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SlicerSALT: Shape AnaLysis Toolbox

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Abstract

SlicerSALT is an open-source platform for disseminating state-of-the-art methods for performing statistical shape analysis. These methods are developed as 3D Slicer extensions to take advantage of its powerful underlying libraries. SlicerSALT itself is a heavily customized 3D Slicer package that is designed to be easy to use for shape analysis researchers. The packaged methods include powerful techniques for creating and visualizing shape representations as well as performing various types of analysis.

Keywords

Shape analysis; Statistics; Software

1 Introduction

Statistical shape analysis is an active area of research in the medical imaging community with many groups working on novel methods of representing and analyzing the shape of anatomical structures. Unfortunately, due to the sheer number of data formats and software packages created in a variety of programming languages, it can be difficult to pull together pipelines making use of methods created by different groups. In addition, much of the available software is written only to be used by other computer scientists, making it difficult for the wider medical community to make use of these powerful analysis techniques.

SlicerSALT [3] is an open-source platform for the dissemination of state-of-the-art methods for performing statistical shape analysis. The goal of SlicerSALT is to provide an easy to use end-to-end solution for performing statistical shape analysis of anatomical objects. As shown in figure 1, SlicerSALT provides methods for importing segmentation data in several formats, performing a variety of pre-processing and quality control tasks, deriving shape represtations with good correspondences from these segmentations, and performing statistical analysis using a variety of powerful techniques. SlicerSALT is a heavily customized version of 3D Slicer[1, 5] that is designed to streamline the importing and

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running of the included methods to make it easy for even non-experts to perform powerful shape analysis studies as well as remove the non-relevant modules of 3D Slicer to avoid confusion.

SlicerSALT is built as a series of extensions to 3D Slicer. This enables SlicerSALT to leverage the power of Slicer's underlying toolkits as well as its large and active developer community. It also makes contributing to SlicerSALT easy, as additional functions can be created as indepdendent Slicer extensions and incorporated into SlicerSALT's build system. This is combined with a strong software infrastructure including automatic building, unit testing, and dashboards. The end result is a robust software package that is easy to both extend and maintain as new methodology continues to be developed.

2 Available Extensions

This section describes the extensions developed as part of SlicerSALT. These are available as part of the SlicerSALT distribution as well as individually in 3D Slicer via the Slicer Extension Manager. Because the methods are packaged as 3D Slicer modules, non-expert users are able to run them through the SlicerSALT UI while advanced users could also run them from the command line.

2.1 Home

SlicerSALT starts by default on the home module shown in figure 2. This module describes a basic workflow from data loading through the creation and analysis of the target shapes. It also features links to jump directly to each module. This module is designed to guide new and inexperienced users through a typical workflow.

2.2 Data Importer

This extension is designed to make it easy for the user to import data in multiple different formats and perform quick visualizations and quality control prior to analysis. Data can be imported as either binary label maps or surfaces. The Data Importer also has special logic to deal with importing data output from popular segmentation applications such as Autoseg [14], FSL [9], and FreeSurfer [6]. Figure 3 shows the Data Importer interface with an example dataset.

2.3 SPHARM-PDM

SPHARM-PDM [13] is a tool that uses spherical harmonics to compute point distribution models (PDMs) using a parametric boundary description for use in shape analysis. The SPHARM-PDM extension takes one or more binary images as input. The binary images are first processed to ensure spherical topology, then converted to surface meshes using marching cubes. The spherical parameterization was computed from the surface meshes using area-preserving, distortionminimizing spherical mapping. The SPHARM description was then computed from the mesh and its spherical parameterization. Using icosahedron subdivision on the spharm description, a set number of points is sampled to create correspondent PDMs. These resulting PDMs have been shown to provide a strong foundation for a variety of statistical studies of the shape of anatomical objects, particularly

in the brain. SPHARM-PDM provides a basis on which many of the other included methods operate.

Also included is ShapePopulationViewer [2], shown in figure 4, for visualizing the resulting PDMs and their parameterizations to ensure good correspondence.

2.4 Group-wise Registration For Shape Correspondence (GROUPS)

GROUPS[11] is a method for improving correspondence of a population of PDMs, such as those resulting from SPHARM-PDM, using a group-wise registration and optimization strategy. This optimization works by minimizing the entropy of the distribution of curvedness of the surface at corresponding point locations, ensuring that corresponding points are in positions with similar geometric features across the population. This method is particularly helpful in improving correspondences on objects with complicated geometry where the standard SPHARM-PDM correspondences may prove inadequate.

