



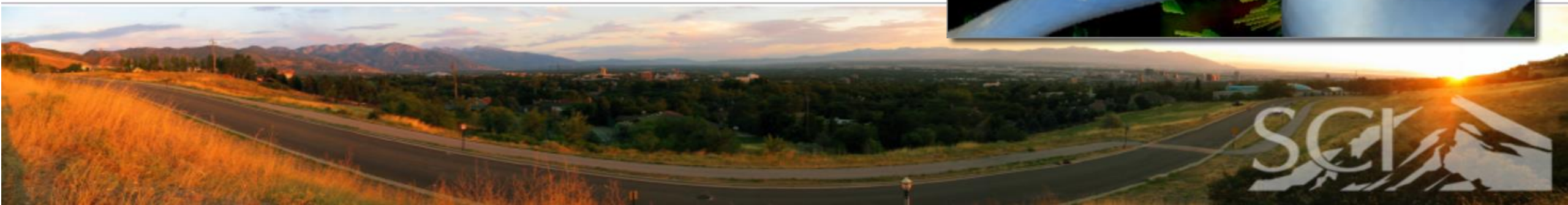
THE  
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OF UTAH

# Statistical Shape Analysis

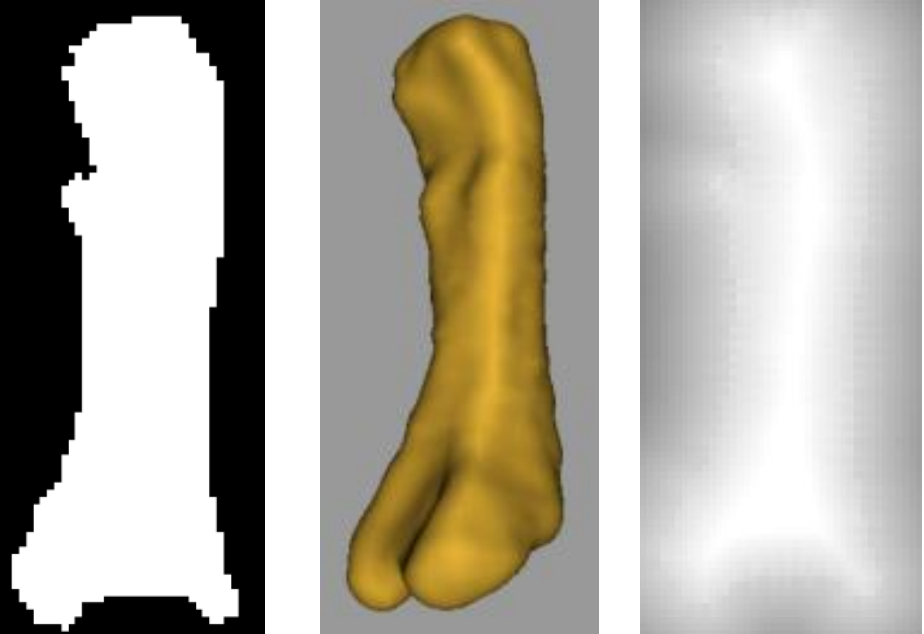
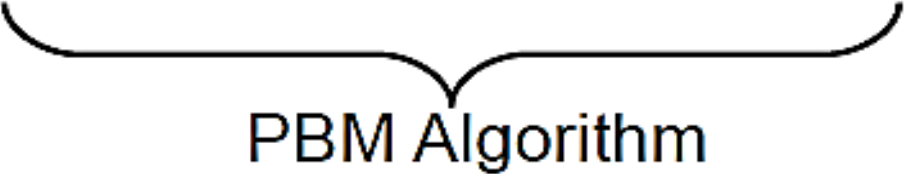
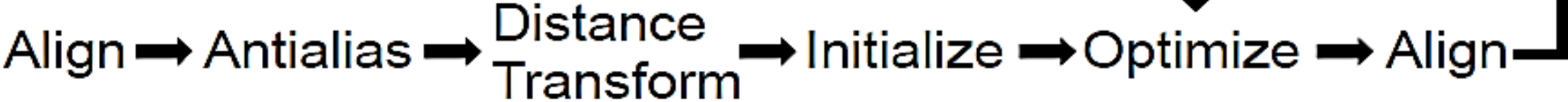
## Tutorial

Shireen Elhabian, Prateep Mukherjee  
and Ross Whitaker

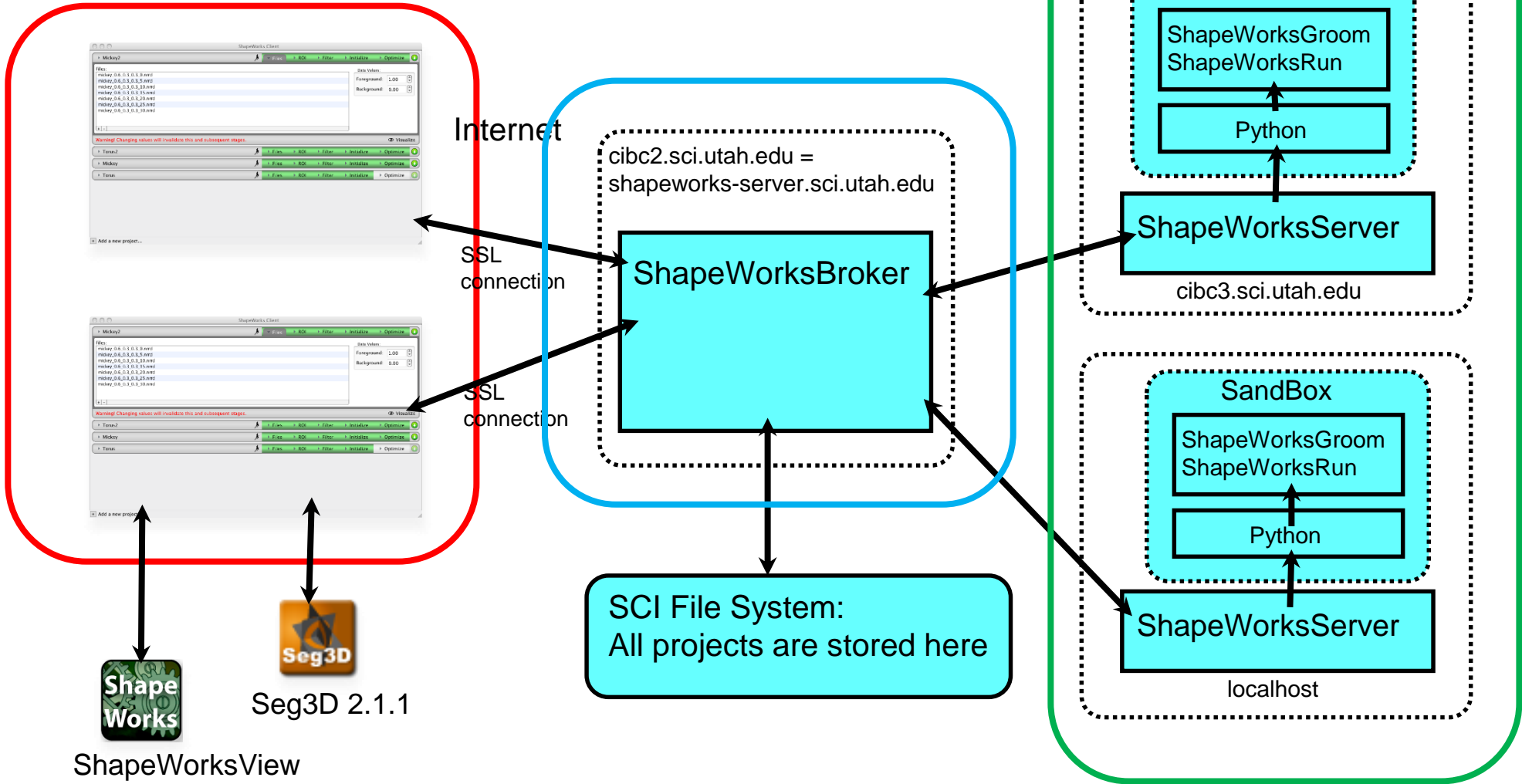
Saturday, January 4<sup>th</sup>, 2014



# Correspondence Pipeline



# Main Components



ShapeWorks Client

ShapeWorks Broker

ShapeWorks Server

# Let's Get Started

- Copy all the software given in the USB stick at a convenient location in your computer
- Click on start menu and type 'cmd.exe' to start a command prompt
- First, start ShapeWorks Broker

```
ShapeWorksBroker.exe broker_address=localhost \  
broker_rootdir=c:\shapeworks_run
```

