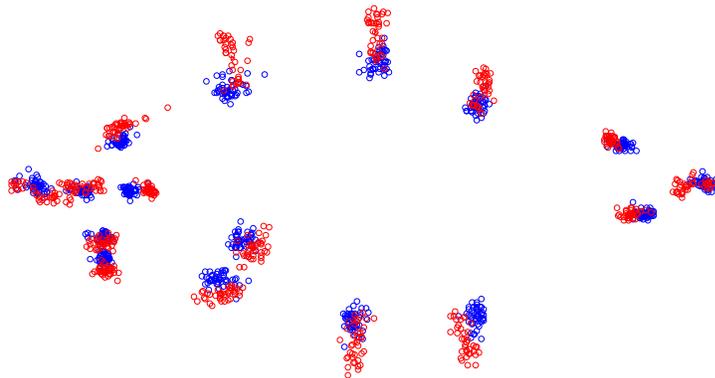


## IMP TwoGroup6

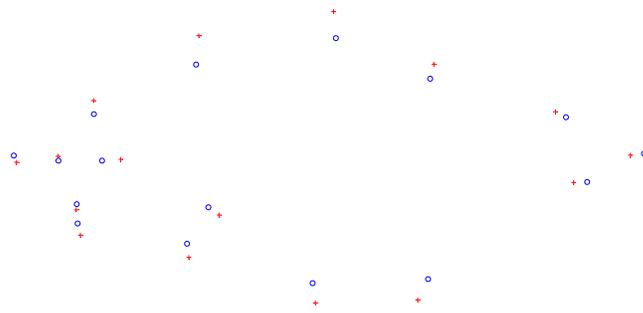
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The program TwoGroup is part of the IMP software suite for analysis of 2D landmark based geometric morphometric data. TwoGroup offers a variety of statistical tests; Goodall's F-test and Hotelling's  $T^2$  test for significant differences in shape between two groups, as well as bootstrap versions of these tests. TwoGroup uses the usual IMP file format system. TwoGroup will also calculate the Full and Partial Procrustes Distances between the means of two groups, and a bootstrap estimate of the variance in this distance. The distance between the groups may also be determined for the means under a SBR superimposition.

### Example of the Use of TwoGroup



Landmark configurations of specimens of two species of piranha, using 16 landmarks in 2 D, the superimposition shown here is a Partial Procrustes Superimposition of the two data sets produced by TwoGroup.



The mean shapes of the two distributions shown above. The Partial Procrustes Distance between the two mean forms is 0.0785, Goodall's F-test yields  $F=48.21$ ,  $df_1=28$ ,  $df_2=2296$ ,  $p=0$  to 4 decimal places. Hotelling's  $T^2$  on the same data in Bookstein Two-Point registration yields  $F=55.3$ ,  $df_1=32$ ,  $df_2=51$ ,  $p=0$  to 4 decimal places. Bootstrap tests done using Partial Procrustes Distances and Sliding Baseline registration both yield  $F=48.21$ , and  $p<0.01$  (no instances of an F value over 48.21 in 100 bootstrap sets, in either case).

### **Using TwoGroup**

If you are not familiar with IMP, read the files WhatIsIMP and the manual for the CoordGen program. You will need to use CoordGen prior to proceeding. This manual also assumes that you are familiar with Goodall's F-test and Hotelling's  $T^2$  test, if you are not see the morphometrics website at Stony Brook for references.

To use TwoGroup, you need to load the data files of specimens into TwoGroup. Each group needs to have a separate data file in the IMP file format (the X1Y1....CS format). To carry out the analytic forms of Goodall's F-test or Hotelling's  $T^2$ , simply

press the appropriate button on the program. TwoGroup will automatically carry out the necessary superimposition of the data, so it does not matter what superimposition your input data files were in. You do need to specify the endpoints of the baseline used for the Bookstein Coordinates or SBR methods prior to carrying out the test. The default baseline endpoints are landmarks 1 and 7, these may be changed by typing values into the appropriate windows on the program.

The Bootstrapped based tests determine an F-score using either a Procrustes Superimposition or the SBR method. Bootstrap tests are then carried out to determine if the probability the observed F-value could have been produced by chance. To carry out the bootstrapping procedure, the two groups are merged into a common pool, and then two groups with the same sample size as the original data sets are drawn with replacement from the common pool. The distribution of bootstrapped F-values over a large number of bootstrap data sets is used to determine the probability that the observed F-value could have arisen by chance.

Be sure to set the desired number of bootstrap sets using the Number of Bootstrap Sets option prior to running the test. Start with a small number of bootstrap sets to get some idea how long it will take to carry out the procedure on your data using a given computer, it varies quite a bit. Make sure if you are using the SBR option to set the endpoints of the baseline.

You can also use TwoGroup to calculate the Full or Partial Procrustes Distance, or the Euclidean distance under the SBR superimposition between the means, as well as a bootstrap estimate of the confidence interval of this distance.

It is also possible to display the data and the means of the data under a variety of different superimpositions (see the images above), and to copy these images to the Windows clipboard and to an Encapsulated PostScript (EPS) file.