

Introduction to Geomorph Package

Analytical Paleobiology Course 2018

Geometric Morphometrics Module

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Adams, D. C., M. L. Collyer, A. Kaliontzopoulou, and E. Sherratt. 2017. Geomorph: Software for geometric morphometric analyses. R package version 3.0.5. <https://cran.r-project.org/package=geomorph>.

Downloading course package ‘qpal’

- Download “devtools” package in r if you don’t already have it
- Install package using:

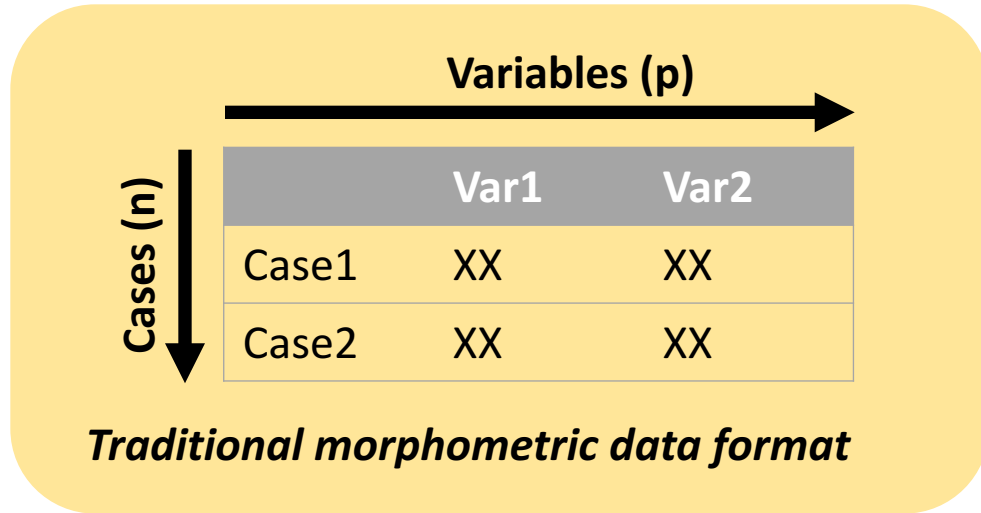
```
devtools::install_github("katrinajones/qpal", build_vignette=T)
```

- Load it into your environment: `library(qpal)`
- External data (e.g., photos) required for this course is saved within the package. To access it, save its location as an object:

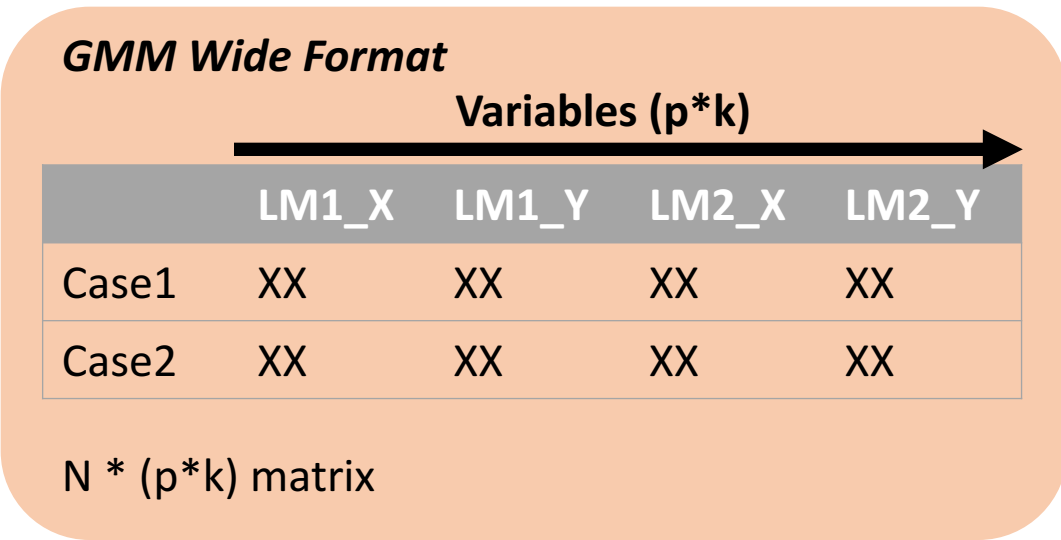
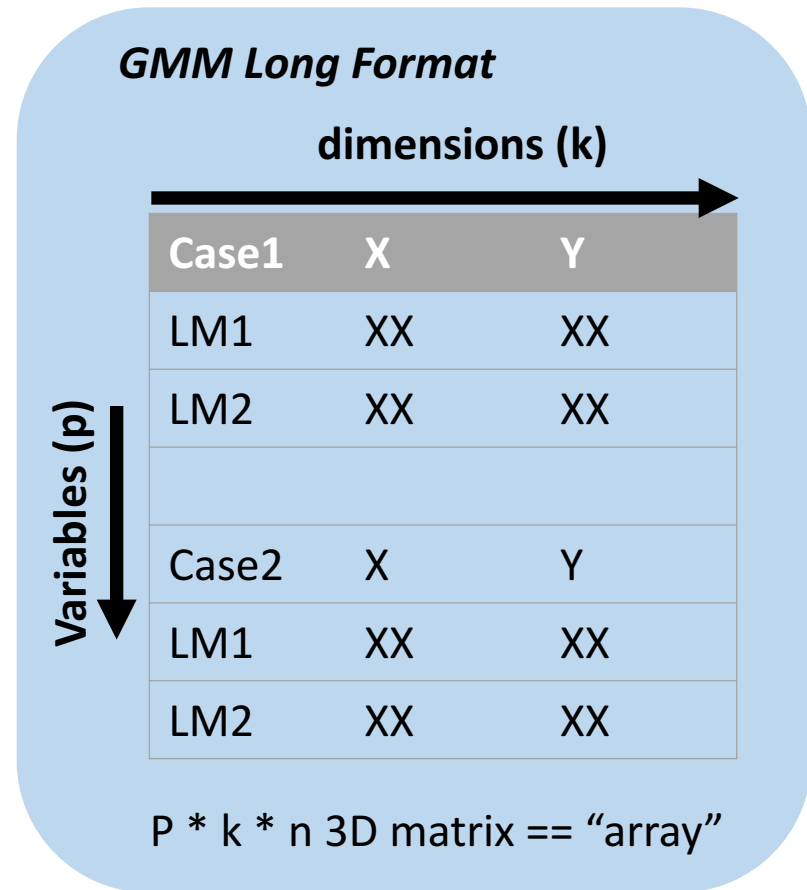
```
Dir.data<-system.file("extdata",package="qpal",mustWork = T)
```