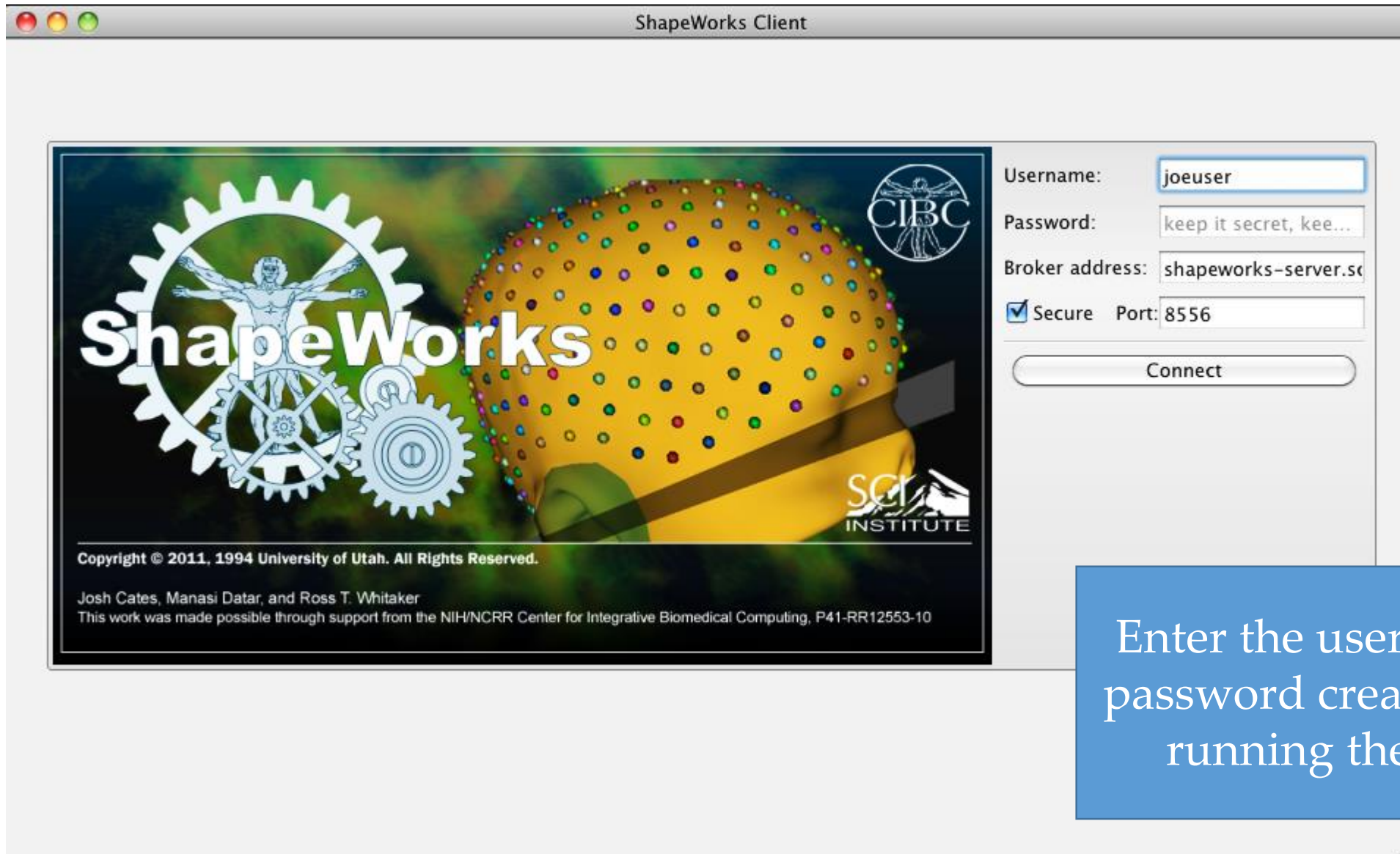
- Make note of password generated. It will be required to start ShapeWorks Client
- Click on start and start another command prompt
- Start ShapeWorks Server

```
ShapeWorksServer.exe broker_address=localhost \  
shapeworks_dir=c:\Shapeworks
```

\* Refer to lab document(Section 2) for more instructions

# Connecting to a Server

ShapeWorks Client



The image shows a screenshot of a software window titled "ShapeWorks Client". The window contains a splash screen on the left and a login form on the right. The splash screen features the "ShapeWorks" logo, a Vitruvian Man figure surrounded by gears, and a 3D model of a yellow brain with colored dots. It includes the CIBC logo and SCI INSTITUTE logo. Copyright information for the University of Utah and the names of the developers (Josh Cates, Manasi Datar, and Ross T. Whitaker) are also present. The login form has fields for Username (joeuser), Password (keep it secret, kee...), Broker address (shapeworks-server.sc), and a checked "Secure" checkbox with a Port field (8556). A "Connect" button is located below the form.

Username:

Password:

Broker address:

Secure Port:

