

R functions to plot Westermann Morphospace

Supplement to Ritterbush and Bottjer, 2012. Westermann Morphospace displays ammonoid shell shape and hypothetical paleoecology. *Paleobiology*, 38(3), 424-446.

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- Creates an object with parameters, scaled parameters, etc.

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- Creates an object with parameters, scaled parameters, etc.

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Westyspace()

Description

Plots a Westermann Morphospace ternary diagram derived from measurement data.

Usage

Westyspace(data, identifier, obj.name, title, color)

Arguments

data	a data.frame object that contains measurement data for ammonoid specimens.
identifier	a character string, in quotes, that matches a column name of object data, which the user would like to use to identify specimens in the ternary diagram.
obj.name	a character string, in quotes, that will become the name of the object created by Westyspace().
title	a character string, in quotes, that will be displayed as the title of the Westermann Morphospace ternary diagram in the quartz window.
color	a character string, in quotes, or a number, designating the color for the added data points; see par() for options.

Details

The data object should have at least two rows and five columns, and must have columns with these exact column names: Diameter, Umbilical.Diameter, a, and b. Only these columns and the column of identifier information will be used by Westyspace(), though other cells may be useful for indexing by the user.

After plotting the morphospace, Westyspace() calls function identify(), and the R console will pause for the user to identify the points or pass this step if desired. To identify the points, left click on each point in Westermann Morphospace. A character string (ie, species name) will appear next to each identified point, based on which column from data was chosen as identifier. To stop, right click in the quartz window.

Westyspace() generates an object given the name specified by the obj.name argument. This object is a list containing the following matrices: Parameters, Scaled, Percents, and Coordinates. This follows the steps in Ritterbush and Bottjer 2012, Figure 4. These matrices are handy for other indexing and plotting functions.

Examples

```
Jacobs.demo<-read.csv(file=file.choose())  
# this opens the computer's user interface (explorer, finder,
```

etc) window to find and click on the intended csv file.
Alternately, copy the data table in the demonstration on the last page of this document.

```
Source("WestermannMorphospace.R") # imports the functions to R
```

```
Westyspace(Jacobs.demo, "Genus", "Jacobs.Westy", "Ammonoid shell shapes from Jacobs 1992", "black")
```

```
Westypoints()
```

Description

Adds data points to a Westermann Morphospace diagram already displayed in the quartz window by deriving the coordinates from a data object with measurement values.

Usage

```
Westypoints(data, identifier, color)
```

Arguments

data	a data.frame object that contains measurement data for ammonoid specimens.
identifier	a character string, in quotes, that matches a column name of object data, which the user would like to use to identify specimens in the ternary diagram.
color	a character string, in quotes, or a number, designating the color for the added data points; see par() for options.

Details

Unlike Westyspace(), Westypoints() does not create a list object with matrices of parameters, etc.

Examples

```
Westypoints(Guex, "Species", "red")  
# or use indexing:  
Westypoints(Jacobs.demo[1:3,], "Genus", "blue")
```

Westyplot()

Description

Plots a ternary diagram using the coordinates from an object created via Westyspace().

Usage

Westyplot(coordinates, title, color)

Arguments

coordinates	x, y coordinates.
title	a character string, in quotes, that will be displayed as the title of the Westermann Morphospace ternary diagram in the quartz window.
color	a character string, in quotes, or a number, designating the color for the added data points; see par() for options.

Details

Once Westyspace() has already been used on a dataset, then the list of matrices is available for further use. Westyplot() calls on the coordinates designated and does not deal with measurement data, parameters, etc. It does not generate objects.

By default, Westyplot() calls identify, and uses the row names of the coordinate object as the labels. In the case of objects created using Westyspace(), these row names will match the column initially chosen as the identifier.

Examples

```
Westyplot(Jacobs.Westy$Coordinates, "Ammonoid Shapes from Jacobs  
1992", "red")
```

WestypointsAdd()

Description

Like Westyplot(), this function adds data points to a ternary diagram using coordinates that have already been derived by Westyspace().

Usage

```
WestypointsAdd(coordinates, color)
```

Arguments

coordinates x, y coordinates.

color a character string, in quotes, or a number, designating the color for the added data points; see par() for options.

Details

Once Westyspace() has already been used on a dataset, then the list of matrices is available for further use. Westyplot() calls on the coordinates designated and does not deal with measurement data, parameters, etc. It does not generate objects.

By default, Westyplot() calls identify, and uses the row names of the coordinate object as the labels. In the case of objects created using Westyspace(), these row names will match the column initially chosen as the identifier.

Examples

```
Westyspace(Chamberlain, "Specimen", "Chamberlian.Westy", "Shapes  
from Chamberlain 1976", "black")
```

```
Westypoints(Jacobs.Westy$Coordinates, "red")
```

Demonstrate the 3d projection of ternary diagrams

Example data (from Jacobs, D., 1992, Shape, drag, and power in ammonoid swimming: Paleobiology, v. 18, no. 2, p. 203–220.)

```
Jacobs.demo<-data.frame(matrix(nrow=11,ncol=5))
colnames(Jacobs.demo)<-c("Genus", "Diameter", "a", "Umbilical.Diameter", "b")

Jacobs.demo[1,]<-c(0,5.13,3.220436,0.3175665,1.00)
Jacobs.demo[2,]<-c(0,4.84,2.035338,1.3532569,1.00)
Jacobs.demo[3,]<-c(0,4.80,2.220215,1.1465710,1.50)
Jacobs.demo[4,]<-c(0,4.32,2.222255,0.7829191,1.10)
Jacobs.demo[5,]<-c(0,4.11,1.934417,0.9036098,2.15)
Jacobs.demo[6,]<-c(0,5.02,2.158499,1.3130785,3.10)
Jacobs.demo[7,]<-c(0,4.23,1.35312,1.8087713,1.35)
Jacobs.demo[8,]<-c(0,5.77,2.128687,2.0196039,1.91)
Jacobs.demo[9,]<-c(0,4.88,2.309564,1.1643509,1.89)
Jacobs.demo[10,]<-c(0,5.32,2.699867,1.2918991,2.25)
Jacobs.demo[11,]<-c(0,3.50,1.932218,0.4815402,1.60)

Jacobs.demo[,1]<-
c("Sphenodiscus", "Cardioceras", "Anahoplites", "Oppelia", "Stephanoceras", "Cadoceras",
"Microceras", "Lytoceras", "Otohoplites", "Gastropilites", "Scaphites")

triangle<-matrix(nrow=3,ncol=3)
triangle[1,]<-c(1,0,0)
triangle[2,]<-c(0,1,0)
triangle[3,]<-c(0,0,1)

Display the data in 2 and 3 dimensional space:

library(rgl)

source("WestermannMorphospace.R")

Westyspace(Jacobs.demo, "Genus", "Jacobs.Westy", "Jacobs 1992")

# left click to identify points or right click to move on

plot3d(Jacobs.Westy$Scaled, col="green", size=5,
xlim=c(0,1),ylim=c(0,1),zlim=c(0,1))

points3d(Jacobs.Westy$Percents, col="black", size=5)

triangles3d(triangle, front="fill", col="grey",alpha=.5)

play3d(spin3d(axis=c(0,1,0), rpm=5),duration=12)
```