

IMP: TMorphGen6- Traditional Morphometrics Variables Generation Utility

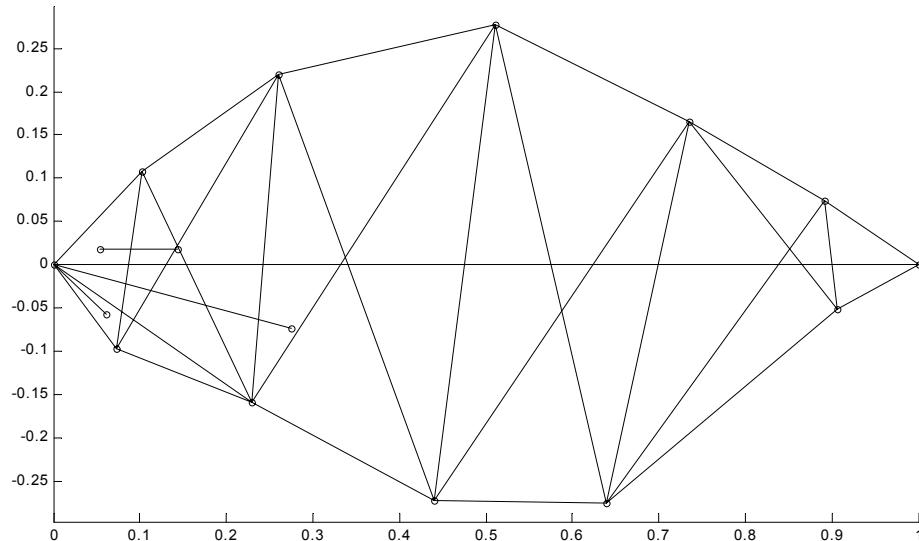
Part of IMP- Integrated Morphometrics Package

Updated 8/16/05 to allow for angular measurements as well as linear measurements

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

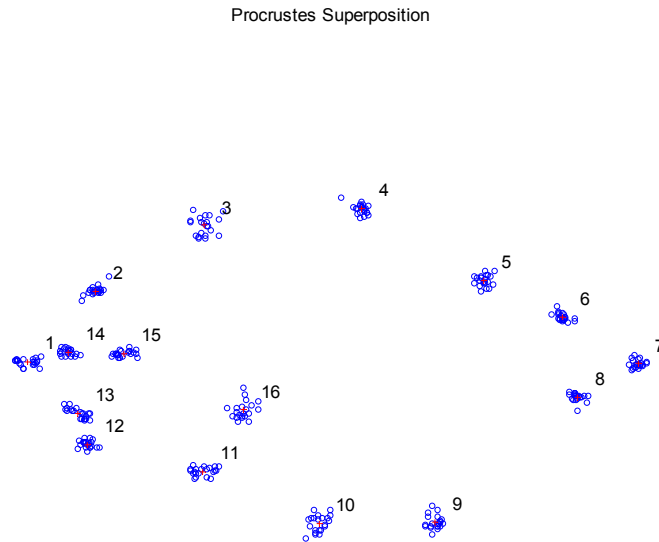
TmorphGen6 has limited image property options available, allowing minor alterations to the plotted image.