ShapeWorks

CIBC

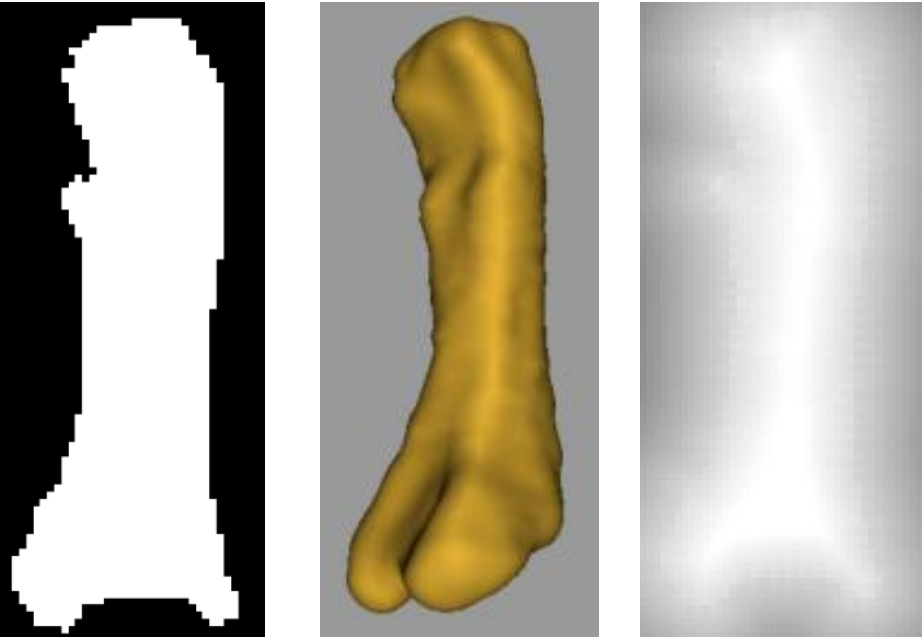
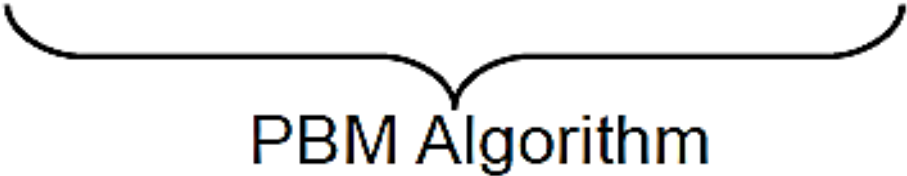
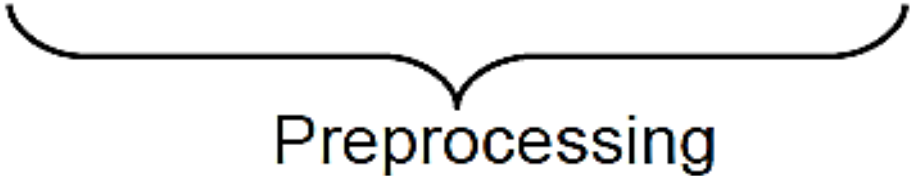
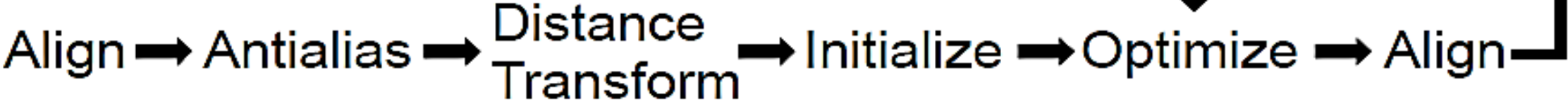
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Josh Cates, Manasi Datar, and Ross T. Whitaker  
This work was made possible through support from the NIH/NCRR Center for Integrative Biomedical Computing, P41-RR12553-10

Enter the username and password created during running the broker

# Correspondence Pipeline



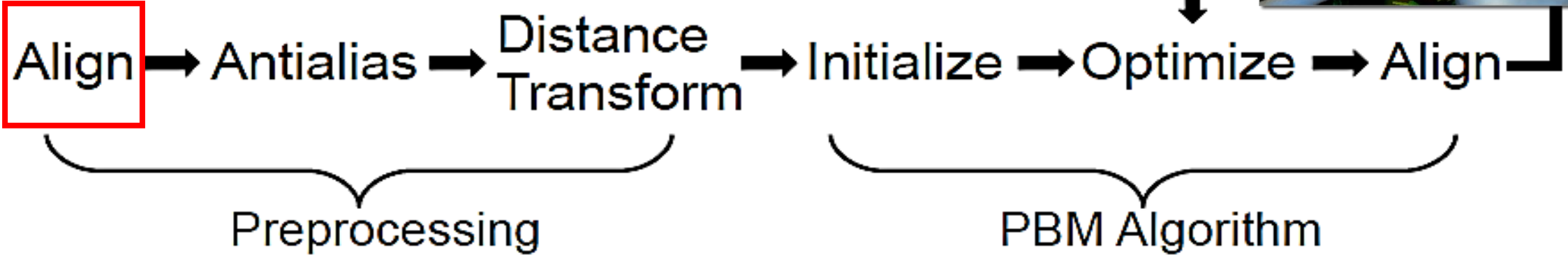
# Configuring a Project



The screenshot shows the ShapeWorks Client interface with the following configuration options:

- Fill Holes  
Description: Fill any holes in the binary segmentation of interest.
- Auto Crop  
Description: Use this option to find the largest bounding box containing all input shapes, and crop all input volumes accordingly.
- Center  
Description: Center the data.
- Isolate  
Description: Find and isolate the largest connected component.

Buttons at the bottom right include "Run this stage" and "Visualize".



# Configuring a Project



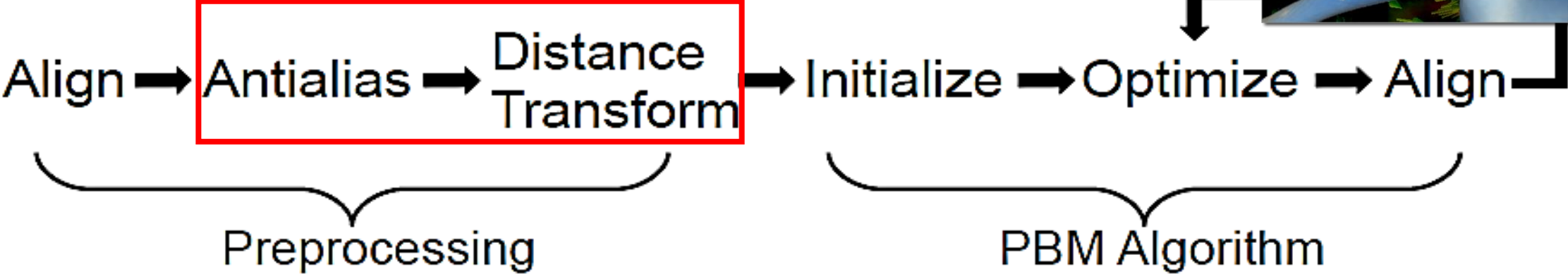
ShapeWorks Client

Torus

Files ROI Filter Initialize Optimize

- Antialias  
Description: Antialias the binary input volumes.  
Iterations: 20  
 Iterative Closest Point  
Description: Run iterative closest point (ICP) for the specified number of iterations to coregister the datasets. Iterations: 10
- Fastmarching  
Description: Levelset based computation of a distance transform volume from a specified isovalue. Isovalue: 0.00
- Blur  
Description: Gaussian blurring to remove high frequency artifacts. Sigma: 2.00

Run this





# Configuring a Project



ShapeWorks Client

▶ Torus ▶ Files ▶ ROI ▶ Filter ▶ Initialize ▶ Optimize

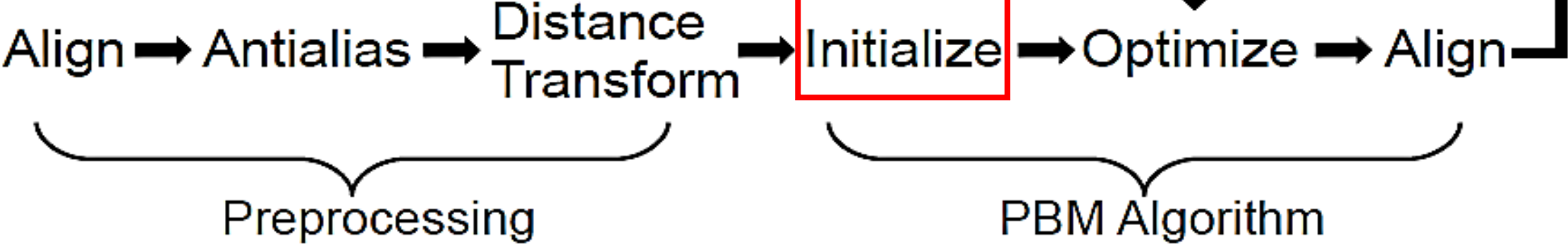
Number of Particles  
Description: Particles: 256  
Specifies the number of particles to be used to represent each shape in the ensemble.

