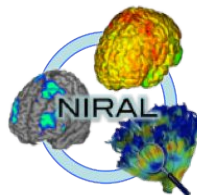




Slicer Shape Analysis ToolBox: SlicerSALT



THE UNIVERSITY
of NORTH CAROLINA
at CHAPEL HILL



NYU

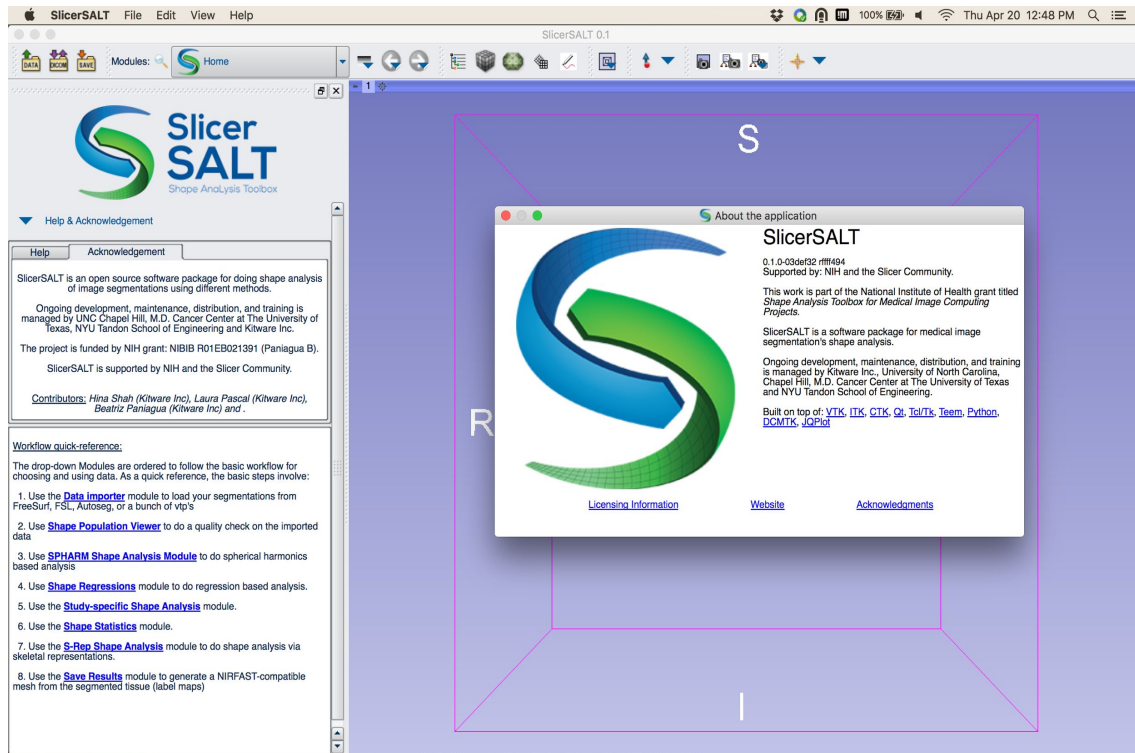
THE UNIVERSITY OF TEXAS
MD Anderson
~~Cancer~~ Center

Slicer Shape AnaLysis Toolbox



❖ Description: open-source shape analysis SPT (Slicer Project Template) which support 6 different analysis methodologies

❖ Purpose: precisely locate **shape changes** in biomedical imaging studies



SlicerSALT's Maintenance

Software Infrastructure

Creation of the SlicerSALT packages nightly for all the platforms using 2 scripts:

1. Shell Script
2. Cmake Script

```
#####
# OS :
# Hardware:
# GPU :
#####
# WARNING - The specific version and processor type of this machine should be reported
# in the header above. Indeed, this file will be sent to the dashboard as a HOSTS file.
#
# On linux, you could run:
# 'uname -a' and 'cat /etc/*-release' to obtain the OS name.
# 'lscpu' to obtain hardware details.
# 'lshw -l grep OpenCL' to obtain GPU details.
#####
cmake_minimum_required(VERSION 3.8)

# You could invoke the script with the following syntax:
# ctest -S /path/to/scripts/ctests.cmake -C <CTEST_BUILD_CONFIGURATION> -v
# Note that '-C <CTEST_BUILD_CONFIGURATION>' is mandatory on windows

# Macro allowing to set a variable to its default value only if not already defined
macro(setDefaultIfNotDefined var defaultvalue)
    if(NOT DEFINED ${var})
        set(${var} "${defaultvalue}")
    endif()
endmacro()

set(CTEST_PROJECT_NAME SlicerSALT)

#
# Repository
#
setOnlyIfNotDefined(CTEST_REPOSITORY git@github.com:Kitware/SlicerSALT.git)
setOnlyIfNotDefined(CTEST_TAG master)

#
# Type of dashboard:
# Experimental:
# - run_ctest() macro will be called "ONE" time
# - binary directory will "NOT" be cleaned
# Continuous:
# - run_ctest() macro will be called EVERY 5 minutes ...
# - binary directory will "NOT" be cleaned
```

