

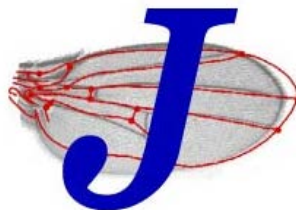
Lab 5

Geometric Morphometrics (GMM) using MorphoJ

- This week you'll learn to perform some basic analyses of model shape using geometric morphometrics. For this we're using the program **MorphoJ** (Klingenberg, 2011).

I. File management and Checking your data

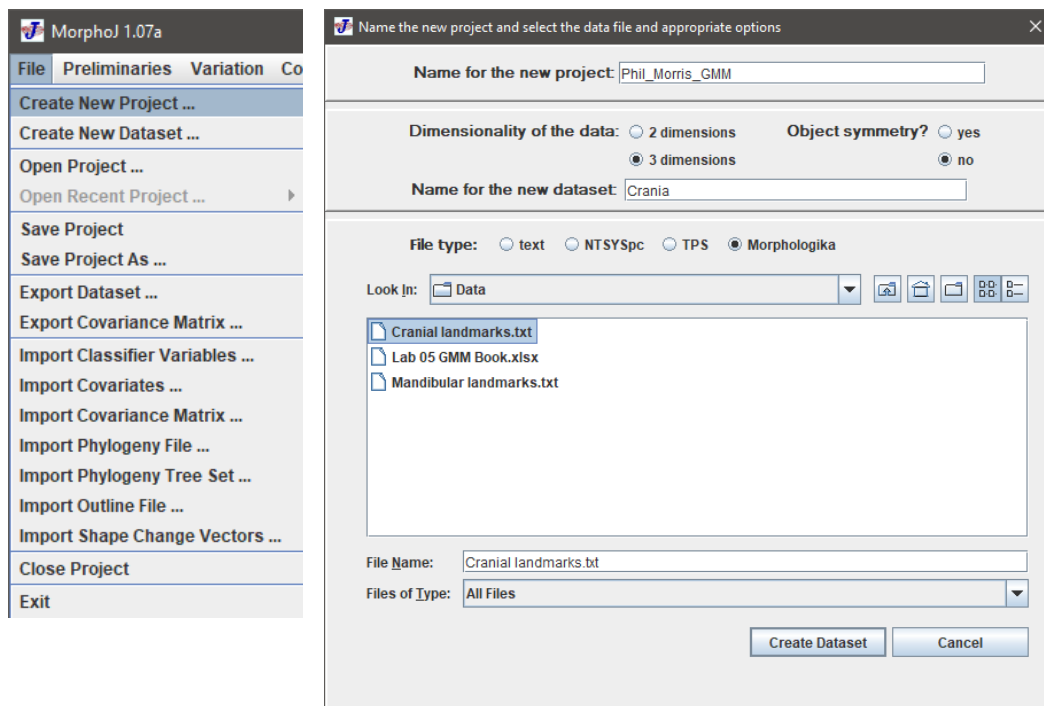
- 1). Create a folder on your desktop called **Lab 5 GMM**, include a **data** subfolder and a **saves** folder.
- 2). **Data:** from Canvas > Files > Lab_05_GMM > download files **Cranial landmarks.txt**, **Mandibular landmarks.txt**, and **Lab 05 GMM book.xlsx** and drop them into your Lab_05 folder.
- 3). Open up **Cranial landmarks.txt** in Notepad and take a look at the formatting of the file. This is called a Morphologika file, and contains the raw coordinate data collected from landmarking (not covered in this lab), organized according to specimen, and listed in columns according to the number of dimensions of data (in this case 3 - X, Y, Z).
 - At the top of **Cranial landmarks.txt** is noted how many individuals (specimens), landmarks, and dimensions the data is in. Below that you can see the names of all your specimens, and below that the list of landmark data associated with each specimen.
 - Quickly compare the number of landmarks the file says should be there with the number of rows of coordinates for the first specimen to double check there are the correct number of landmarks (each row equals one landmark). If the numbers don't match, let me know.
 - Usually you'd do this for every specimen and all your files, but this is just to get you familiar with the file format.
- 4). Now open up the program **MorphoJ**.