Iteration per split  
Description: Iterations: 200  
Specifies the number of iterations to run between successive particle splits during an initialization phase.

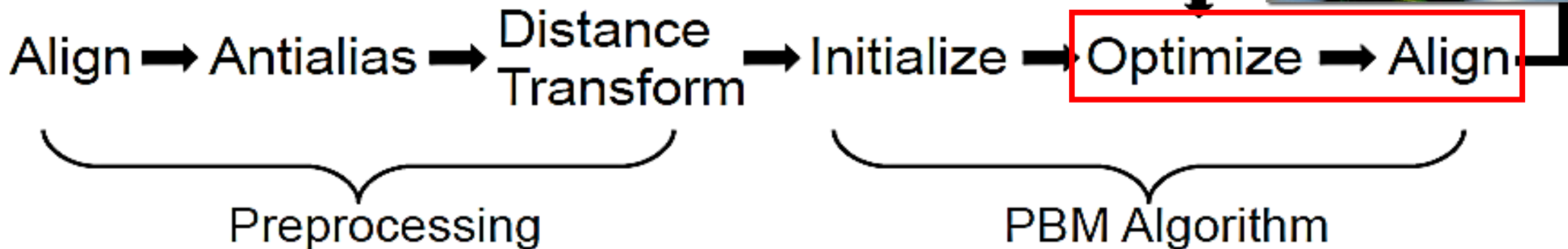
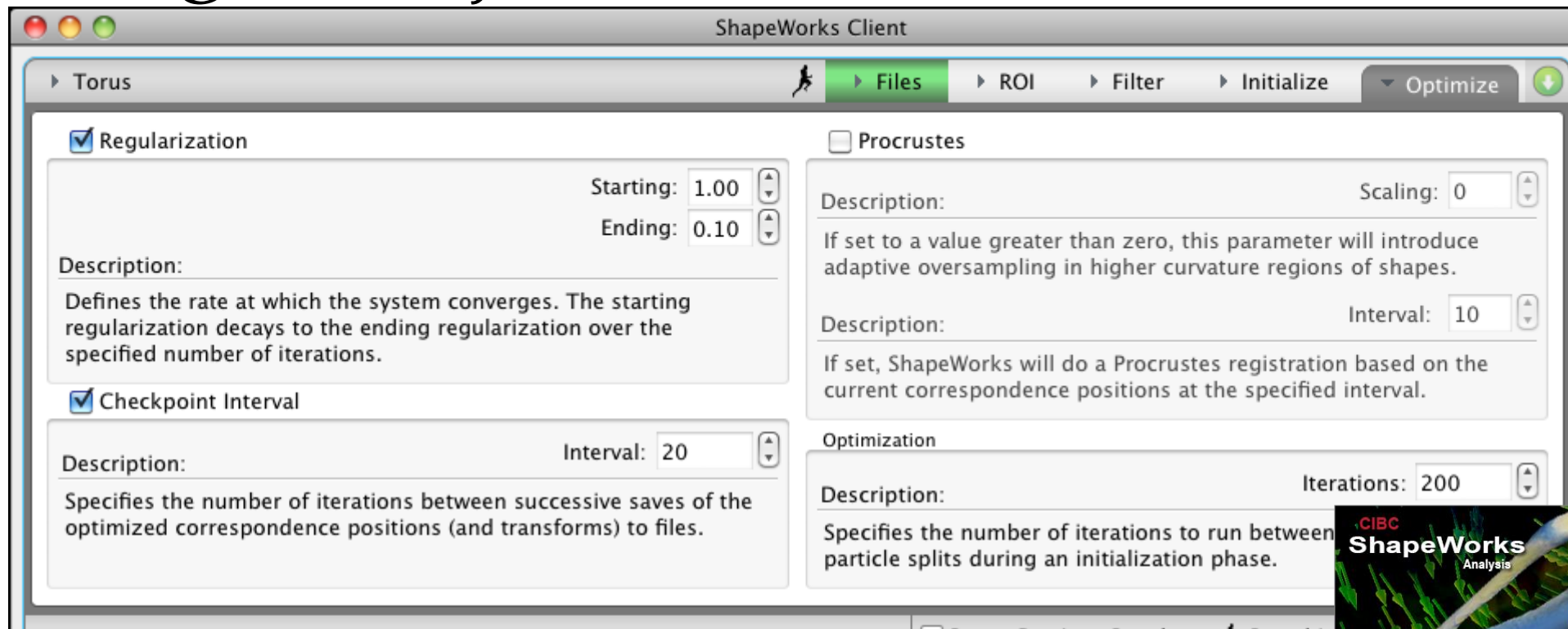
Relative Weighting  
Description: Weighting: 0.10  
This is the value of parameter  $\alpha$  from Equation 1.

Adaptivity Strength  
Description: Strength: 0.10  
If set to a value greater than zero, this parameter will introduce adaptive oversampling in higher curvature regions of shapes.