Upload of the SlicerSALT packages in the [Girder instance](#):



Kitware Data

Collections

Users

Groups

NIH Shape Analysis Toolbox

This project will develop a comprehensive software that will allow biomedical scientists to precisely locate shape changes and allow researchers to find shape changes with higher statistical power. Altogether this constitutes a crucial resource


NIH Shape Analysis Toolbox / SlicerSALT-Public-Packages

- ☐ SlicerSALT-0.1.0-c988d2d-linux-amd64.tar.gz
- ☐ SlicerSALT-0.1.0-c988d2d-macosx-amd64.dmg
- ☐ SlicerSALT-0.1.0-c988d2d-win-amd64.exe

Metadata

Automatic tests monitored using an online [dashboard](#):





SlicerSALT

Dashboard
Calendar
Previous
Current
Project

No file changed as of Wednesday, January 03 2018 - 01:00 UTC

6 hours ago: 125 warnings introduced on Darwin clang 700.0.31-440a-CF4.8.7-Release-master

7 hours ago: 1000 warnings introduced on Windows VS2013-640a-CF4.8.7-Release-master

11 hours ago: 100 warnings introduced on Linux GCC-4.8.5-640a-CF4.8.7-Release-master

1 days ago: 125 warnings introduced on Darwin clang 700.0.31-440a-CF4.8.7-Release-master

6 days ago: 100 warnings introduced on Linux GCC-4.8.5-640a-CF4.8.7-Release-master

See full feed 3 Data

Nightly		Update	Configure	Build	Test			Start Time		
Site	Build Name	Revision	Error	Warn	Error	Warn	Not Run	Fail	Pass	Start Time
Macosx.kitware	Windows-VS2013-640a-CF4.8.7-Release-master	719d1c1	0	0	0	100%	0	0	0	11 hours ago
Platform.kitware	Linux-GCC-4.8.5-640a-CF4.8.7-Release-master	719d1c1	0	0	0	100%	0	0	0	14 hours ago
Macosx.kitware	Darwin-clang 700.0.31-440a-CF4.8.7-Release-master	719d1c1	0	0	0	100%	0	0	0	9 hours ago

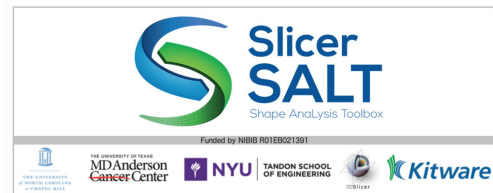


Support Infrastructure

Website:

<http://salt.slicer.org/>

SlicerSALT



What can I do using SlicerSALT?

SlicerSALT is the dissemination vehicle of powerful shape analysis methodology based on 3D Slicer open-source software.

- Compute Point Distributed Models (PDM) using Spherical Harmonic Representation (SPHARM-PDM)
- Run 4D regression in a collection of 3D PDMs associated to a linear variable (i.e. age)
- Perform correspondence optimization using study-wise shape analysis
- Fit skeletal representations (s-reps) to a collection of binary volumes
- Compute image-based correspondence in binary volumes of different topologies
- Use advanced shape statistics for scientific hypothesis testing
- Visualize, edit, and register multimodal data using 3D Slicer tools
- Access all functionality through the graphical user interface
- Perform command line batch processing
- Extended and improved shape analysis functionality is coming soon in Slicer...