- Some datasets are also saved directly as r datasets, and so can easily be accessed using: `data("mammals")`
- The tutorial associated with this course can be accessed using:
`vignette("GMM_Tutorial",package="qpal")`

Data formats



However, Geometric Morphometric data is either 2 or 3 Dimensional (k=2/3)!



Preferred for Non-GMM software

Preferred for GMM software

Landmark data in r

```
#Load geomorph
library(geomorph, quietly=T)
#> Warning: package 'rgl' was built under R version 3.4.4
#> Warning: package 'ape' was built under R version 3.4.4

#Get example data - plethodon salamander heads
data("plethodon") #Load data into environment

#What's included in the dataset
summary(plethodon)
#>      Length Class  Mode
#> Land      960  -none- numeric
#> Links       28  -none- numeric
#> species     40  factor numeric
#> site        40  factor numeric
#> outline 7262  -none- numeric
```

Landmark data from Plethodon salamander heads

Description

Landmark data from Plethodon salamander heads

Author(s)

Dean Adams

References

Adams, D. C. 2004. Character displacement via aggressive interference in Appalachian salamanders. *Ecology*, 85:2664.

All Bundled together:

- Landmark data
- Wireframes
- Species/site information
- 2D Outlines

Very handy!

Manipulating arrays

```
#Converting between wide and long formats
```

```
#Long to wide
```

```
wide<-two.d.array(plethodon$land)
```

```
wide[1:5,1:5]
```

```
#Wide to long
```

```
long<-arrayspecs(wide, 12, 2)
```

```
long[,1]
```

However, arrays are much more handy for handling GMM data in R because you can easily access all elements with simple code

```
#Indexing arrays
```

```
#Get first specimen
```

```
long[,1]
```

```
#Get first landmark of all specimens
```

```
long[1,,]
```

```
#Get X coordinates of all landmarks
```

```
long[,1,]
```

Geomorph Data Frames

Geomorph data frames are a useful way of tidying all your data associated with your landmarks together into a single object, and are the native and sometimes required format for geomorph functions

```
#Create geomorph data frame
plethgdf<-geomorph.data.frame(landmarks=long, species=plethodon$species,
                              site=plethodon$site)

summary(plethgdf)
#>           Length Class  Mode
#> Landmarks 960    -none- numeric
#> species    40     factor numeric
#> site       40     factor numeric
```

This format is based on a standard r list, thus you can access elements using \$ or [[]]

#Access species information

plethgdf\$species

plethgdf[[2]]

However, unlike a standard list, geomorph checks to ensure you have the same number of individuals in each object, depending on the object types

List objects can be Procrustes residuals (coordinates) arrays, matrices, variables, distance matrices, and phylogenetic trees

Manipulating geomorph data frames

Once your data is all combined into a single geomorph data frame, its very useful to be able to subset it all at once, keeping track of all your separate variables. I've included a custom subsetting function I wrote for this purpose.