Reuse Previous Results Run this sta

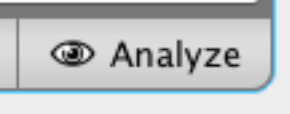


# Configuring a Project

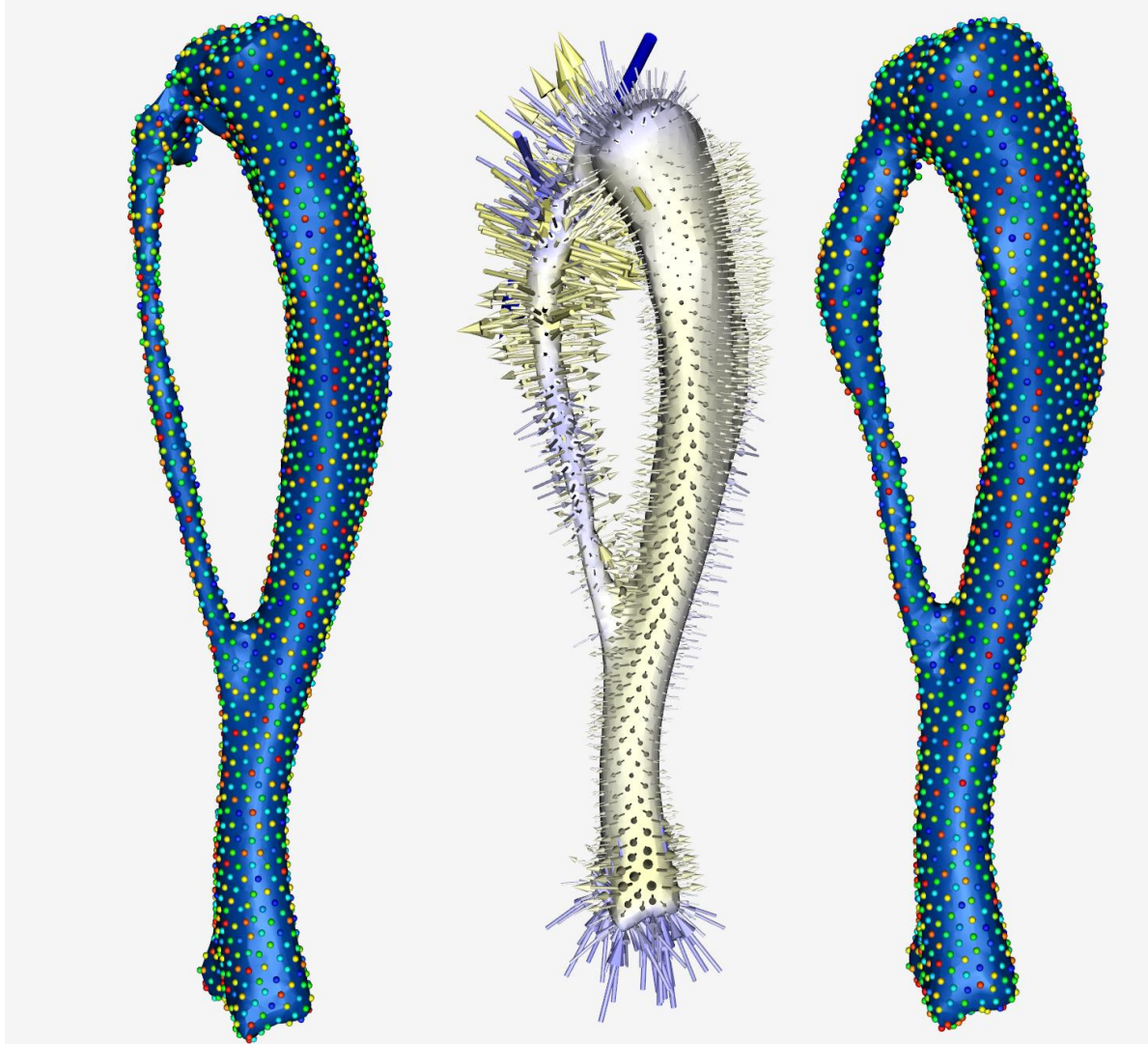


# ShapeWorksView

## Multiple Osteochondromas



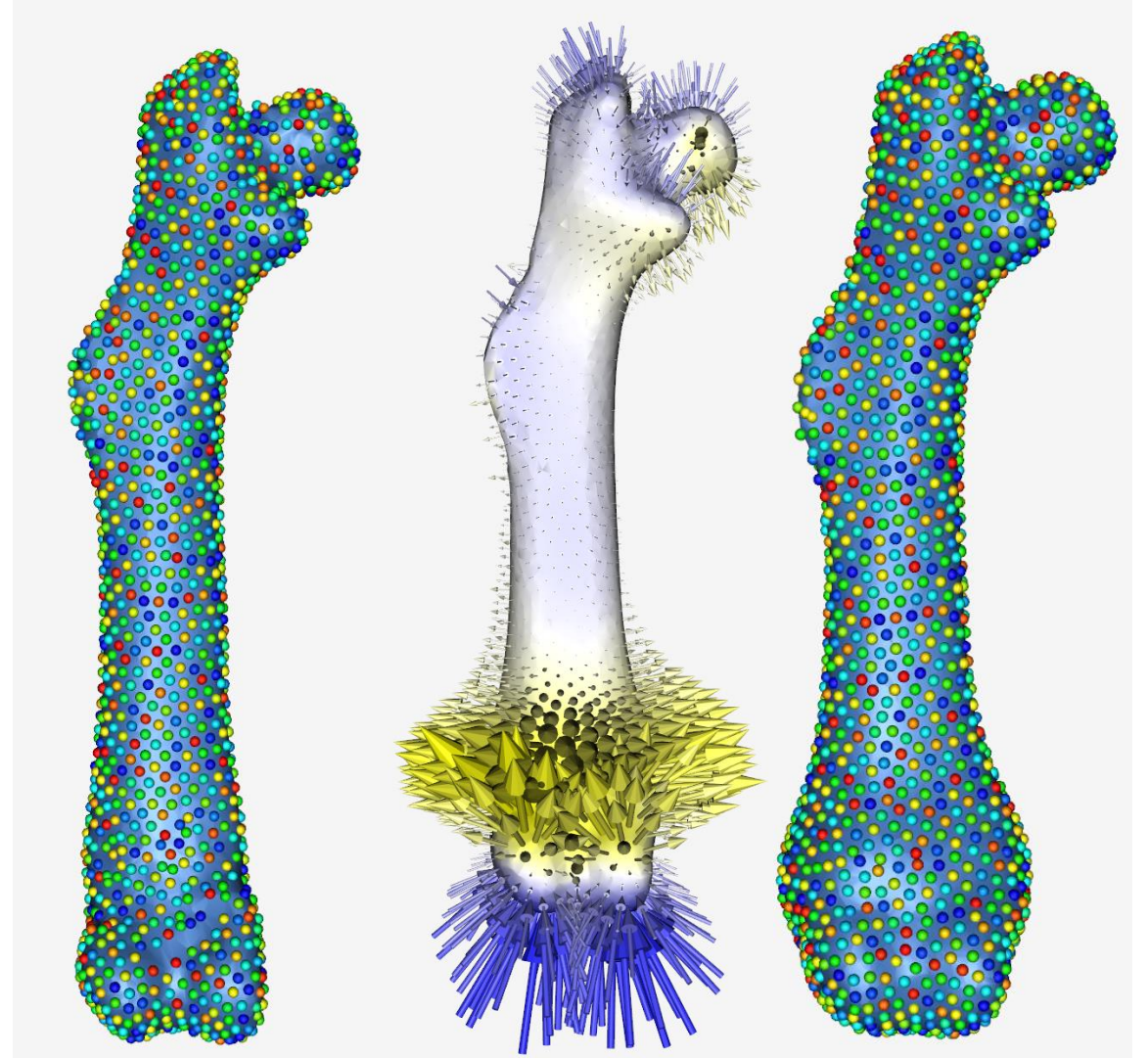
Group mean differences for tibia+fibula – young



