# **ShapeWorks Workflow**

### **Section 1: Installation**

- To get ShapeWorks, first install miniconda if you don't already have it.
- Visit ShapeWorks's GitHub and download the latest stable release.
- Install ShapeWorks using the installer you downloaded
- Open a miniconda terminal and navigate to the ShapeWorks folder
  - Default location is C:\Program Files\ShapeWorks
- Run install\_shapeworks in the miniconda terminal
  - NOTE: If this step takes a while to complete, try deleting the shapeworks folder and updating your miniconda
- Once that is complete, navigate to C:\Program Files\ShapeWorks\bin and run ShapeWorksStudio.exe

### Section 2: Importing a dataset

- For our purposes, we are using ShapeWorks to analyze .stl files.
- Download our shoulder dataset from here
- Once it is downloaded, clone the nick-dev branch from the Shoulder-Keypoint repo on GitHub and create a folder named "Projects" in the root of that folder

igit .git	2/25/2022 2:43 PM	File folder	
config	2/15/2022 8:32 PM	File folder	
Projects	2/25/2022 3:24 PM	File folder	
gitignore	2/16/2022 12:41 AM	GITIGNORE File	1 KB
🎝utility.py	2/15/2022 8:32 PM	Python File	7 KB
🗟etl.py	2/15/2022 8:32 PM	Python File	3 KB
🞝 _train.py	2/15/2022 8:32 PM	Python File	9 KB
🎝 _test.py	2/15/2022 8:32 PM	Python File	9 KB
🎝 CreateProject.py	2/25/2022 3:24 PM	Python File	5 KB
👼 FeaturePointDataset.py	2/25/2022 2:11 PM	Python File	26 KB
FeaturePointDataset_tester.py	2/25/2022 2:11 PM	Python File	22 KB
iensen_notes_11.4.21.txt	2/15/2022 8:32 PM	TXT File	1 KB
PointHRNet.ipynb	2/15/2022 8:32 PM	IPYNB File	64 KB
🎝 pose_hrnet.py	2/15/2022 8:32 PM	Python File	20 KB
README.md	2/15/2022 8:32 PM	MD File	1 KB
requirements.txt	2/15/2022 8:32 PM	TXT File	1 KB
tester.ipynb	2/25/2022 2:11 PM	IPYNB File	0 KB

- Open the repo in VSCode and run the file "CreateProject.py"
  - The program will prompt you first for a name for the project file.
  - Next, get the path to the shoulder data you downloaded earlier and paste it into the program. It should be that path to a folder that contains the two datasets,
     "Akira\_Organized" and "Keisuke\_Organized"
  - Next, choose which bones to import. Type 1 for scapula, 2 for humerus, or 3 for clavicle.
  - Lastly, choose the amount of bones to import. I would recommend 9 at most if you're just trying to get optimization to work correctly and mess around with parameters.
  - If you're trying to generate data for the whole dataset, however, type "all"
  - The project file will be saved in the Projects folder you created earlier
- Open ShapeWorks and click "Open Existing Project", then navigate to the Projects folder and select the file you created above to import your desired .stl files.

## Section 3: Using ShapeWorks to create point clouds

- ShapeWorks uses three steps in order to generate a point cloud:
  - Groom, which smooths out the models and makes them easier for the program to process
  - Optimize, which is what we use to actually generate the points on each mesh
  - *Analyze*, which we can use to visualize the different point clouds for each individual mesh and see how well our optimization parameters did

#### Section 3a: Grooming

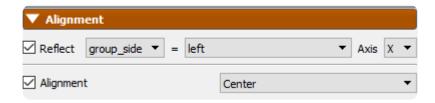
#### **Mesh Grooming**

- Mesh Grooming has three main options:
  - Fill Holes
  - Smooth
  - Remesh
- Fill holes should always be selected for our purposes, as many of the scapula meshes have...you guessed it: holes!
  - NOTE: If the grooming step is taking a long time for Scapulae, de select this option.
     Not recommended, but it was not completing on some computers so do this if needed.
- Smoothing is prety self explanatory: it smoothes out the mesh. This *can* be useful, but if you enable it be sure to keep iteration amounts between 1 and 3, as going higher loses the surface detail that we need to generate accurate clouds.
- Remesh modifies the mesh so that the triangles that make it up have more similar areas.
   This is very useful, but keep it at default.

