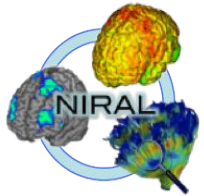
Slicer Shape AnaLysis ToolBox: SlicerSALT

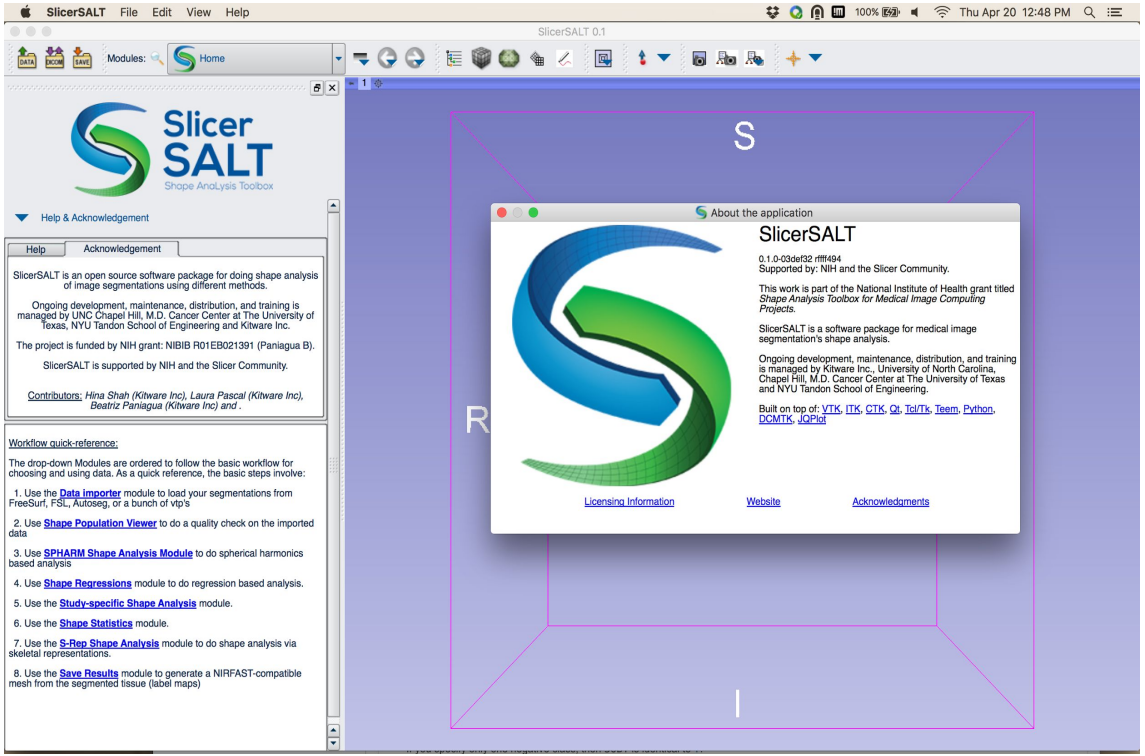
THE UNIVERSITY of NORTH CAROLINA at CHAPEL HILL



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

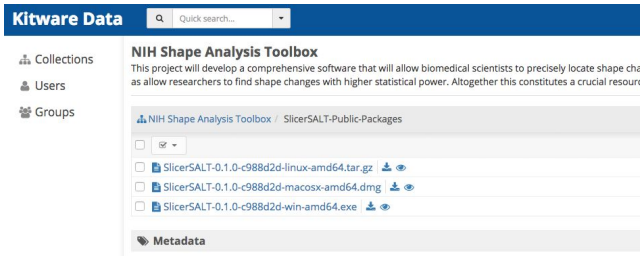
Creation of the SlicerSALT packages nightly for all the platforms using 2 scripts:

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 send to the dashboard as a NOTE file.
#
# On linux, you could run:
#     'uname -o' and 'cat /etc/*-release' to obtain the OS name.
#     'uname -mpi' to obtain hardware details.
#     'glxinfo | grep OpenGL' to obtain GPU details.
##########################################################################

cmake_minimum_required(VERSION 3.0)

# You could invoke the script with the following syntax:
#  ctest -S /path/to/<scriptname>.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(setOnlyIfNotDefined var defaultvalue)
  if(NOT DEFINED ${var})
    set(${var} "${defaultvalue}")
  endif()
endmacro()

set(CTEST_PROJECT_NAME SlicerSALT)