normal

mutated

Group mean differences for femur – young



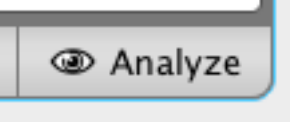
normal

mutated

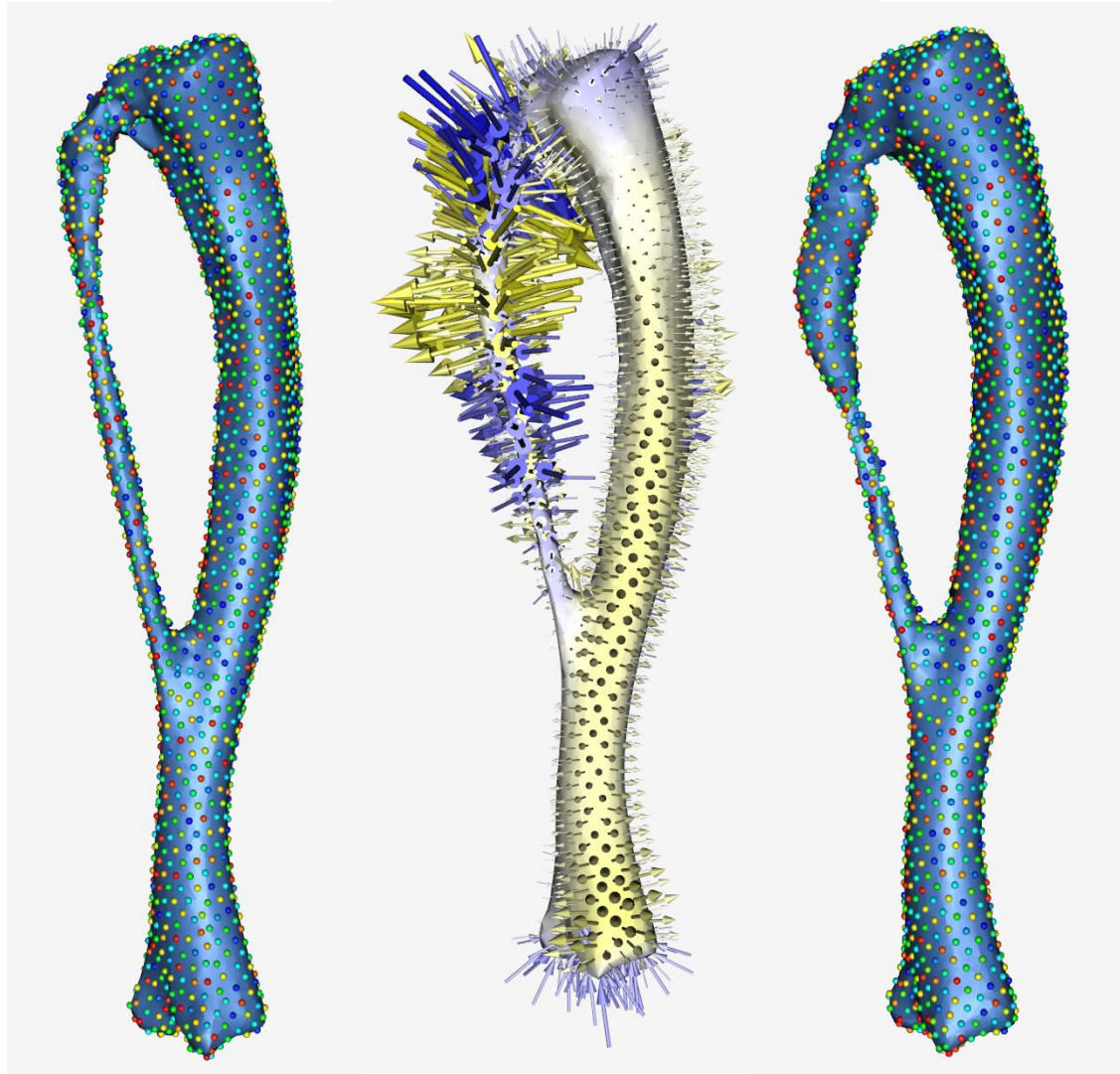
# ShapeWorksView

## Multiple Osteochondromas

Group mean differences for tibia+fibula – middle-aged

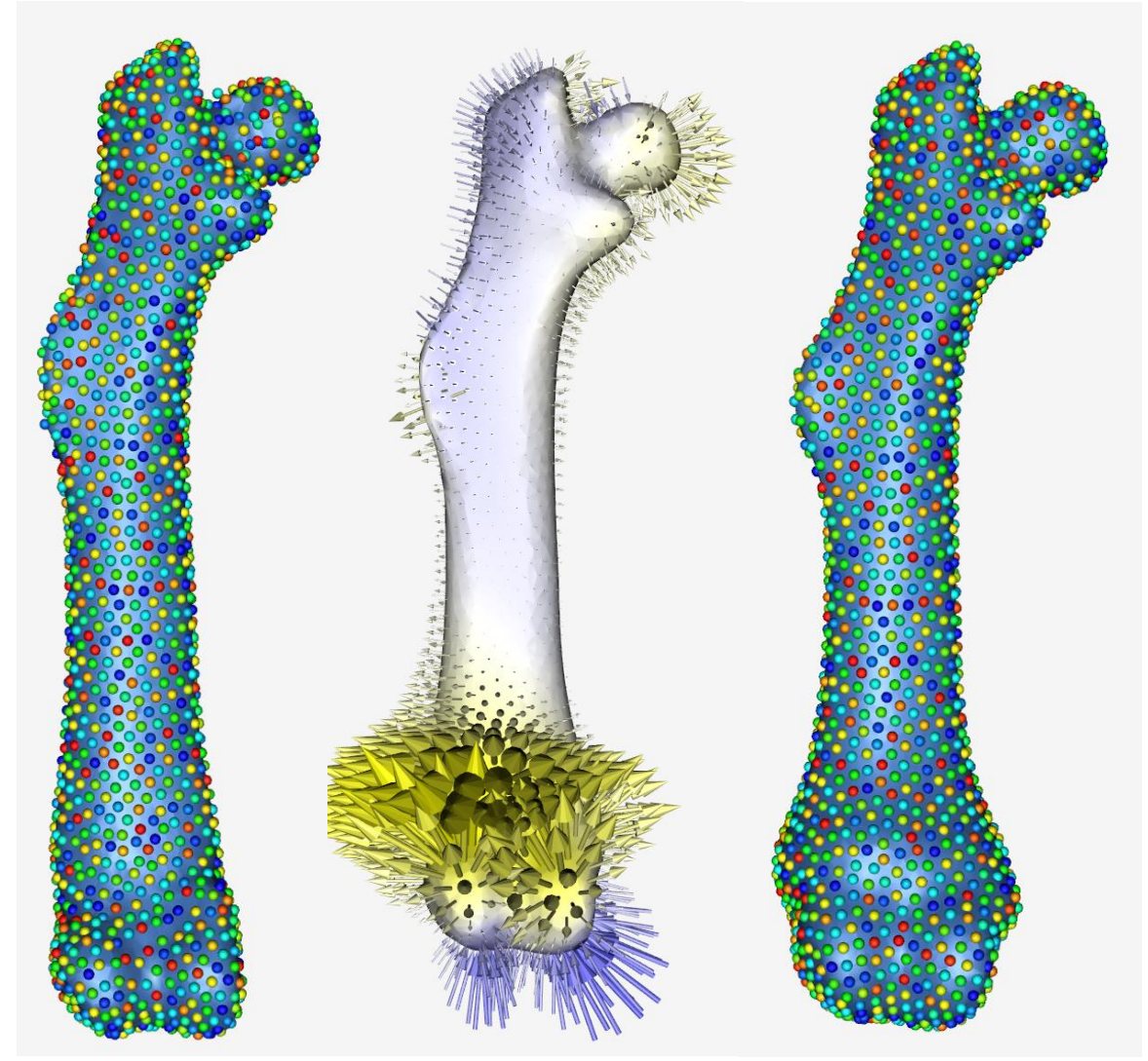


Group mean differences for femur – middle-aged



normal

mutated