II. Importing data

1). Create a new project in MorphoJ.

- File > Create New Project
- Name the new project “**Lastname_Firstname_GMM**”
- 3 Dimensions
- No object symmetry
- Name for the new dataset: “**Crania**”
- File type “Morphologika”
- Select file **Cranial landmarks.txt**
- Create dataset

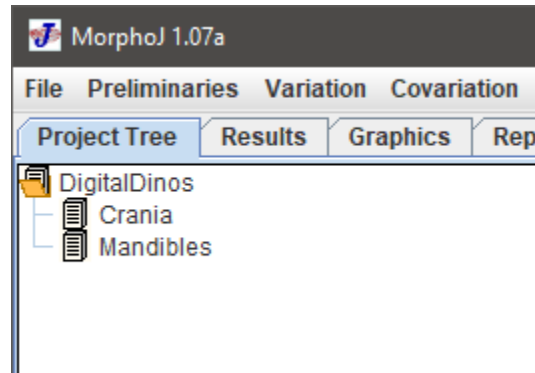


2). Create new dataset

- File > Create New Dataset
- 3 Dimensions
- No object symmetry
- Name for the new dataset: “**Mandibles**”
- File type “Morphologika”
- Select file **Mandibular landmarks.txt**
- Create dataset

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3). Switch from Reports tab to Project tree - you should now have a Project Tree looking like the figure below.



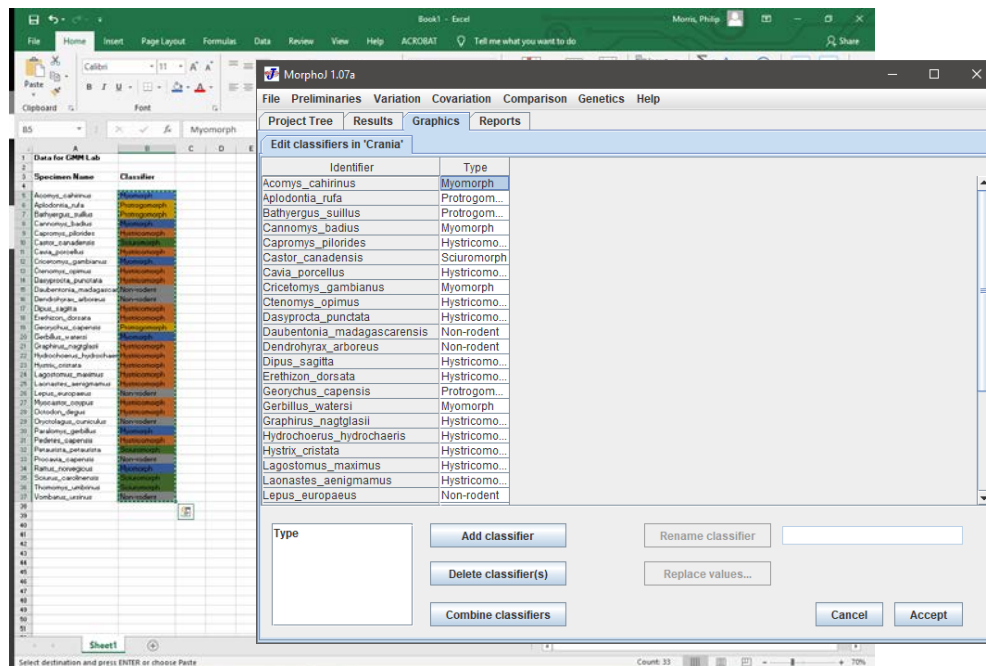
III. Preliminaries

1). **Add classifiers** to your data – these are keywords that allow you to group your data during analysis and will be important later on.

- On the **Project Tree** select the **Crania** dataset > Preliminaries > Edit classifiers > click “Add classifier” and name it “**Type**”
- Open the Excel document **Lab 05 GMM book.xlsx** and copy all of the classifier column (from B5 to B37).

