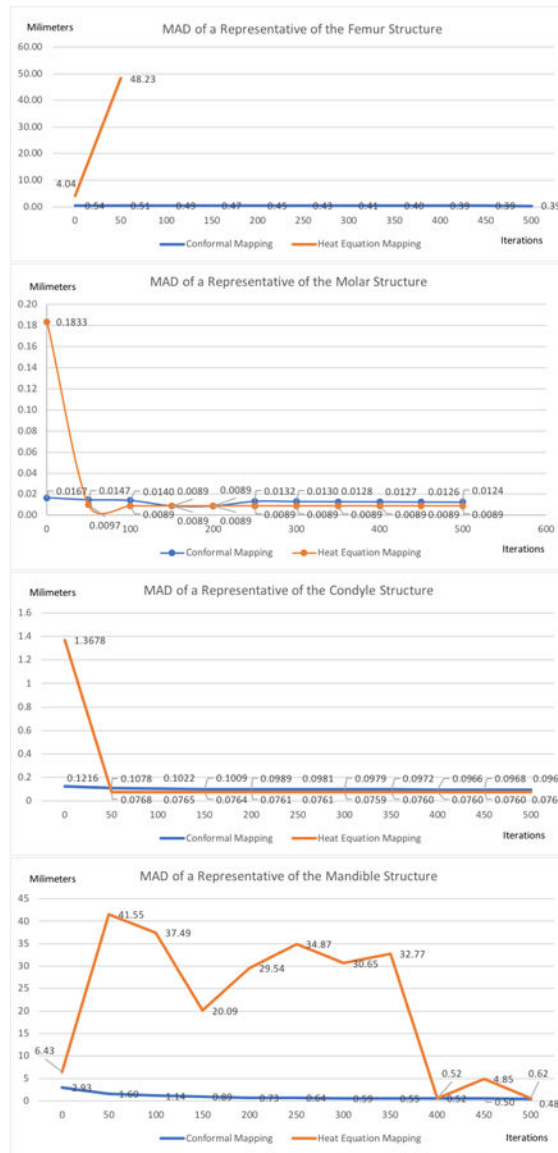
Figure 4.
From top to bottom: Mean Absolute Distance of (1) the femur, (2) the molar, (3) the condyle, and (4) the mandible structure

Figure 5.
From top to bottom: Coefficient of Variation of Cell Area of (1) the femur, (2) the molar, (3) the condyle, and (4) the mandible structure