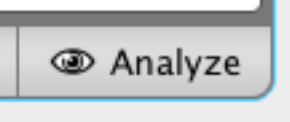


normal

mutated

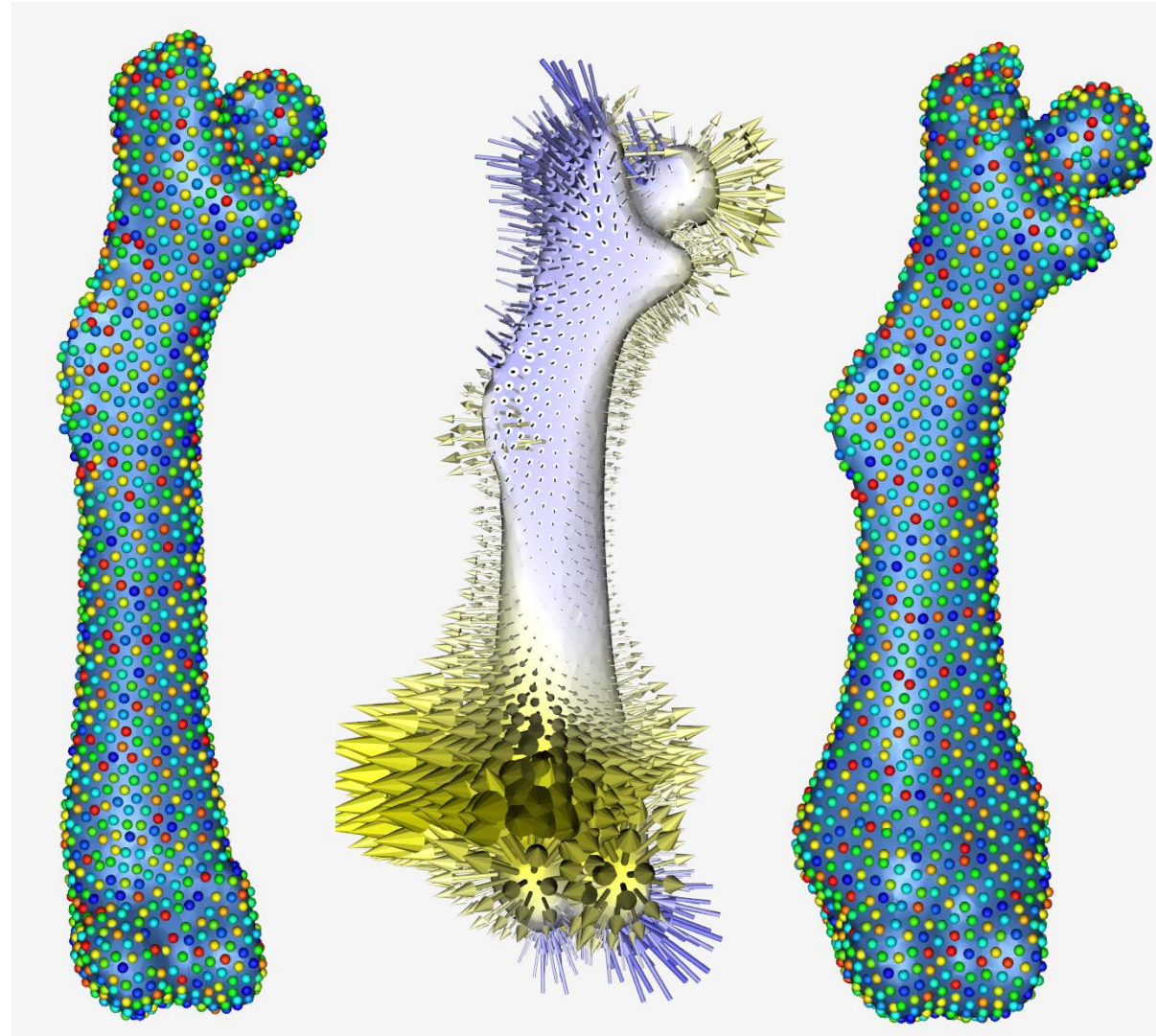
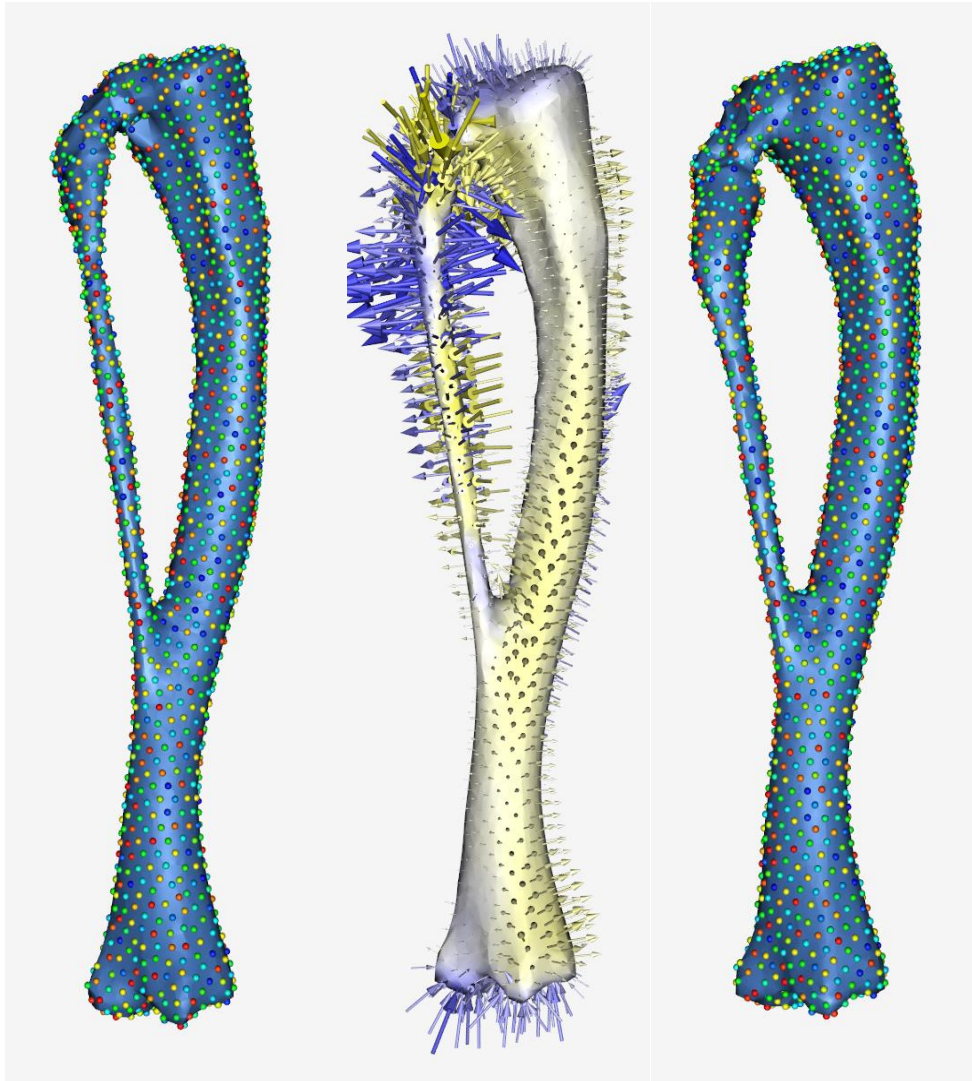
# ShapeWorksView

## Multiple Osteochondromas



Group mean differences for tibia+fibula – old

Group mean differences for femur – old



normal

mutated

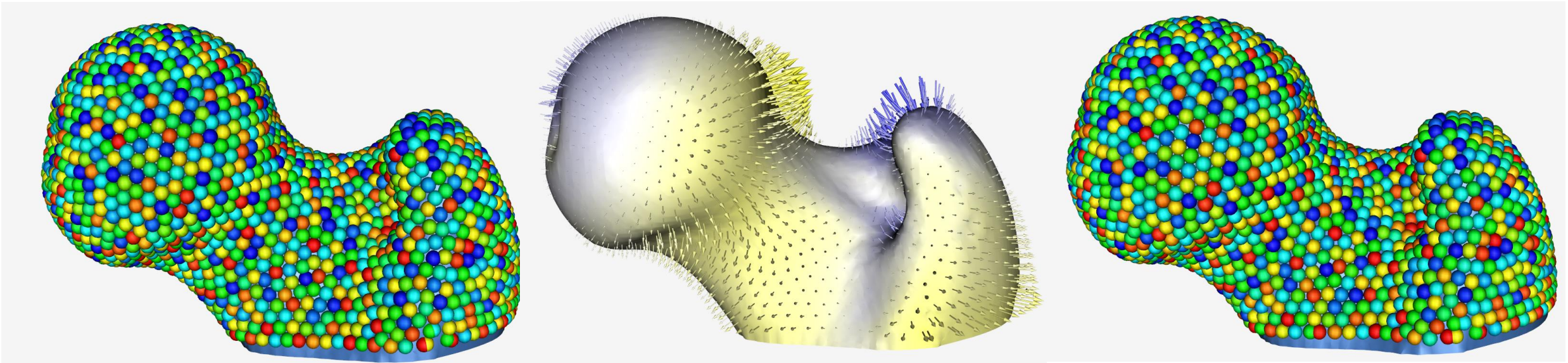
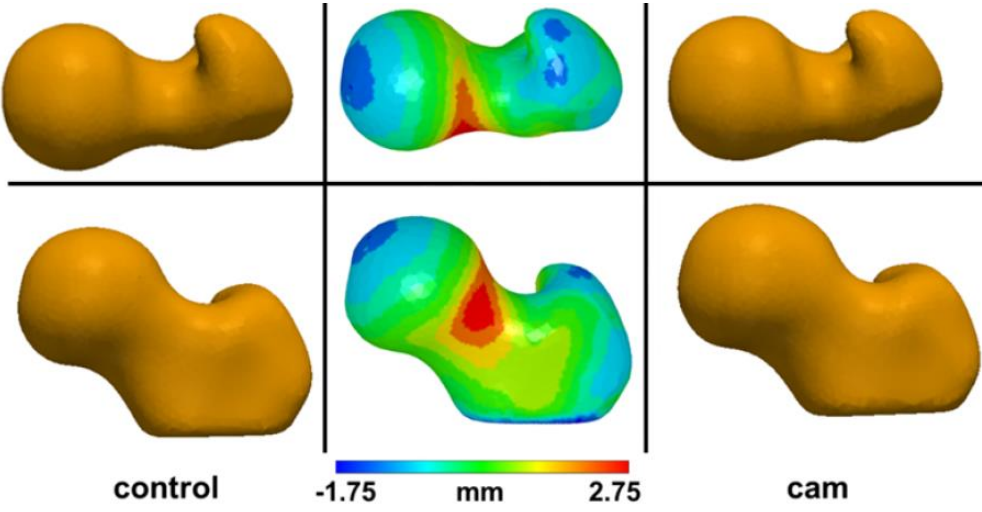
normal