- (if your computer does not have Excel, here is a Google sheets version you can use:

<https://drive.google.com/open?id=1oTJOxtmBK2Bj3sZ3d8MxWAYnnRGUxSNh2GefrngalZY>

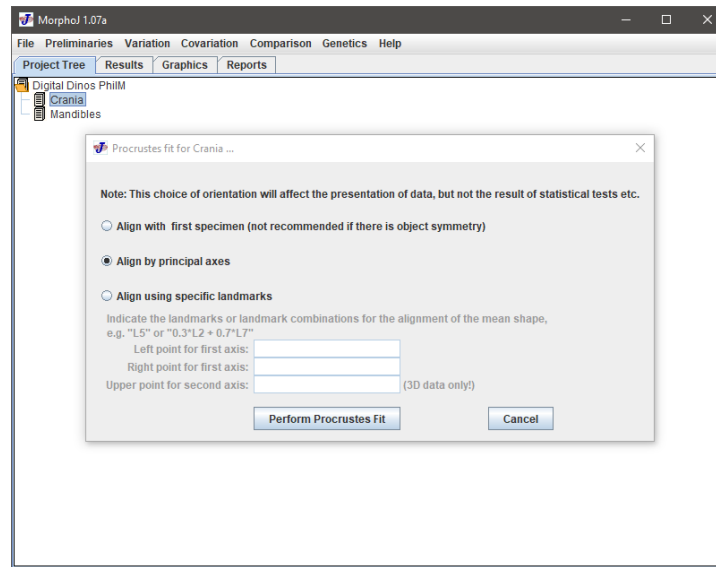


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- Return to MorphoJ and click the first box in the new column that you named “Type” and paste the data in with ctrl + V.
- Click accept.

2). Perform a **New Procrustes Fit** (aka. Procrustes superimposition) on the **Crania** dataset.

- On the **Project Tree** select the **Crania** dataset > Preliminaries > Perform New Procrustes fit
- Align by principal axes
- Perform Procrustes Fit



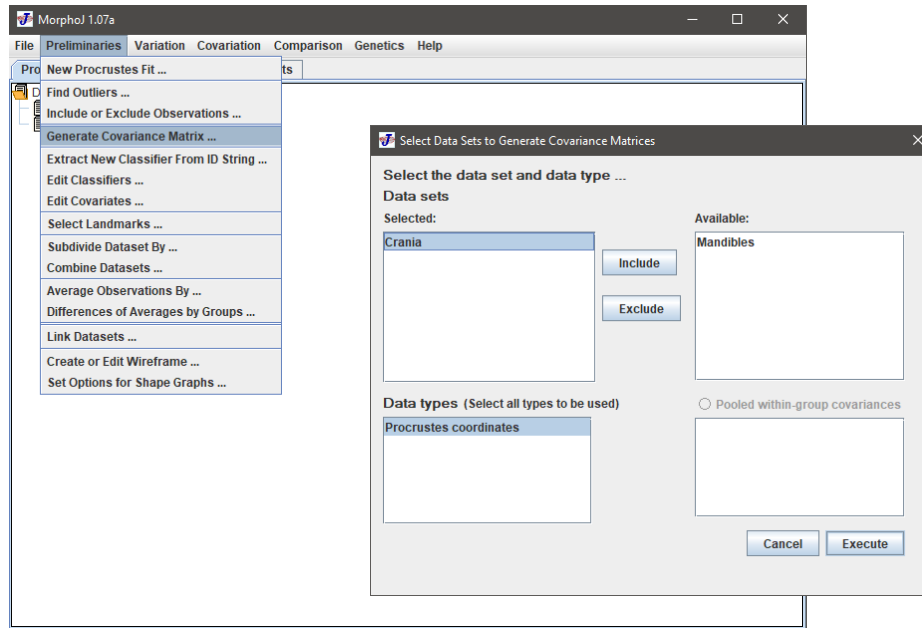
3). Take a look at the result of the Procrustes Superimposition and see if you can make sense of what you’re looking at.