#-----------------------------------------------------------------------------
# Repository
#-----------------------------------------------------------------------------
setOnlyIfNotDefined(GIT_REPOSITORY git@github.com:Kitware/SlicerSALT.git)
setOnlyIfNotDefined(GIT_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
```

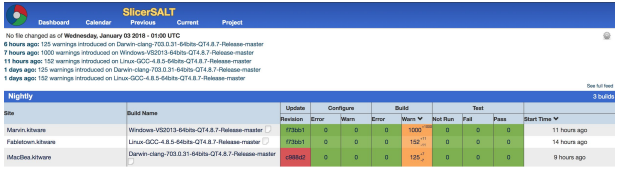
Upload of the SlicerSALT packages in the Girder instance:

Girder



Automatic tests monitored using an online dashboard:

CDash



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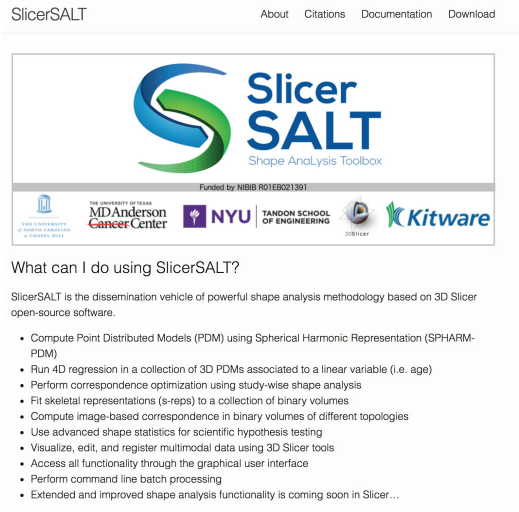
Support Infrastructure

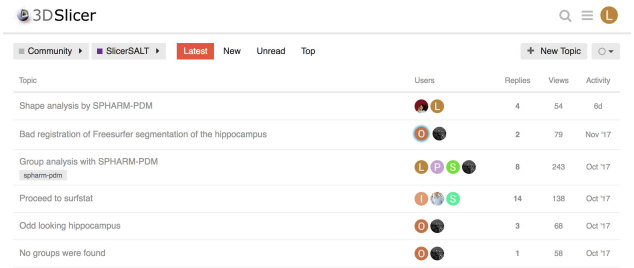
Website:

http://salt.slicer.org/

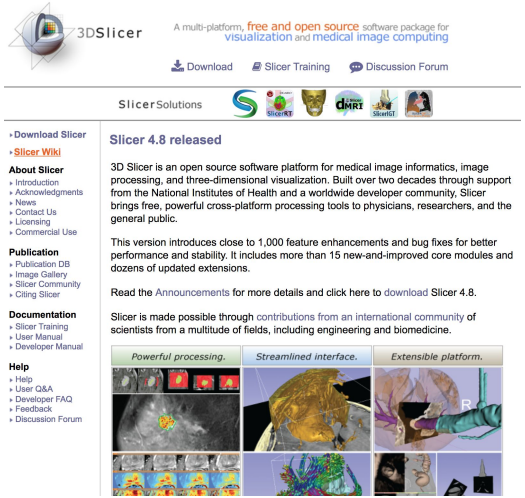


Forum:

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



Presence in the Slicer landing page:



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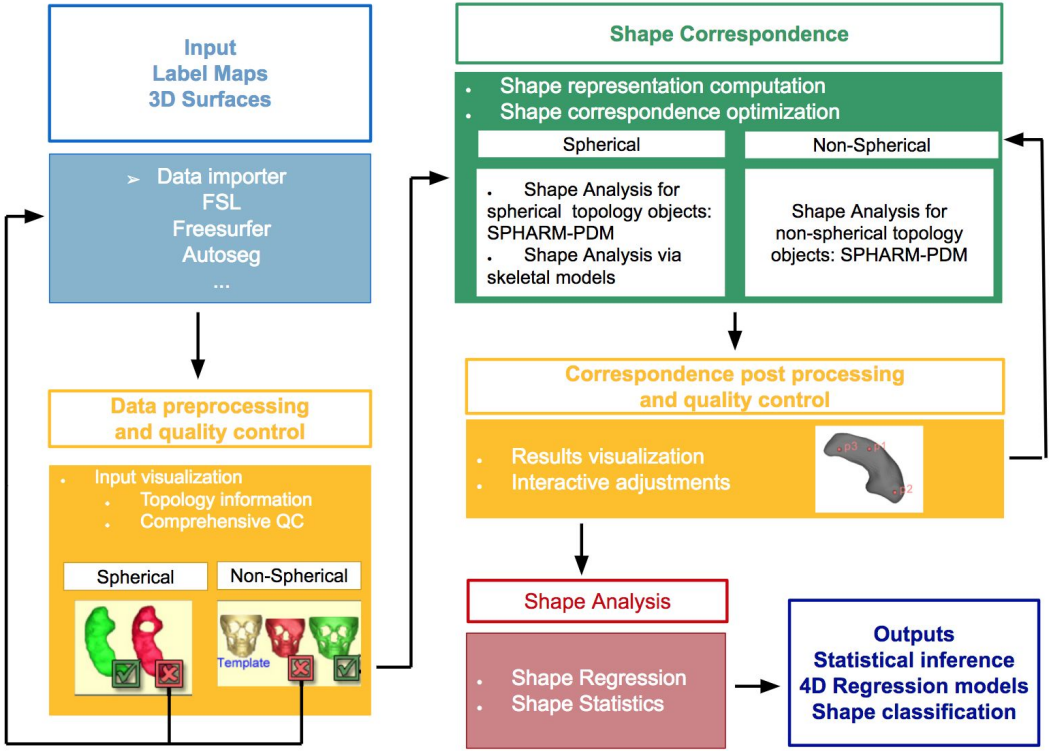
Methods

SlicerSALT workflow