Forum:

<https://discourse.slicer.org/c/community/slicer-salt>



3DSlicer

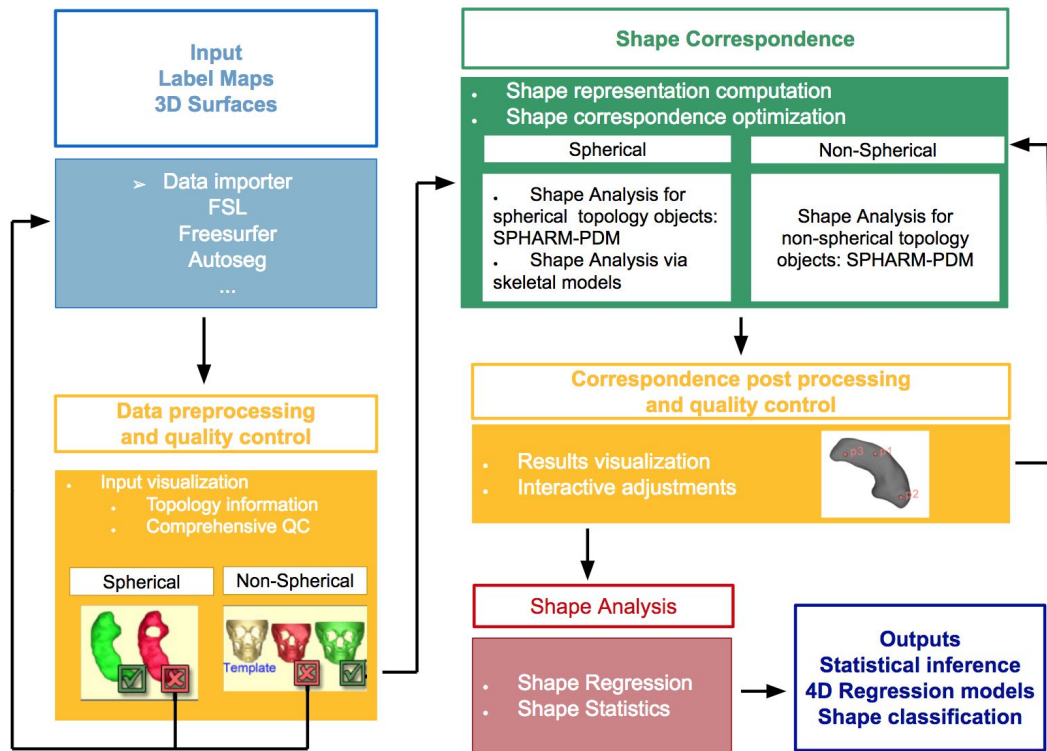
Community	SlicerSALT	Latest	New	Unread	Top	New Topic	
Topic	Users	Replies	Views	Activity			
Shape analysis by SPHARM-PDM		4	54	6d			
Bad registration of Freesurfer segmentation of the hippocampus		2	79	Nov '17			
Group analysis with SPHARM-PDM spharm-pdm		8	243	Oct '17			
Proceed to surfstat		14	138	Oct '17			
Odd looking hippocampus		3	68	Oct '17			
No groups were found		1	58	Oct '17			

Presence in the
Slicer landing page:



Methods

SlicerSALT workflow



Shape Correspondence Methods

SPHARM-PDM Extension

Description: Creation of a corresponding model population only applicable on spherical topology objects (condyle, hippocampus, or caudate, ...) where each generated densely 3D model will have the same number of points placed at geometrically corresponding positions.

Method: The binary segmentations or 3D surfaces inputs are converted into corresponding spherical harmonic descriptions (SPHARM) and then are sampled into triangulated surfaces (PDM).

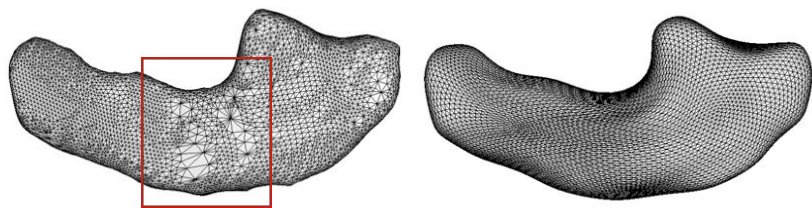


Figure a. Creation of 3D surfaces without (left) and with (right) the use of SPHARM-PDM extension

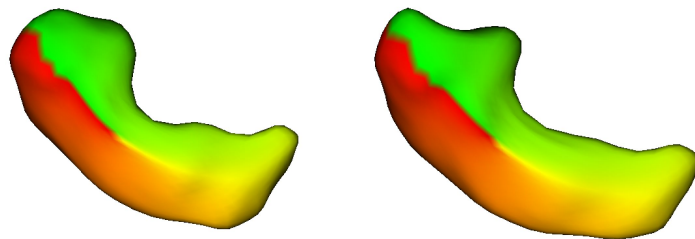


Figure b. Results of SPHARM-PDM extension: Surfaces colored by vertex index for two different hippocampus