- **Note:** Each individual dot represents a landmark, and each cluster of dots is the variation in landmark coordinates from throughout all the specimens in your dataset. Right away this gives us a good idea of how much difference in shape there might be and where, based on how big the spread of dots is for each landmark. Take a look through different tabs and see what results each offers.

4). Generate a **Covariance Matrix**.

- On the **Project Tree** select the **Crania** dataset > Preliminaries > Generate Covariance Matrix
- In the “Selected” box click **Crania** > Now select “Procrustes coordinates”
- **Execute**

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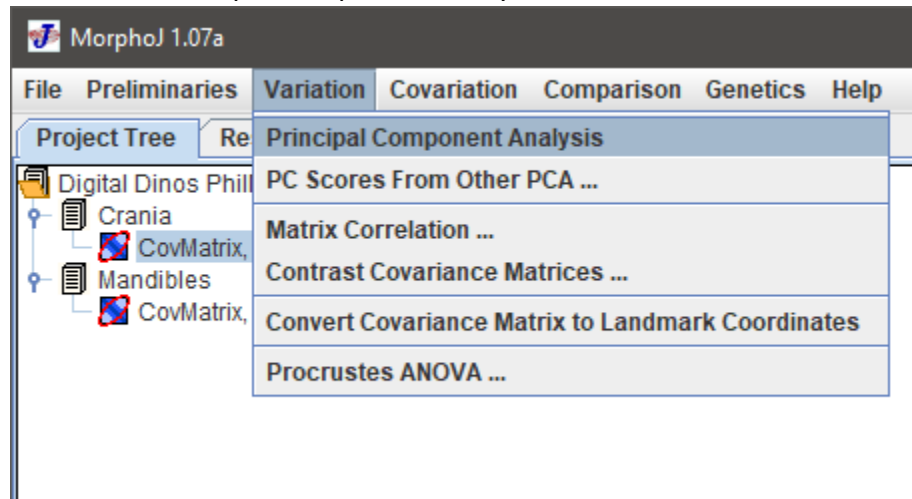


- 5). Perform steps 2 to 4 of section III again, but this time for the **Mandibles** dataset.

IV. Analysis (Shape variation – Principal components analysis - PCA)

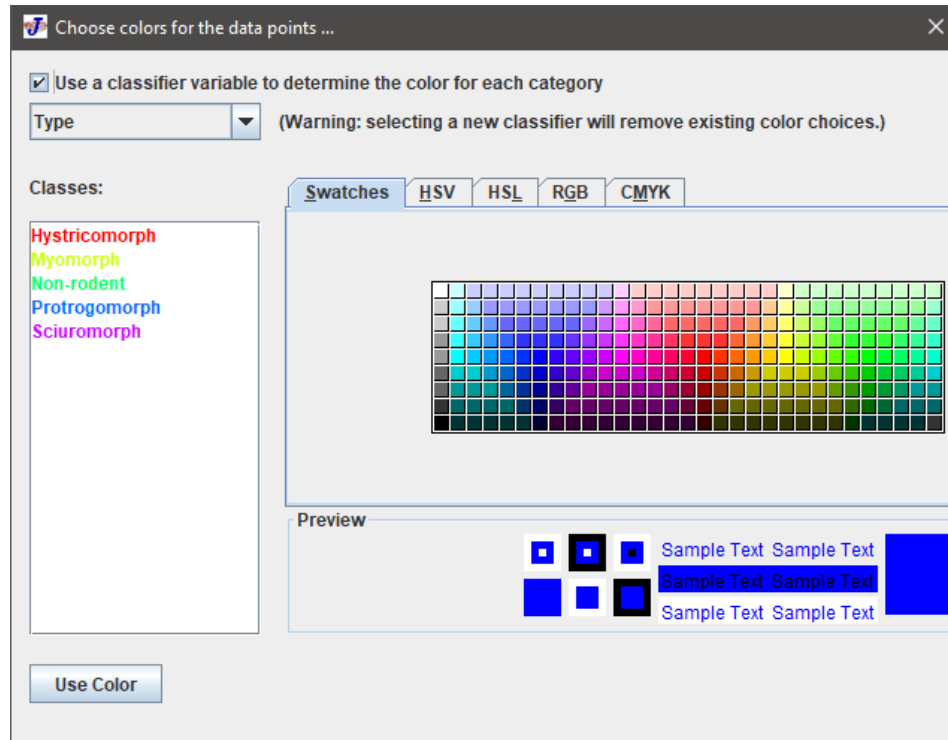
- 1). Perform a **Principal Components Analysis**

