Geometric morphometrics R setup

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1 Introduction

For the session on geometric morphometrics, we will use some R-packages as well as some of my own code (written in an .r-file). All source and data files from my side are made available to you on the summer school website, but perpetually updated code for geometric morphometrics and other analyses is also freely available in my GitHUB repository.

All code has been tested in R v. 4.2.1. Mostly, minor updates to the R core engine do not impact functionality. This means that everything should run fine with any 4.x version and likely with 3.x or even 2.x versions of R. Should you experience any problems with the code provided in any of the exercises, check if you have a recent version of R and compatible versions of all required packages installed. You can, at any point, re-install packages to repair or update them.

2 Installing required packages

A number of packages need to be installed on your system to successfully complete the exercises. You can run the following code to easily install all these packages.

```
#Install the packages, only needed once
install.packages(c("shapes", "Momocs", "geomorph", "Morpho", "devtools", "stringr",
                                 "abind", "sfsmisc", "pixmap", "tiff", "splancs", "jpeg", "vegan",
                                "sp", "MASS", "grDevices", "ape", "cluster", "pls", "pcaPP",
                               "mclust", "mvoutlier", "robust"))
library(devtools)
install_github("klapaukh/hangler")
#Load any or all packages for use in R
library(shapes)
library(momocs)
library(geomorph)
library(Morpho)
```

library(hangler)
library(stringr)

3 Loading source code

To load the functions provided in my source code files into the namespace of the session, you need to navigate to your working directory (the directory where the .r file containing the source code is stored) and use the source()-command.

```
#Replace the following address with the path to your own working directory
setwd("C:/R_Data/Erlangen_Morphometrics")
```

#Load the functions into namespace: Replace the following file name with the name of the # file containing the relevant functions source("MorphometricExtraction_Functions.r")

4 Example datasets

On the website, you find two datasets from my own work. The first is a dataset containing outline data of belemnite hooks (available as raw outline coordinates and smoothed outline coordinates) and the second is a dataset of landmarks from planktonic Foraminifera shells.

Despite the datasets that are available from the website, you are encouraged to use data that are included in the packages to practice the methods we learn. Some of these datasets are:

```
#FOR OUTLINE ANALYSES
#From package 'shapes'
data(cortical) #cortical outlines of 68 humans, separated by age,
    normal vs. schizophrenia, sex, and symmetry
data(sand)#49 sand grain outlines, separated into sea and river sand
#From package 'Momocs'
data(bot)#40 bottles, separated into type and fake
data(apodemus)#30 woodland mouse mandibles, separated by site, species, location
#
    and with area and perimeter values
data(molars) #360 human molars, separated into types
data(mosquito)#126 mosquito wings
data(mouse) #30 mouse molars, separated into populations
data(olea) #210 olive seeds, separated into varieties
data(trilo)#50 trilobite cephalons, separated into ontogenetic stages
#FOR LANDMARK ANALYSES
#From packages 'shapes'
data(apes)#167 specimens, separated into males and females
data(brains) #58 human brains, separated by sex, age, and handedness
data(macaques)#18 macaque skull data, separated into males and females
data(mice) #76 mice vertebrae T2, separated into normal, small, and large mice
data(rats) #18 rat skulls observed over ontogeny
#From package 'geomorph'
data(hummingbirds)#44 hummingbird specimens
data(larvalMorph)#114 larval salamanders, separated into herbicide treatments and
```

```
# taxonomic families
```

```
data(lizards)#98 lizard skulls, 2 replications of data extraction
data(mosquito)#40 mosquito wings, with replications of data extraction
data(plethodon)#40 salamander skulls, separated into species and ecological group
data(plethShapeFood)#Salamander skulls, separated by food source
data(pupfish)#54 fish, separated by sex and population
```