Skeletal Models Method

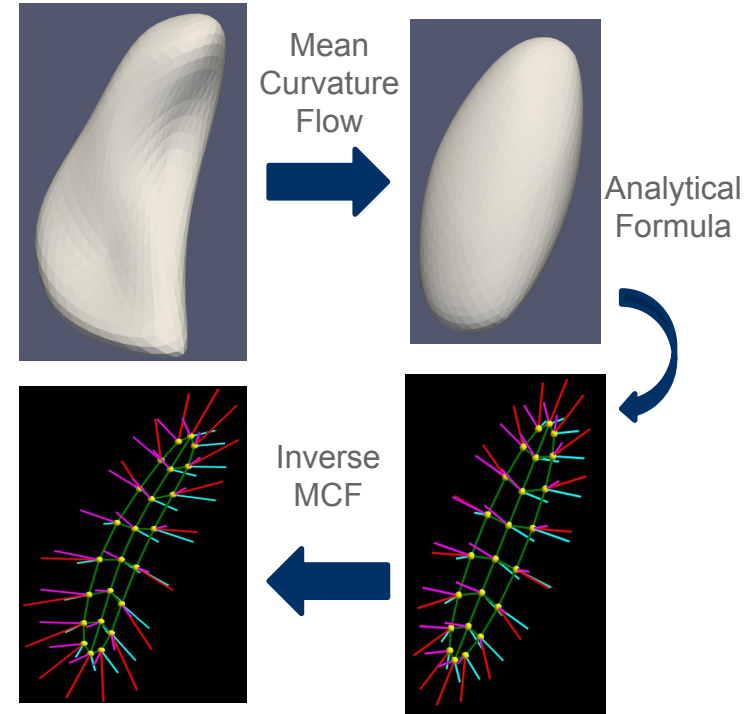
Description: The skeletal shape assessment will allow a more intuitive interpretation of the detected morphometric effects by separating the ones due to local deformations from those due to local size differences

Method: Automatically generate a skeletal representation (s-rep) that has similar local geometrical measure as the target surface:

Step 1: Apply Mean Curvature Flow (Iterate until the deformed surface is roughly ellipsoidal)

Step 2: Compute analytical the skeletal representation that fit the approximate ellipsoid

Step 3 : Apply inverse MCF to the skeletal representation

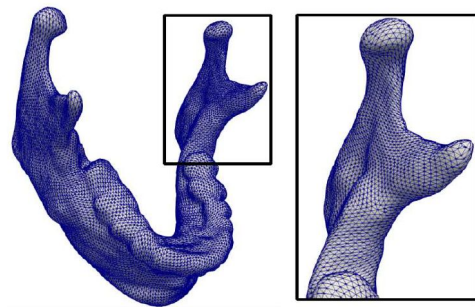
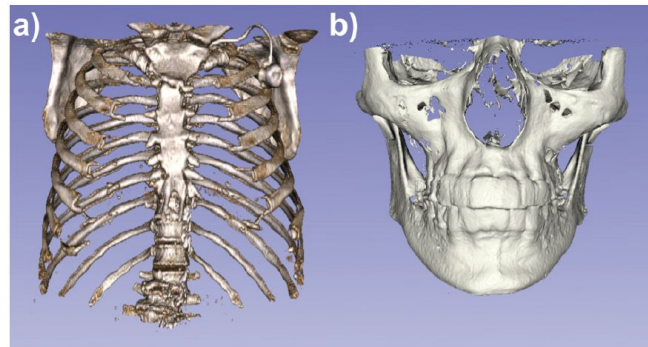


Estimation of shape correspondence for population of objects with complex topology

Limitation of SPHARM-PDM: The method is only applicable on spherical topology objects which excludes a great number of anatomical structures (vertebrae, pelvibones or skulls)

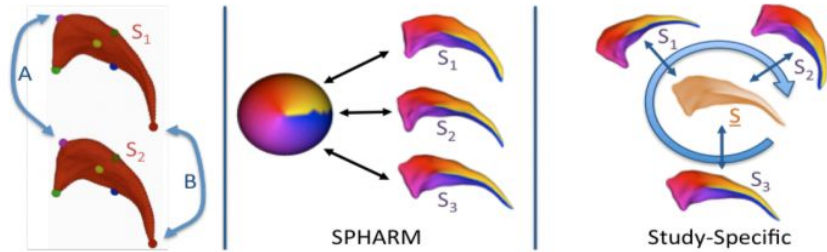
Description: Research of a method to estimate a corresponding model population of non-spherical topology objects where each generated model will have the same numbers of points at corresponding positions

Example: Existing shape analysis methods such as SPHARM-PDM or s-reps have not been able to properly densely represent mandibular shapes, due to its highly concave and thin shape.