#### Alignment

- This section allows you to modify the alignment and the reflections of meshes
- For our purposes, the *CreateProject.py* file mentioned above assigns the "right" group to any bone that contains "Raxes" in its name. Otherwise, it assigns the "left" group
  - This is done because the Keisuke dataset is the only one with meshes from both sides
    of the body Akira has only the left. The Keisuke dataset names corresponding
    meshes "Raxes" for the right side, and "Laxes" for the left, resulting in the above
    logic for the script.
- Select the "Reflect" option to reflect the meshes so that they all have the same orientation.

Change the "shape\_file" option to "group\_side" to enable this feature



#### Section 3b: Optimizing

- There are a lot of options to choose from here, and they all have different effects. Here is what I have found through trial and error, and the page on what the parameters mean and some quick tips on optimization from ShapeWorks:
  - Number of particles
    - The amount of particles the program generates
    - Keep this number low while fine-tuning your parameters (x<64) but increase and decrease by factors of x\*2 if you need to.
    - Increasing it provides a mesh with higher detail at the end, but takes much longer
  - Initial Relative Weighting
    - How the initial correspondence is weighted
    - Increase this number (by a factor of 0.01) in order to make particles correspond better
  - Relative Weighting
    - Relative weighting of correspondence during optimization
    - Decrease this number (by a factor of 1) to help particles spread more evenly across the mesh
  - Starting Regularization & Ending Regularization
    - Don't worry about modifying these(?)
  - Iterations Per Split
    - How many times the optimization occurrs per split of points
    - Keep this around 1000, increase it to help get particles to be in the "right places" but there are diminishing returns on increasing it.
    - This affects processing time quite a lot, especially with higher amounts of particles
  - Optimization Iterations
    - How many times the program will optimize point location per iteration. Keep this around 1000.
  - Geodesic Distance

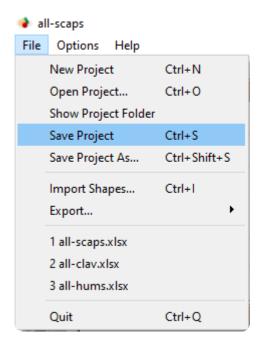
 Don't enable this. Increases computing time by a factor of 10x and is not useful for our application.

#### Normals

- Tells the algorithm whether to consider surface normals and the xyz of a particle in correspondence
- Should be enabled to avoid particles flipping sides on thin structures
- Seems like it may be needed in order to get particles to place correctly on most smaller structures
- Normals Strength
  - How much the algorithm ascribes strength of surface normals relative to position.
- Procrustes
  - These options provide minimal changes and have little documentation. Would recommend to just avoid for now.
- Multiscale Mode
  - No documentation on this option and it hasn't provided meaningful improvements. Would recommend avoiding this.
- Multiscale Start
  - After how many particles should multiscale mode begin.
- Narrow Band
  - Doesn't affect optimization. Don't worry about this.

### **Section 3c: Exporting Data**

• To export the key point data, just save the project! This will save all of the current particles in a folder with the same name as the project, just with "\_particles" appended.



Name	Date modified	Туре	Size
all-clav_particles	3/22/2022 3:21 PM	File folder	
all-hums_particles	3/22/2022 3:21 PM	File folder	
all-scaps_particles	3/17/2022 10:35 AM	File folder	
groomed	3/22/2022 3:16 PM	File folder	
🕦 all-clav.xlsx	3/22/2022 3:54 PM	Microsoft Excel W	6 KB
🕦 all-hums.xlsx	3/22/2022 3:54 PM	Microsoft Excel W	6 KB
all-scaps.xlsx	3/22/2022 3:54 PM	Microsoft Excel W	6 KB