Exit

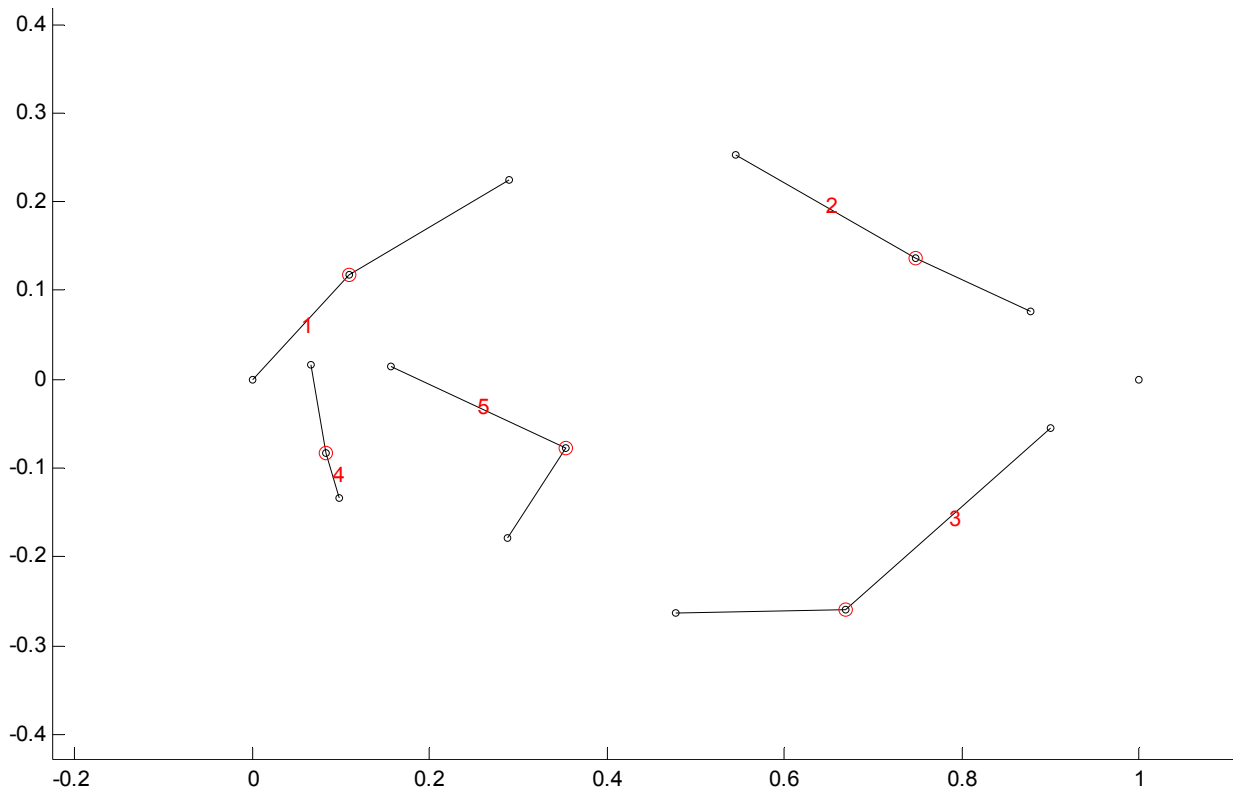
Just hit the button!

Updates 8/17/05 to Handle Angular Measurements

At the suggestion of Sarah DeGroot of the Rancho Santa Ana Botanic Garden, the program will now calculate angles between lines joining landmarks. To use this function, one loads a set of landmarks into the program and a protocol file which includes a list of angular measurements to be made. For the piranha example, we have the landmarks (included in the example file carbc.txt):



The example angle file (piranha_angles.txt) lists the 5 angles to be measured as shown in the diagram below. Each angle must have a landmark at the vertex, and at both ends of the line segments leading away from the vertex. The program will display the angles specified by the input protocol on the mean landmark configuration.



The program can then save the requested angles for each specimen (as either radians or degrees). Each specimen is on a single line in the output file, and the angles are in the same order as in the angle protocol file. These angles may be submitted to statistical analysis in other pieces of software.

162.506	172.892	142.844	172.929	80.1701
163.355	176.731	133.687	177.352	74.9774
162.876	177.973	143.131	172.974	74.0439
161.917	178.297	137.495	170.765	76.485
161.274	176.406	136.669	169.144	72.9717

Using the Angular measurements

1.) Digitize your specimens and convert the data to IMP format files.

2.) Use a Word Processor (Word), text editor (Notepad) or spreadsheet (Excel) to create the protocol file you will need. Each line in the protocol file indicates a single angle. The first integer on each line is the number of the angle (starting with 1 and counting upward). The next three integers specify the landmarks that form the angle. The middle of these three values is the landmark forming the vertex of the angle, the other two are the landmarks forming the ends of the lines coming out from the vertex. Save this as an ASCII format file (it may also be called a tab-delimited text file, or an MS-Dos text file). Excess line feeds at the end of the file can cause errors, so make sure you have no excess line feeds. See the example file "piranha_angles.txt" included with the program, it is meant to be used with the carbc.txt data file.

3.) Load the data file (of landmark coordinates) into TMORPHGEN.

4.) Use the "Load Angle Protocol" button to load your angle protocol file. When you do this, the program will plot the angles on top of the data.

5.) You can use the "Show Angles" button to display only the angles, without the rest of the information. Make sure the protocol is producing the

6.) Use the "Save Angles" buttons to save the angles in either degrees or radians as desired. The output will have one specimen per row (in the same order as your input data file) and the angles in columns in the same order you loaded them. The output is in an ASCII text file that most programs should load.