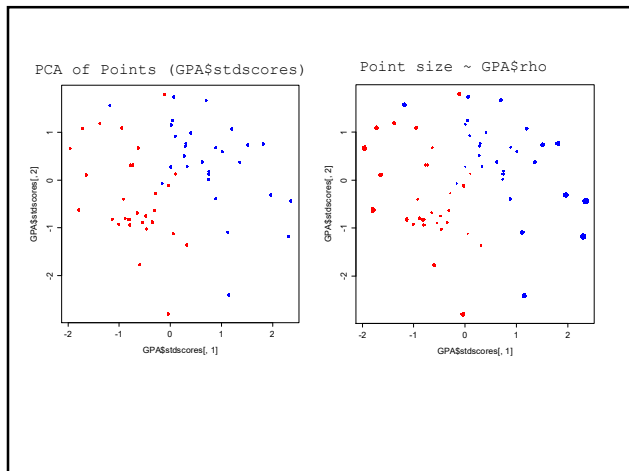
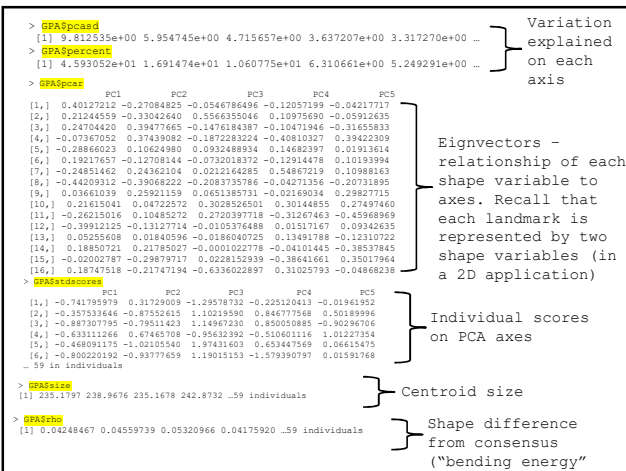
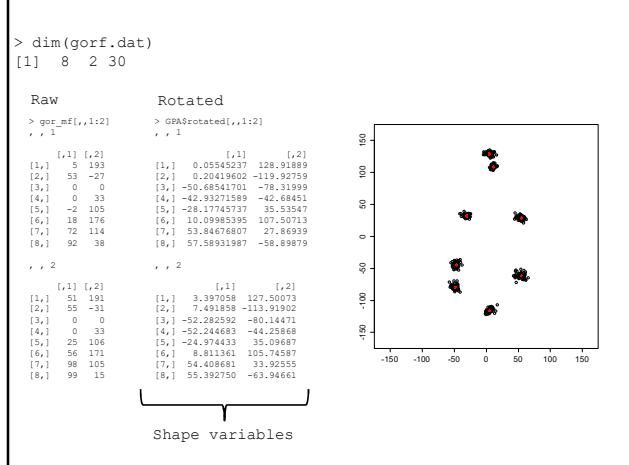


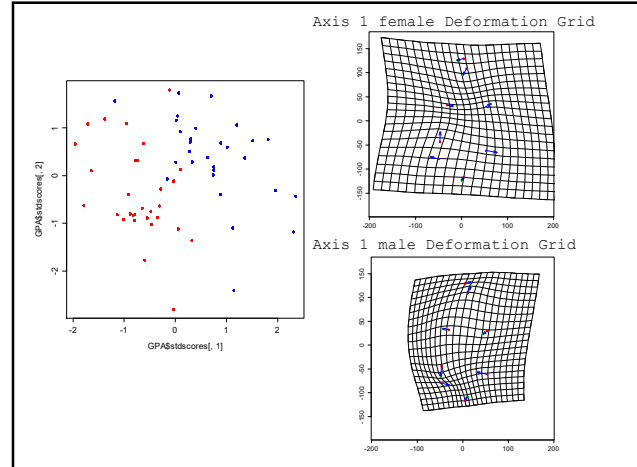
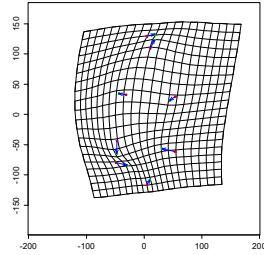
procGPA function

- GPA<-procGPA(gor_mf)
 - Performs general procrustes analysis followed by principal components analysis of shape variables
 - Options
 - scale – scaling of raw data
 - tol – options for tolerance in procrustes rotation
 - tangentcoords – different handling of tangent coordinate
 - Output
 - mshape – consensus (mean) shape
 - rotated – the procrustes rotated shape variables
 - pcar – eigenvectors
 - pcsad - eigenvalues
 - percent – percent of shape variation explained by axes
 - stdscores – sample pca scores