2.5 Multivariate Functional Shape Data Analysis (MFSDA)

MFSDA[10] packages a powerful set of advanced statistical tools that can efficiently correlate shape data with clinical and demographic variables such as age, gender, and genetic markers. Users can load in sets of additional data corresponding to each input shape and determine whether there is a statistically significant morphological difference caused by some combination of the covariates.

2.6 Shape Regression

This extension allows for modeling the continuous evolution of anatomical objects via geodesic regression and creates a 4D shape model [7]. There are two separate modules as part of this extension: RegressionComputation for computing the regression and RegressionVisualization for visualizing the resulting shape model. A visualization of a regression on a set of brain data is shown in figure 5.

2.7 Shape Evaluator

The Shape Evaluator module is designed to take in a set of corresponding PDMs such as those generated by SPHARM-PDM or GROUPS and use principal component analysis (PCA) to compute a mean shape and its major modes of variation. The user can then visualize the mean shape as well as how moving along each principal component changes the shape of the object. This module allows for a quantitative comparison of the generated shape space to those created by other methods by examining the percent of variation explained by the modes of variation as well as computing generalization, specificity, and compactness measures on the distribution.

2.8 Skeletal Representations (S-reps)

This module packages methods for creating and visualizing skeletal representations, known as s-reps, of anatomical objects. S-reps are powerful shape representations that have been shown to have beneficial properties compared to pure boundary models [12] in applications such as classification and segmentation.

Currently only s-rep visualization is included, but there will soon be support for fitting sreps to objects and eventually for estimating probability distributions and performing classification. These statistical methods are designed to work on s-reps as data from a non-Eucliean manifold and will be applicable to other representations such as PDMs as well. An example of an s-rep loaded into SlicerSALT is shown in figure 6.

3 Software Infrastructure

SlicerSALT is set up with a modern open-source software infrastructure. In addition to information about the individual methods available in the package, the SlicerSALT website [3] has a variety of information on using and contributing to SlicerSALT. The code for SlicerSALT itself is hosted on GitHub [4] and includes information on how to build the software locally as well as guidelines for contributing to SlicerSALT.

The main SlicerSALT repository has code for pulling in and building a lightweight version of 3D Slicer and its dependencies as well as links to the external repositories where the code for the various included methods is stored. During the building of SlicerSALT, the code for each method is checked out from its own Git repository and built as a 3D Slicer extension. During packaging these extensions are then pulled in along with the customized version of 3D Slicer to create the final SlicerSALT package.

SlicerSALT is built nightly and the results of these builds are uploaded to a dashboard to track and diagnose problems with building Slicer or any of the individual extensions. Additionally each extension has its own set of tests to ensure they are functioning correctly as well as documentation and tutorials.

4 Discussion

The first release of SlicerSALT packages a number of powerful tools for performing statistical shape analysis with an easy-to-use interface. It is designed as a platform for disseminating these methods to the broader medical community.

SlicerSALT development is ongoing. Several of the methods described here are still under active development and we will continue to improve the existing modules as well as introduce new methods for representing and analyzing shape.

In particular, there is ongoing work [8] to establish correspondence between shapes with complex geometry, including those with non-spherical toplogy, that cause traditional methods such as SPHARM-PDM to fail. This work establishes correspondences by using a diffeomorphic registration technique to deform a template shape representation into each member of a population.

SlicerSALT is open to contributions of other shape representation and analysis methods. New methods can be contributed by packaging them as 3D Slicer extensions. Detailed contribution guidelines can be found in the SlicerSALT GitHub repository.

Future work will also include user evaluations and usability testing of the software to ensure that it is easily usable by both expert and non-expert users.

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Fig. 1. The SlicerSALT workflow





The SlicerSALT home module with direct links to the available extensions.





The Data Importer module after loading lateral ventricle segmentations.



Fig. 4.

ShapePopulationViewer visualizing a set of brain segmentations



Fig. 5.

The RegressionVisualization module showing the result of a regression computation on a set of brain segmentations.



Fig. 6.

An example skeletal model (s-rep) loaded into SlicerSALT.