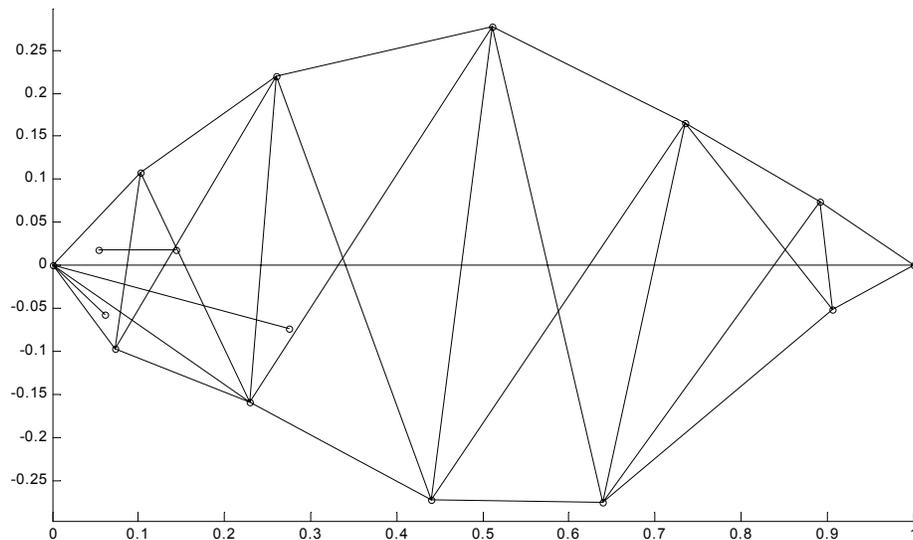# IMP: TMorphGen6- Traditional Morphometrics Variables Generation Utility
Part of IMP- Integrated Morphometrics Package

Introduction

This piece of software is part of IMP and requires data files in the X1Y1X2Y2...CS format, or the TPS file format. If you have not used CoordGen6 by now, go and read the WhatIsImp file and the CoordGen6 manual before proceeding.

TmorphGen6 (Tradition Morphometrics Generator) generates a set of traditional morphometrics variables (length measurements) from a geometric landmark data set, of paired coordinate measurements. This allows rapid comparison of results based on geometric morphometric methods with earlier work based on traditional morphometric methods.

The set of length measurements used in the traditional morphometric studies of piranha. This figure shows a set of interlandmark distances to calculated by TradMorphGen, as specified by a Measurement Protocol

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Using TradMorphGen

Load Data Set

This button loads a data set that is in X1Y1X2Y2..CS format. The superposition used is not relevant for these calculations, any one will do. When the data is loaded it will be displayed on screen.

Load Data (TPS format)

This option loads data in the TPS file format used by James Rohlf's software. When the data is loaded it will be displayed on screen.

Load Measurement Protocol

This is an ascii data file of the interlandmark distances you want measured. The file should have the following format,

measurement number   landmark 1   landmark 2

for example the following file

1   1   2
2   2   3
3   1   3
4   1   4

would indicate that your protocol called for 4 length measurements, between landmarks 1 and 2, 2 and 3, 1 and 3, 1 and 4, output in that order.

When a protocol is loaded, it will be plotted on top of the data, drawn using the mean specimen in the data set. This allows you to see that your protocol has been drawn correctly.

There is an example file, dummypairs.txt, showing a sample, rather simple protocol included with the compressed program files. This protocol can be used with the piranha data file sdent.txt (denticula) included in the package.

Calculate Length Set

Calculates all the lengths. Do this before trying to save the file.

Save Traditional Length set

This button saves a data set of the lengths you have requested for each specimen. The file output is an ASCII data mata, with each specimen on a row, and each column representing a length measurement, in the sequence given in the protocol. Note that the rows of specimens will be in the same order as they were in your input file. The specimens are not labelled, but since the order is preserved you can cut and paste labels into a file using excel if desired. This data matrix should also load easily into SAS or SPSS etc.

Clear Input Data, Retain Protocol

Sets up the software to produce the same set of length measures using for a new data set.

Show Protocol Only

This is intended to allow you to produce a diagram of the protocol easily, without showing all the data points on top of it.

Copy Image to Clipboard

Copies the current onscreen image to the Windows clipboard. From there, it may be pasted into Word, or your favorite graphics editor, etc.

Image Properties Menu

TmorphGen6 has limited image property options available, allowing minor alterations to the plotted image.

Exit

Just hit the button!