

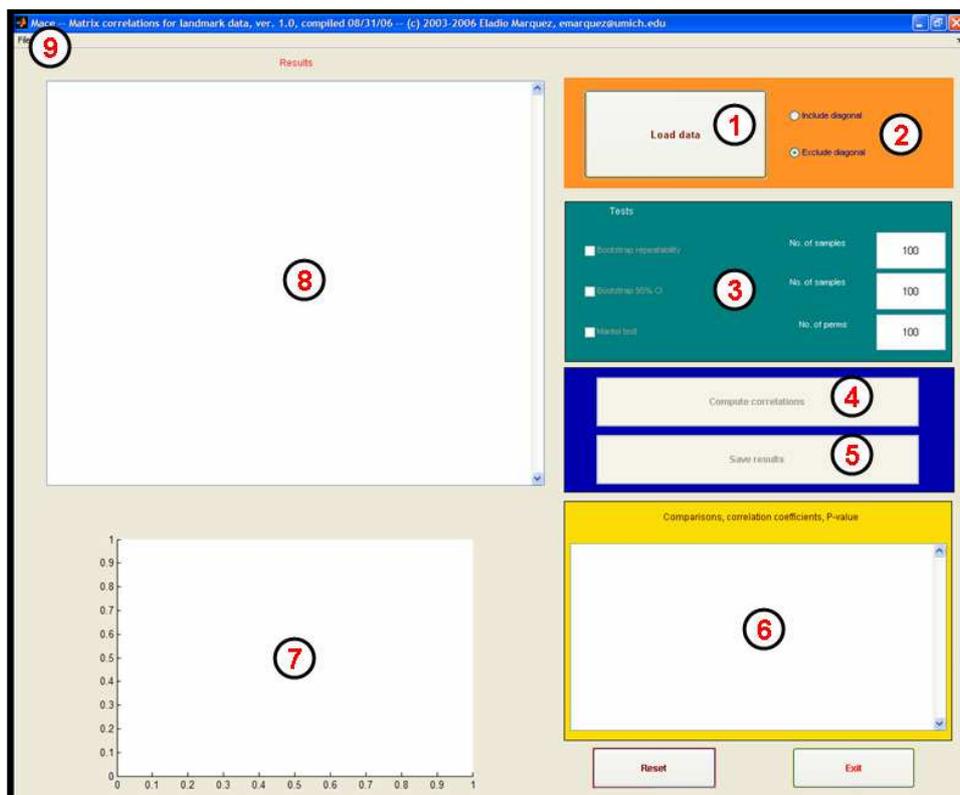
## Mace and Mace3D: Matrix Correlations for Landmark Data Version 1.03/1.02 (compiled 03/11/14)

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### Reference Guide

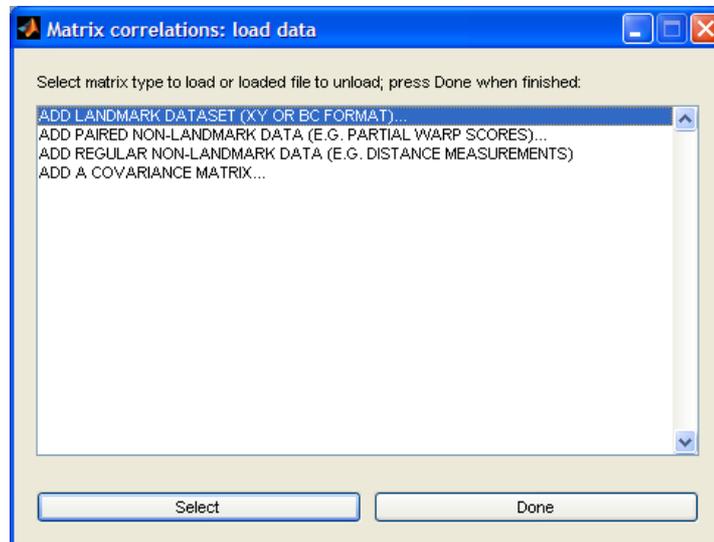
The following instructions apply to both Mace and Mace3D, which are identical in every respect besides the type of landmark data each expects, except where noted. Instructions will therefore refer simply to Mace, even though they apply for both programs. Sample datasets are packaged with Mace (but not Mace3D), containing two XY-format datasets (faland.dat, symland.dat), and their corresponding covariance matrices (facova.dat, symcova.dat), from a study comparing fluctuating asymmetry and symmetric covariation patterns in mice skulls.

Most functions in Mace are accessible from the main panel. Additional functions may be found in the **File** menu. An overview of the main functions available through Mace is schematized in the following figure and explanation:

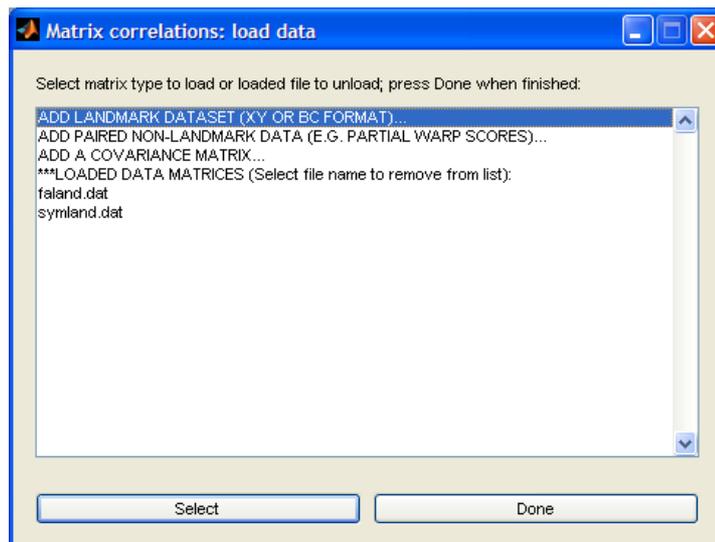


Description of functions:

1. **Load data** button: you must load at least two datasets to compute matrix correlations. When clicking this button, the following dialog box will appear:



From this dialog, you may select to upload any number and combination of landmark datasets, non-landmark datasets consisting of paired variables (e.g. partial warp scores), non-landmark datasets consisting of unpaired variables (e.g. traditional measurements; **Mace only**), or covariance matrices. The number of variables must coincide in all loaded files. Data formats allowed for landmark datasets are XY ( $X_1, Y_1, \dots, X_n, Y_n$ , where each coordinate is in a column), and David Sheets' IMP ( $X_1, Y_1, \dots, X_n, Y_n, CS$ , where each coordinate is in a column and CS stands for centroid size of each individual configuration).



Each time a new file is loaded, its filename will appear at the bottom of the list of options, as in the dialog shown above, where two files have been loaded. Selecting or double-clicking a file will unload it from the list.

2. You may choose to include or exclude the diagonals of the covariance matrices from the calculation of the matrix correlations. In the case of landmark data, these diagonals consist of 2×2 blocks of variances and covariances for each landmark's  $x, y$  coordinates. Keep in mind that mixing covariances and variances in a matrix correlation analysis can produce spuriously high correlations simply driven by the difference in magnitude between them—variances are usually higher than covariances.
3. From the Tests panel, choose any number of analyses. If none is chosen, clicking on 'Compute correlations' (see below) will only compute the correlation coefficient between the matrices. Note that bootstrapping requires actual data, as opposed to covariance matrices, to be loaded. These three tests consist on the following procedures:
  - a. *Bootstrap repeatability*: if data points are loaded, selecting this procedure will produce mean, SD, and 95% confidence limits for the correlation of each matrix with itself, which gives an empirical maximum of the value of a particular correlation. These statistics are computed directly from the distribution of correlation coefficient values between  $N$  bootstrapped datasets and the original one, where  $N$  is entered by the user. The mean can be used to adjust the observed correlation between two matrices by their repeatabilities (see Marroig and Cheverud, 2001, *Evolution* 55:2576-2600).
  - b. *Bootstrap 95% CI*: if data points are loaded, selecting this procedure will produce two mean, SD, and 95% confidence intervals for the correlation between the two matrices under comparison. These two values correspond to the two datasets, since only one is bootstrapped at a time. The number of bootstrapped samples is entered by the user.
  - c. *Mantel test*: selecting this option will cause the program to compute a permutation-based P-value for each matrix correlation. This P-value corresponds to the null hypothesis that the two matrices being compared are as different from each other as two random covariance matrices would.
4. **Compute correlations** button: click here to perform computations. All possible correlations between pairs of loaded datasets will be computed.
5. **Save results** button: click here to save ALL results from current analyses. The first row contains labels for columns. The first column contains labels for comparisons, each of which occupies a row. Labels and data on a row are separated by commas. Saving a set of results in an existing file causes the new

results to be appended to whatever the original file contains, even though a replace file warning is displayed.

6. In this box, each row will correspond to a comparison between two datasets. Clicking different rows will change the comparison whose results are currently shown (see 7 and 8).
7. In this space, a plot of the covariances is shown. Clicking on the graph changes the current comparison being shown.
8. In this box, results are displayed as verbal descriptions. Depending on what analyses were selected (see 3), different sets of results are displayed here. These descriptions can be copied to the clipboard as ordinary text. An example of the results from a comparison is shown below. In this example, all three kinds of analyses were selected. If none is selected, the results consist only on the first item shown here. Abbreviations: MC stands for matrix correlation, STD is the standard deviation from bootstrap replicates (or standard error for the bootstrap mean), and CI is confidence interval.

- Observed MC in std10d\_adind.dat vs. std15d\_adind.dat comparison was 0.37402.

- Repeatability: (1) for the matrix on the left, mean bootstrapped correlation with itself was 0.81298 (STD 0.054102), with 95% CI [0.69602,0.8983]; (2) for the matrix on the right, mean bootstrapped correlation with itself was 0.78673 (STD 0.061988), with 95% CI [0.67346,0.88074]).

- MC statistics: (1) mean correlation between left and right matrices was 0.31216 (STD: 0.035731 95% CI: [0.24359, 0.37538]) when left matrix is bootstrapped; and (2) mean correlation between left and right matrices was 0.30125 (STD: 0.059954 95% CI: [0.19248, 0.40647]) when right matrix was bootstrapped.

- A p-value of 0.01 was estimated for the observed correlation, based on 100 random permutations.

9. The **File** menu contains the following options:
  - **Save covariance matrix:** will save any covariance matrix employed in analyses being performed (one at a time).
  - **Transform covariance matrix:** allows constructing additional covariance matrices based on the matrices already loaded (or computed from data). Currently, the two transformations available are: to make a matrix “isotropic” by setting off-diagonal values to zero and all diagonal values to a constant (equal to the mean of the variances), and to make a matrix to have off-diagonal elements equal to zero and diagonal elements as in the original matrix. These matrices can then be uploaded to current analyses.