- On the **Project Tree** select the **CovMatrix** for the dataset **Crania**.
- Variation > Principal Component Analysis

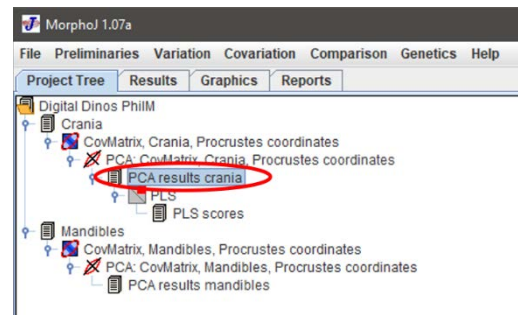


- This will immediately open multiple tabs, all with varying different kinds of figures which tell you about your data.
- Go to the PC Scores tab, right click the graph and select "Label data points". This adds the name for each specimen. You can remove it if it's in the way.

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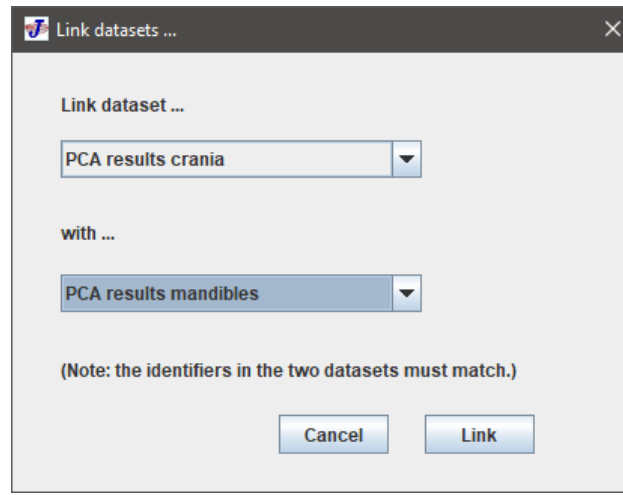


- Right click on the graph again and this time select “Color the data points”. This opens a new window. Select the box that starts “Use a classifier variable...” and then click the “Okay” box. This might be hidden by the edges of the window, so just expand this a little and select it.
 - If you want to change the colors of any of the classifiers select the classifier you want to change in the “Classes” box, choose a color, then click “Use color”.
- 2). Take a look at the PCA plot in the **PC scores** tab again. Now the data is colored can you see any obvious groups or relationships? How does this change if you change what is on each of the axes?
- To change what principal component is on each axis, right click the graph, and select “choose principal components for the vertical/horizontal axis”.
- 3). Perform the same steps above (IV. 1-2) again but this time for the **Mandibles** dataset. Depending on time, skip the steps around exploring your data.
- 4). On the **Project Tree** right click rename the PCAs (PC Scores, **circled**) for each dataset “**PCA results crania**” and “**PCA results mandibles**”



5). Link both sets of results

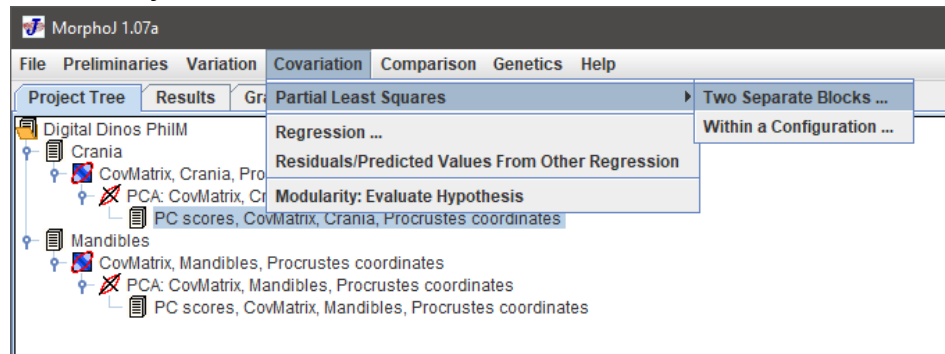
- Preliminaries > Link dataset... “PCA results crania” with... “PCA results mandibles”
- Click “Link”.