#Add to the GDF

```
newvar<-rnorm(length(plethgdf$species))  
plethgdf<-geomorph.data.frame(plethgdf, rand=newvar)  
summary(plethgdf)
```

#Subset by species

#Keep only species='jord'

```
jord<-subsetgeom(plethgdf,'spec',  
which(plethgdf$species=="Jord"), keep=T)  
summary(jord)
```

#Subset by landmarks

#drop first 5 landmarks

```
drop<-subsetgeom(plethgdf,'land', c(1:5), keep=F)  
summary(drop)
```

Graphing in geomorph

#plot first five specimens

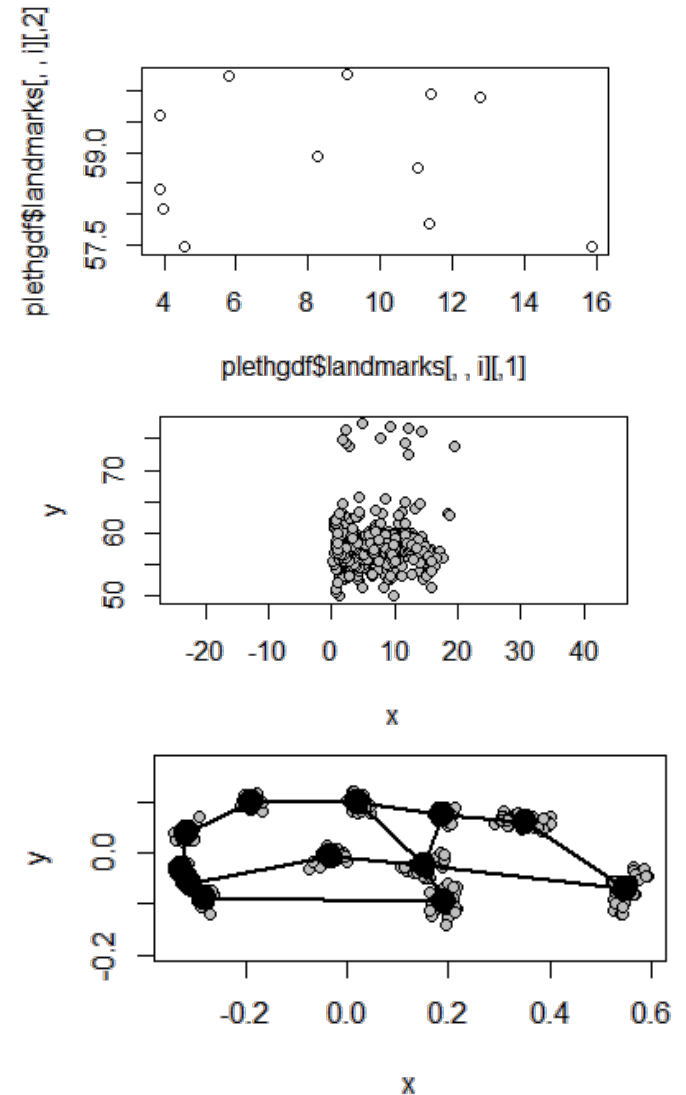
```
for(i in 1:5){plot(plethgdf$landmarks[,i])  
  readline(prompt="Press [enter] to continue")}
```

#plot raw data together

```
plotAllSpecimens(plethgdf$landmarks,  
  mean=F)
```

#plot in same shape space

```
Pcoords<-gpagen(plethgdf$landmarks)  
plethgdf<-geomorph.data.frame(plethgdf,  
  coords=Pcoords$coords,  
  size=Pcoords$Csize)  
plotAllSpecimens(plethgdf$coords, mean=T,  
  links=plethodon$links)
```



Comparing specimens

#Are there any wierd specimens

```
plotOutliers(plethgdf$coords)
```

#Let's compare them

```
shape1<-mshape(plethgdf$coords)
```

```
shape2<-plethgdf$coords[,14]
```

#Thin plate spline

```
plotRefToTarget(shape1, shape2, method=c("TPS"),  
mag=2)
```

#Lollipop

```
plotRefToTarget(shape1, shape2,  
method=c("vector"), mag=10)
```

#Points

```
plotRefToTarget(shape1, shape2,  
method=c("points"), mag=10)
```