Study-specific shape correspondence: Groups-wise Registration (Groups)

Description: The study-specific shape correspondence will accurate the correspondences of SPHARM-PDM or skeletal models method by minimizing the entropy of the distribution of the location and curvedness (a geometric measure of curvature) of corresponding surface locations.



Left: Few anatomical locations allow for precise correspondence, as biological structures present mainly non-sharp features.

Middle: Mapping-based on SPHARM-PDM method

Right: Optimization based study-specific mapping of data into a common average space S.

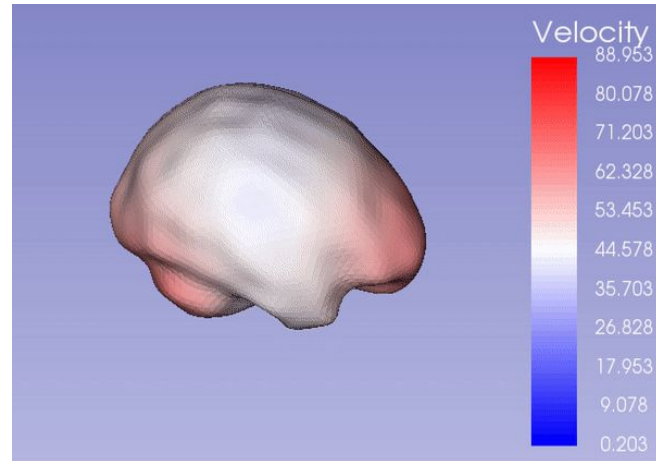
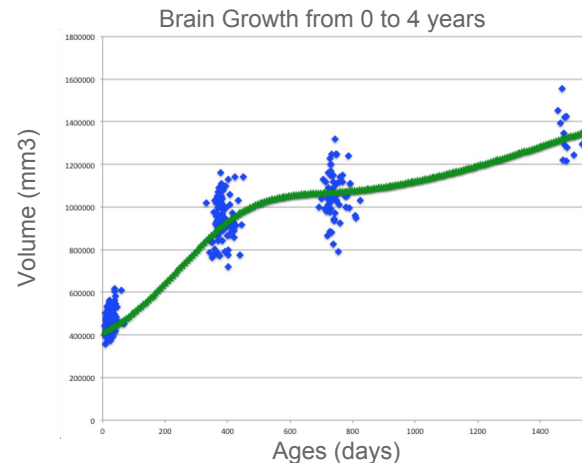
Shape Analysis Methods

Shape Regression Extension

Description: Run 4D regression in a collection of 3D shape inputs associated to a linear variable (i.e. ages)

Modules:

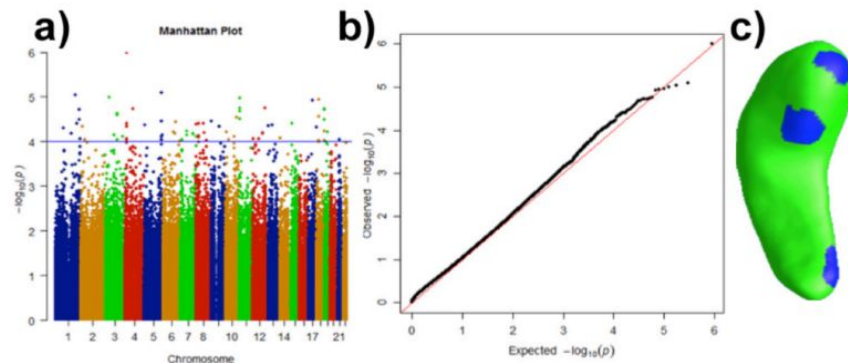
- *RegressionComputation*: compute time-regressed shape effects for objects of any topology
- *RegressionVisualization*:
 - Plot the time-regressed shape volume according to the linear variable
 - Visualize the sequence of the time-regressed shapes generated



Shape Statistics Method: Multivariate Functional Shape Data Analysis (MFSDA)

Description: Efficiently correlate shape data with clinical and demographic variables (such as age, gender or genetic markers) in a population of cases

- ❖ Compute high dimensional correlations between morphological shape differences and clinical/demographic variables
- ❖ Associate the morphological shape differences with the responsible clinical/demographic variables
- ❖ Graphically display on the shape surface the morphological shape difference corresponding to the selected clinical/demographic variable



Preliminary results to correlate shape with genetic markers

- a) Manhattan plot
- b) QQ plot
- c) Significant clusters in the hippocampus in blue, corresponding to the top SNP

Thank you for your attention

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