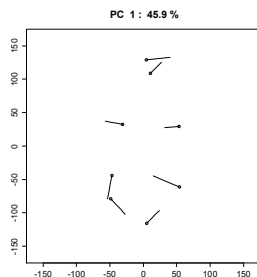
TPS Grids

- Function `tpsgrid`
 - `tpsgrid(xx,yy, [plotting options])`
- Produces TPS (thin plate spline) grids between XX and YY configurations
 - XX and YY could be mean configurations for two groups, one group and the consensus or extreme individuals...etc.
- Options
 - Mag – magnify grid warping to make shape changes easier to see
 - Grid density
 - Line and symbol options
- For your assignment, you will compare the consensus to the skull for *Coelophysis*



Other pertinent functions

- `shapepca(GPA_output, type, mag)`
 - Plots the consensus with vectors for each axis
 - Mag: how much to magnify vectors
 - Type: various ways to show changes



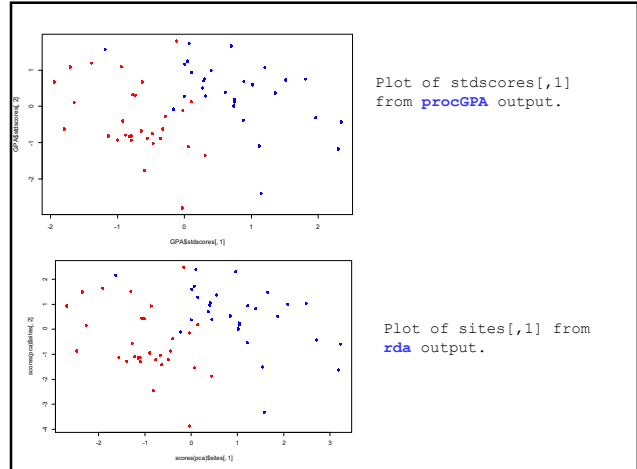
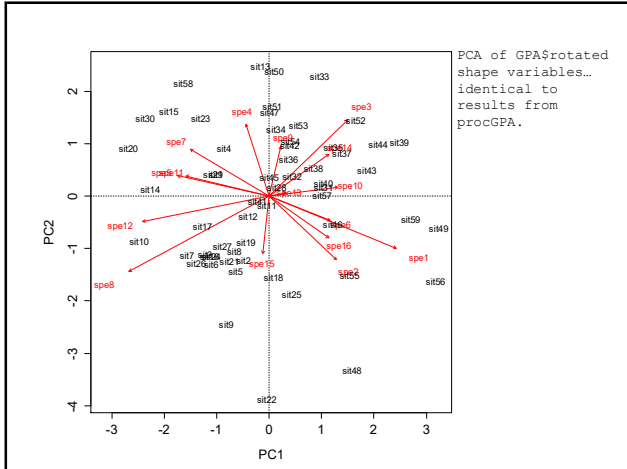
procGPA

- The `procGPA` output can be a bit clunky
- Remember that this is just a PCA of shape variables.
- Convert the `$rotated` 3-D array to a 2-D matrix (individuals by shape variables) and you can use the `rda()` function

```

* shape_variables<-t(matrix(GPA$rotated,16,59))
* pca<-rda(shape_variables)

```



```
GPA$pcasd^2 - (procGPA returns the square root of eigenvalues)
[1] 96.286 35.459 22.237 13.229 11.004 7.923 6.163 5.268 4.794 3.258

GPA$pcasd^2/sum(GPA$pcasd^2) - eigenvalues divided by the sum...
[1] 0.45931 0.16915 0.10608 0.06311 0.05249 0.03780 0.02940 0.02513 0.02287 0.01554

GPA$percent
[1] 45.931 16.915 10.608 6.311 5.249 3.780 2.940 2.513 2.287 1.554

From the rda object (traditional PCA)
rda(X = shape_variables)

Partitioning of variance:
Total Inertia Proportion
Unconstrained 210 1

Eigenvalues, and their contribution to the variance

Importance of components:
      PC1  PC2  PC3  PC4  PC5  PC6  PC7  PC8  PC9
Eigenvalue 96.286 35.459 22.237 13.2293 11.0043 7.9234 6.1625 5.2678 4.7937
Proportion Explained 0.459 0.169 0.106 0.0631 0.0525 0.0378 0.0294 0.0251 0.0229
Cumulative Proportion 0.459 0.628 0.735 0.7976 0.8501 0.8879 0.9173 0.9425 0.9653
```

