

1. Introduction

This is an R implementation of the automated three-dimensional geometric morphometric methods developed in the PhD thesis of [Jesus Puente](#). The utility of the auto3dgm methods was illustrated in [\(Boyer et al., Anatomical Record\)](#) and the R code was written by Chris Glynn.

The R package can be downloaded [here](#).

2. Instructions

To use auto3dgm the an R distribution of at least version 3.0 is required in addition to the following R libraries installed: Matrix, clue, linprog, igraph, MASS.

Once these libraries are installed. Install auto3dgm.tar.gz

The following tutorial provides an example of how to use auto3dgm.

3. A Brief Tutorial

In this example the first five teeth taken from the set of [fifteen teeth](#) are aligned. The meshes to be aligned should be stored as off [\(object file format\)](#) files with an .off designation.

Install Matrix, clue, linprog, igraph, MASS, and auto3dgm.tar.gz

Download the following R code: [Web_Example.R](#)

Edit the following line in Web_Example.R

```
Output_dir = "/Users/sayanm/Desktop/Bones"
```

to

```
Output_dir = "YOUR_DIR"
```

where YOUR_DIR is the path to the directory you want the outputs of the program to be written.

Outputs

When you source/run Web_example.R you will get the following outputs in the Output_dir you specify:

[Aligned Shapes](#): the aligned meshes of the five teeth, for example the [second tooth](#)

[MST.jpg](#): the jpg image of the minimum spanning tree of the five teeth

[alignment.off](#): the mesh file of the five aligned teeth of the lower resolution images, in this case 64 points. There is a marker to designate the first shape and there are ten shapes to a row, see [Figure 1](#). The shapes are ordered according to the sequence of shape ids specified in Web_example.R

[alignment 2.off](#): the mesh file of the five aligned teeth of the higher resolution images, in this case 128 points.

There is a marker to designate the first shape and there are ten shapes to a row, see [Figure 2](#). The shapes are ordered according to the sequence of shape ids specified in Web_example.R

[map.off](#): a 3-dimensional representation of the minimum spanning tree, [Figure 3](#)

[morphologika.txt](#): a [morphologika](#) file for the lower sampling resolution

[morphologika_2.txt](#): a [morphologika](#) file for higher sampling resolution

[morphologika_unscaled.txt](#): an unscaled [morphologika](#) file for the lower sampling resolution

[morphologika_2_unscaled.txt](#): an unscaled [morphologika](#) file for higher sampling resolution

Inputs

The data used in this example consist of

[001.off,...,015.off](#): fifteen teeth that are not aligned, an example [tooth](#)

[lowres](#): a directory of low resolution files for the fifteen teeth

[subsampled](#): a directory of subsampled files for the fifteen teeth

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