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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).

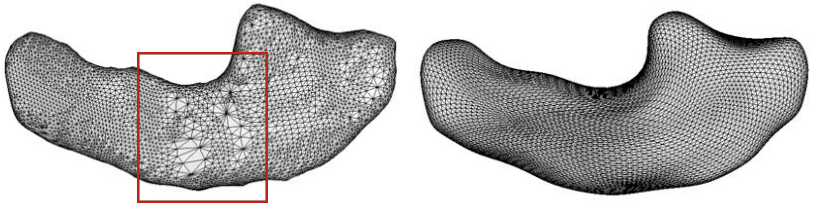


Figure a. Creation of 3D surfaces without (left) and with (right) the use of SPHARM-PDM extension

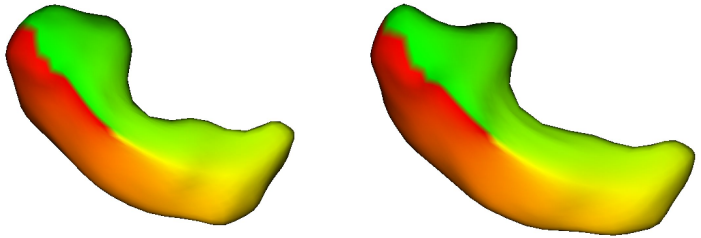


Figure b. Results of SPHARM-PDM extension: Surfaces colored by vertex index for two different hippocampus

Contact: beatriz.paniagua@kitware.com laura.pascal@kitware.com

Skeletal Models Method

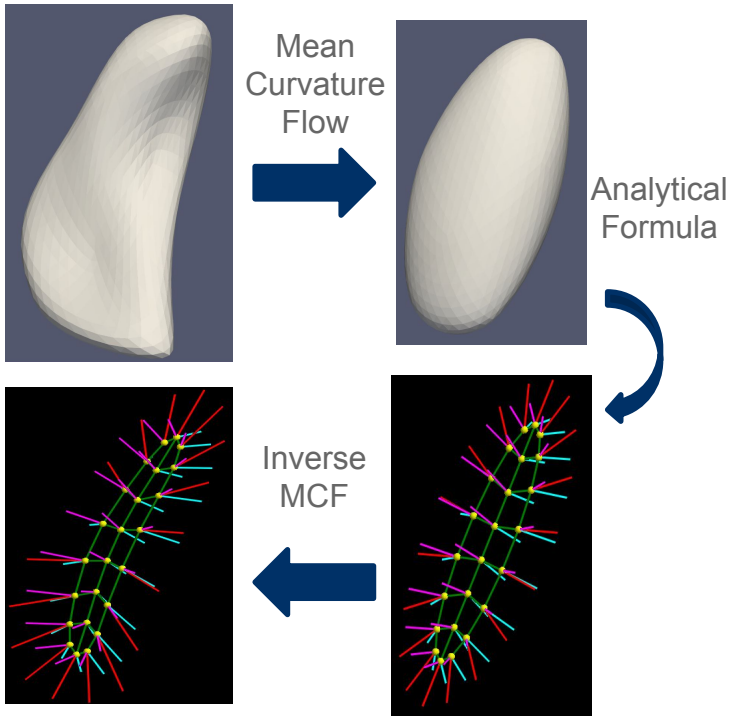
Description: The skeletal shape assessment will allow a more intuitive interpretation of the detected morphometric effects by separating the ones due to local deformations from those due to local size differences

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



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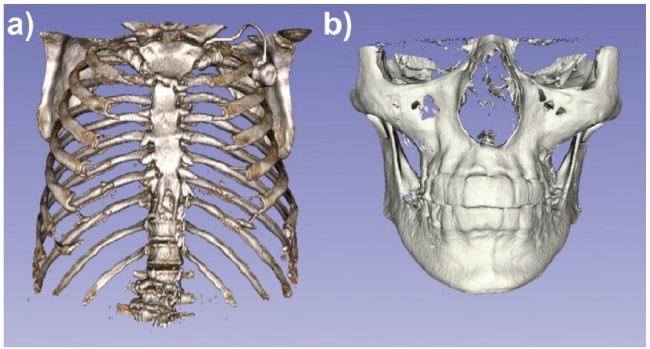
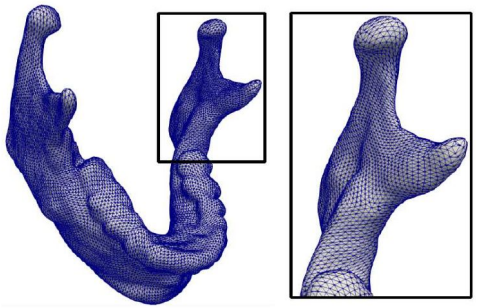
Estimation of shape correspondence for population of objects with complex topology



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