mutated

# ShapeWorksView

## CAM-FAI Characterization

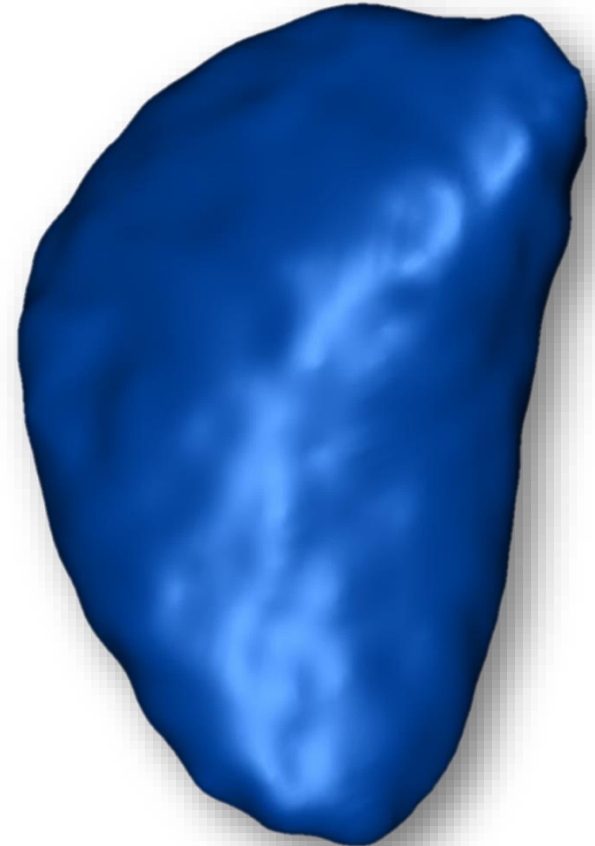
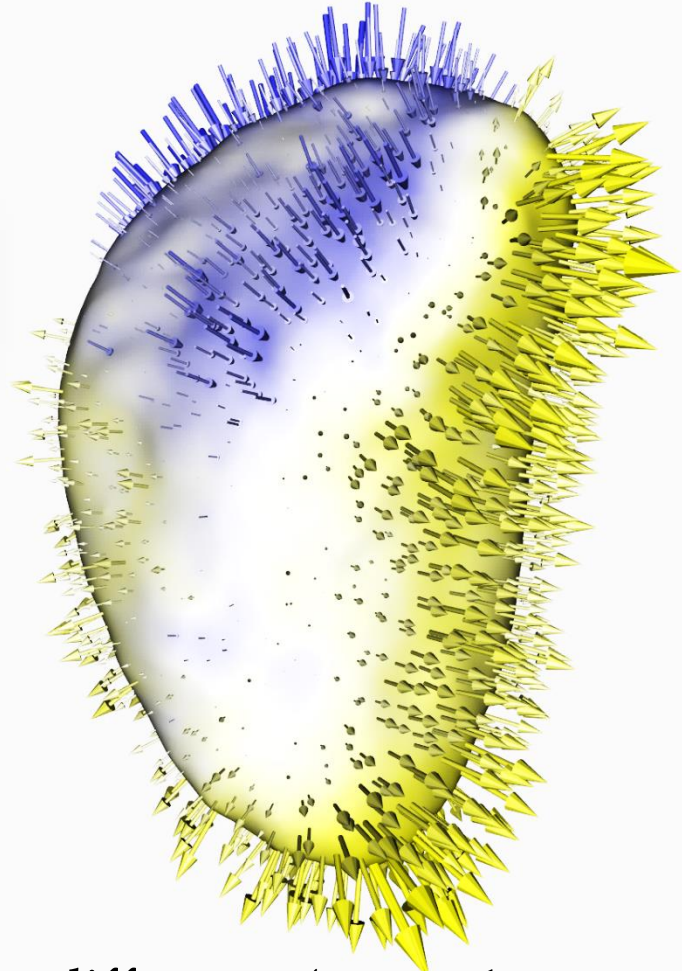
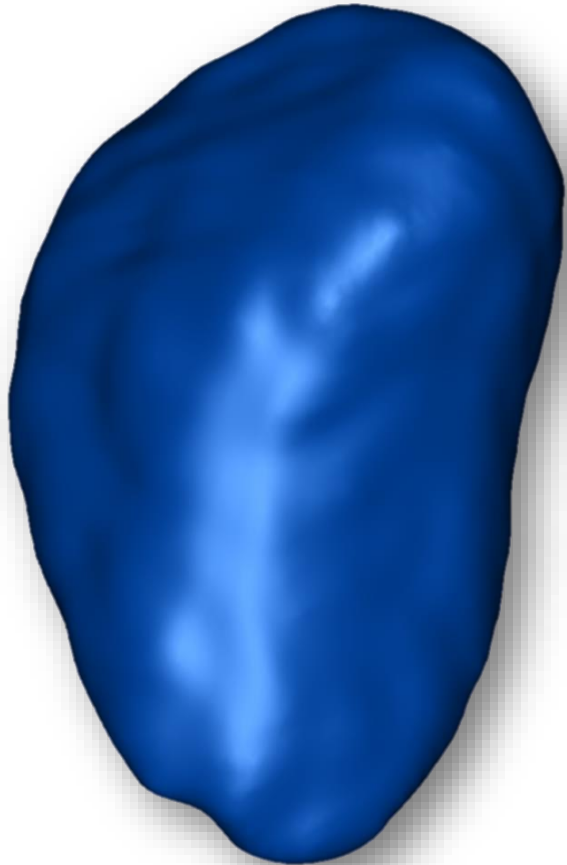
Analyze



# ShapeWorksView

## Left Atrial Appendage

- The LAA of two groups was segmented, one group with no history of having stroke while the other group has evident history of having stroke.



Group 1:  
no history of stroke

Group difference (group 1 to group 2)

Group 2:  
history of stroke

Thanks for your attention