MANOVA

- Shape data are often analyzed by MANOVA to test for shape differences between groups.
- In this case, use the first 10 axes of the PCA and test for sex differences.
 - response_matrix<-cbind(scores(pca, choices = c(1:10))\$sites[,1:10])
 - Or
 - response_matrix<-cbind(GPA\$scores[,1:10])
- Must include size (centroid size) as a covariate.
 - Centroid size is included in the **procGPA** output as **\$size**

```
model<-manova(response_matrix~GPA$size*sex_factor)
summary(model, test="Wilks")

              Df Wilks approx F num Df den Df Pr(>F)
gor_size      1 0.11741   34.577    10  46 < 2e-16 ***
sex_factor    1 0.64840    2.494    10  46 0.01748 *
gor_size:sex_factor 1 0.78022    1.296    10  46 0.26114
Residuals    55
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Geometric Morphometric Software

- TPS Suite
 - <http://life.bio.sunysb.edu/morph/index.html>
 - Series of programs that do standard GM functions
 - TPSDig – very nice digitization program
- MorphoJ
 - All basic GM functions
 - Klingenberg, C. P. 2011. MorphoJ: an integrated software package for geometric morphometrics. *Molecular Ecology Resources* **11**: 353-357.
 - http://www.flywings.org.uk/MorphoJ_page.htm
 - Will also map shape data onto phylogenies
 - Quantitative genetics of shape

Digitizing specimens

- Pictures of specimens
 - Include scale, try and standardize zoom
 - Make sure specimen is flat
 - Landmarks should be clearly visible
- There are a variety of functions posted on the TPSDig webpage.



MorphoJ

MOLECULAR ECOLOGY
15253-1531

COMPUTER PROGRAM NOTE
MorphoJ: an integrated software package for geometric morphometrics

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- **Functions**
 - Procrustes fit for 2D and 3D data with and without object symmetry
 - Import/export of data sets and supplementary information
 - Identification of outliers (with choices for including/excluding observations and fixing some problems)
 - Generating covariance matrices ('standard' and pooled within-group covariances)
 - Principal component analysis
 - Matrix correlation (including automatic adjustment for symmetry/asymmetry for configurations with object symmetry)
 - Two-block partial least squares
 - Regression (arbitrary numbers of dependent and independent variables; also pooled within-group regression, e.g. for allometry correction in multiple groups)
 - Evaluation of modularity hypotheses
 - **Canonical variate analysis**
 - **Linear discriminant analysis, including cross-validation**
 - **Mapping shape variables onto a phylogeny and comparative methods (e.g. independent contrasts)**
 - Various analyses concerning the quantitative genetics of shape and selection for shape

Other R packages for geometric morphometrics

- Morpho
- Geomorph

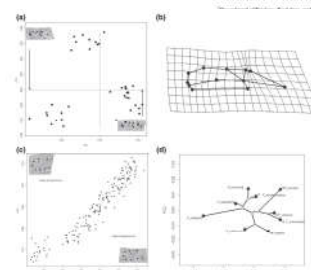


Fig. 3. Example of some of the graphical output from geomorph. (a) Principal components plot of shape variation using the function `pl.pcr(tps2procr(tpsSpecimens, thinShapeDifferences))` between the average (reference) and a target specimen, displayed as a thin-plate spline deformation grid from the function `pl.pcr(tps2procr(tpsSpecimens, thinShapeDifferences))`. (b) Allometric trajectories viewed as the common allometric component (CAC; Mitteroecker et al. 2004) versus size, using the function `pl.pcr(tps2procr(tpsSpecimens, thinShapeDifferences))`. (c) Projections of phylogeny into shape space for tracking evolutionary shape changes obtained with the function `geomorph`.

Outline and Surface analyses

- **Outline analysis** – No homologous landmarks. Specimens digitized by tracing or outlining. Analyses involve functions describing object outline.

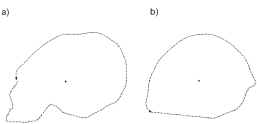
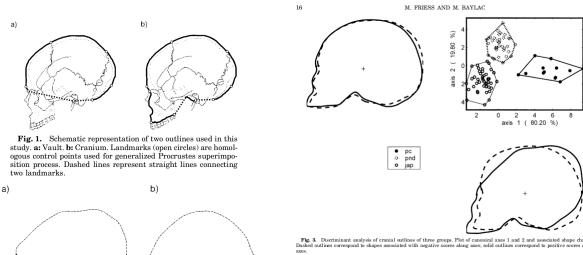


Fig. 3. Shortest analysis of cranial outlines of three groups. Plot of observed axes 1 and 2 and associated shape change. Dashed outlines correspond to shape associated with negative scores along axis 1; solid outlines correspond to positive scores along axis 1.

Fries, M. & Baylac, M. 2003 Exploring artificial cranial deformation using elliptic Fourier analysis of procrustes aligned outlines. American Journal of Physical Anthropology 122, 11-22.