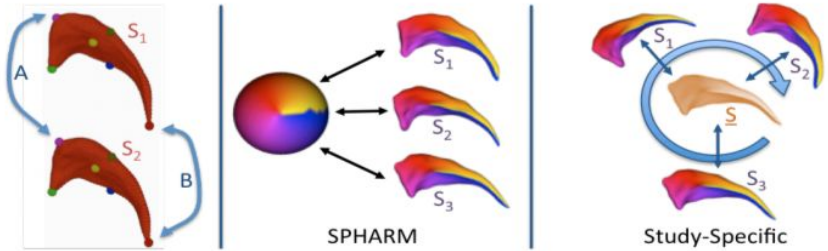
Description: Research of a method to estimate a corresponding model population of non-spherical topology objects where each generated model will have the same numbers of points at corresponding positions

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.

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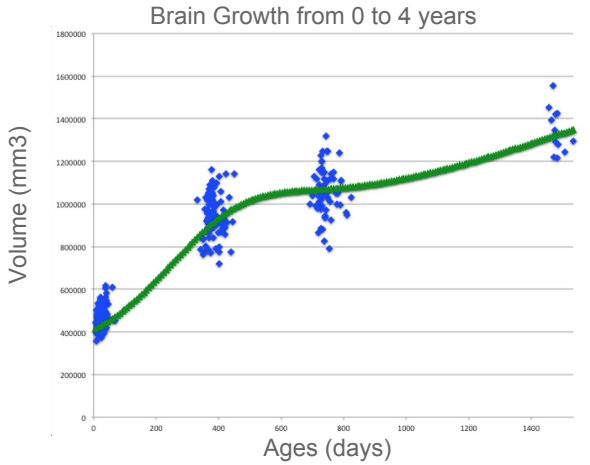
Shape Analysis Methods

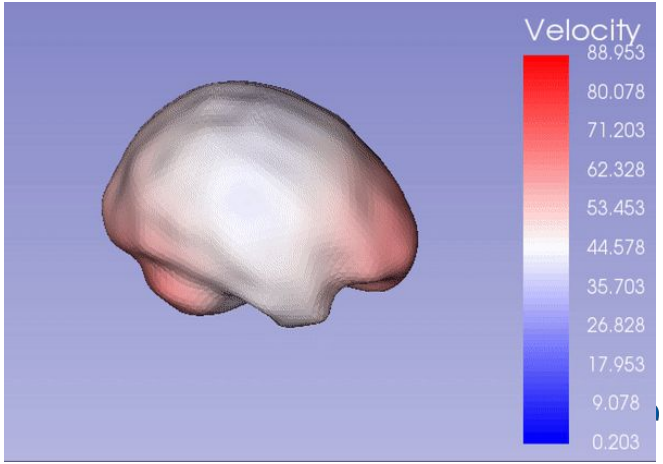
Shape Regression Extension

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



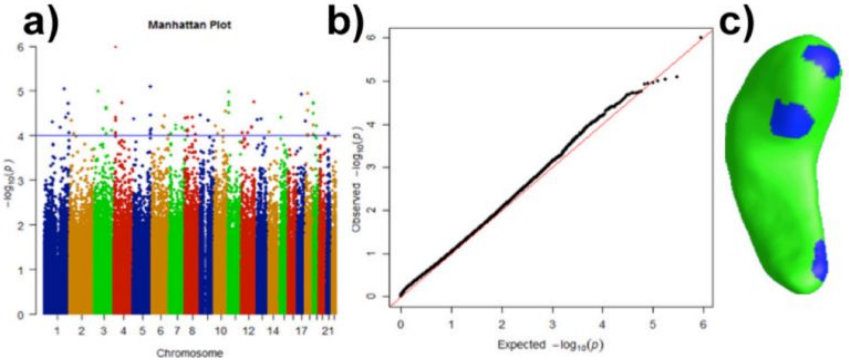


Contact: jfishbaugh@gmail.com laura.pascal@kitware.com beatriz.paniagua@kitware.com

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 responsable 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

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Thank you for your attention

Laura Pascal: laura.pascal@kitware.com
Beatriz Paniagua: beatriz.paniagua@kitware.com

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