V. Analysis (Shape covariation – Partial least squares - PLS)

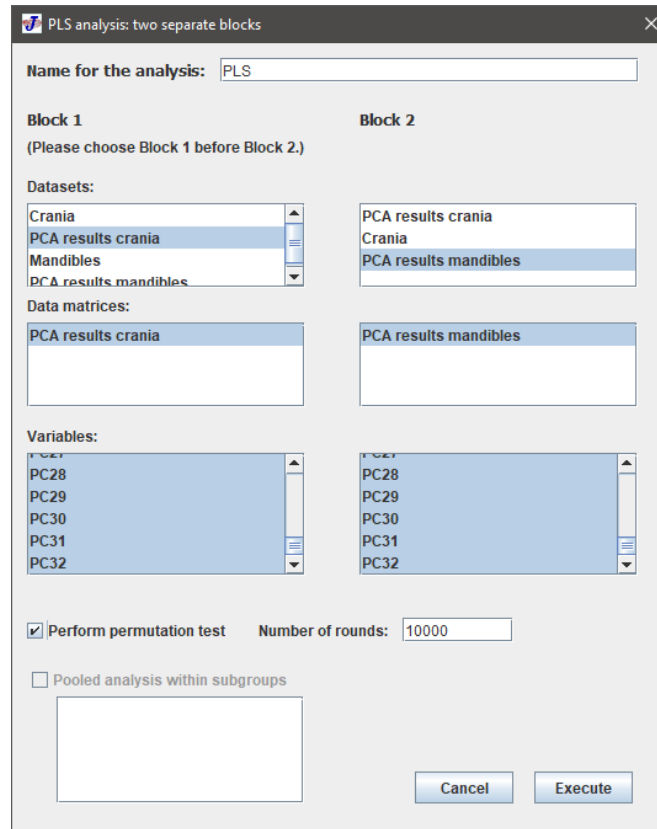
1). Perform a **Partial Least Squares Analysis**.

- On the **Project Tree** select the **PCA results crania** for the dataset **Crania**.



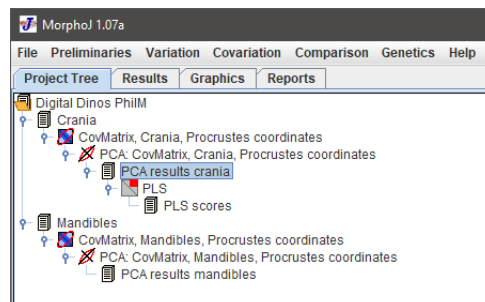
- Covariation > Partial Least Squares > Two Separate Blocks
- This can be a little complicated, so follow the selections in the [figure below]
 - In the **Variables** boxes be sure to select all the PCs for both boxes (Left click PC1, hold shift + left click to bottom of list of PCs).

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- Hit **Execute**

- 2). Take a look at the PLS results,
 - Go straight to the tab called “PLS scores, block 1 vs 2”
 - Explore these results in the same ways you did with the PCA (coloring data points etc).
- 3). Go to the results tab and scroll closer to the bottom and look for the RV coefficient. This is a number between 0 and 1, and is a numerical indicator of how much the two blocks co-vary – with 0 being not at all, and 1 meaning they co-vary perfectly. This indicates the strength of association between the two blocks/datasets.
- 4). Once done, return to the project tree and you should have something that looks similar to the below figure. Now save the project.



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- Select the file in the project tree.
- File > Save Project > Name it “[Lastname_[Firstname] _GMM_Results”

5). **When you’re finished, let me know and we’ll go through the results as a class.**