

# Juan Camilo Arredondo

O título da minha tese é: “Revisão Taxonômica das Serpentes da Tribo Philodryadini Cope 1886 (Serpentes: Dipsadidae); Aplicação de Métodos Comparativos Usando Dados Morfológicos e Moleculares.” e sou orientado pelo Professor Dr. Hussam Zaher.

[exec](#)

[Primeira versão das Propostas](#)

## Proposta Trabalho Final

Escalamento e eliminação do efeito do crescimento alométrico em variáveis morfométricas.

O emprego de variáveis morfométricas e matrizes de dados morfométricos multivariadas são de constante uso em análises de variação morfológica em diferentes áreas da biologia, como taxonomia, evolução, sistemática, e ecologia. No entanto, a natureza destas variáveis não é geralmente tomada em conta na hora de realizar análises que visem compreender a variação da forma e não a variação do tamanho.

A minha proposta consiste em criar uma função que escale variáveis morfométricas <sup>1)</sup> ao aplicar uma técnica de normalização <sup>2)</sup> para escalar variáveis que exibem crescimento alométrico, produzindo um conjunto de dados pronto para análise, sem o efeito do tamanho (size-free). A função receberá uma matriz de dados morfométricos originais e um conjunto de argumentos e aplicará a transformação. No final, haverá dois conjuntos de dados, o original e o escalado. Como resultado, a função realizará um PCA para cada conjunto de dados e apresentará os gráficos de forma comparativa, o original do lado do escalado. Da mesma forma, e com a definição previa de um argumento que selecione alguma variável categórica que defina grupos na matriz morfométrica, uma tabela comparativa apresentará os resultados de um teste de MANOVA realizado a cada conjunto de dados (Original e Escalado). [Leonart et al. \(2000\)](#)

## Página de Ajuda

size.free {unknown}

R Documentation

Data transformation that removes the allometric effect of body size from morphometric data

Description:

Remove the effects of allometric growth on morphometric variables. This removal is performed by applying the proposal of Leonart et al (2000), using a modification of the allometric growth equation.

Usage:

```
size.free(x,vpd=...,vf=...)
```

#### Arguments:

- x** An R object of class "data.frame". In the data set the rows must be the individuals and columns numeric variables, with at least one variable of class "factor".
- vpd** Column number (x[,i]) in the data set (data.frame) that indicates which variable will be used as the standard body size to calculate the constants of growth for each variable.
- vf** Column number (x[,i]) in the data set (data.frame) that indicates the factor variable that will be used to performs an MANOVA on the original and scaled variables.

#### Details:

The transformation is made by applying the equation 13 of Lleonart et al.

(2000:page 88).

$$Y_i^* = Y_i (X_0 / X_i)^b$$

Where  $Y_i$  is the observed value for the individual  $i$  of the variable to be scaled  $Y$ ,  $X_i$  is the observed value for the individual  $i$  of the standard body size variable  $X$ ,  $X_0$  is the mean of the standard body size variable, and  $b$  is the growth constant.

The growth constant is calculated using linear regression.

#### Value:

#### Graphics

Returns a comparative plot (Scaled next to Original data) of principal component analysis (prcomp).

#### MANOVA

Returns the summary of a MANOVA (manova) performed with the Original data followed by other MANOVA made with the Scaled data, both using the factor variable (vf) as factor.

#### File

Saves a file in Comma-separated values format (.csv) with the scaled data in the working directory.

#### Warning:

If there are any NAs or zeros in the input data set, an error message

will indicate in which column are these.

#### Note:

NAs and zero values are not allowed.

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#### References:

Lleonart J., J. Salat, & G. T. Torres. 2000. Removing allometric effects of body size in morphological analysis. *Journal of Theoretical Biology* 205:85–93.

<http://dx.doi.org/10.1006/jtbi.2000.2043>

Thorpe RS. 1976. Biometric analysis of geographic variation and racial affinities. *Biological Reviews* 51: 407–452.

<http://dx.doi.org/10.1111/j.1469-185X.1976.tb01063.x>

#### Examples:

```
## data.frame with NAs and zeros
(df<-data.frame(matrix(sample(c(0,NA,8:10),90,replace=TRUE),ncol=6)))
```

```
## Factor variable
(SP<-sample(paste("SP",1:3,sep=""),15,replace=TRUE))
```

```
## Including the factor variable into the data set
df$SP<-as.factor(SP)
head(df)
```

```
# Applying the function size.free
size.free(df,vpd=2,vf=7)
```

```
## Eliminating NAs
(jn<-df[sapply(df,is.numeric)])
(jn[is.na(jn)]<-sample((jn[!(is.na(jn))]),length(jn[is.na(jn)])))
df[,1:ncol(jn)]<-jn
```

```
# Applying the function size.free
size.free(df,vpd=2,vf=7)
```

```
## Eliminating zeros
(jn<-df[sapply(df,is.numeric)])
jn[jn==0]<-sample(jn[!jn==0],length(jn[df==0]))
df[,1:ncol(jn)]<-jn
```

```
# Apllying the function size.free  
size.free(df,vpd=2,vf=7)
```

## Script da Função

```
## vpd is used as argument to define the standard body size variable and vf  
is the factor variable  
size.free<-function(x,vpd=...,vf=...)  
  
## Extract the numeric variables and store it into a new data frame  
{x1<-x[sapply(x,is.numeric)]  
  
## Extracts the factor variable to a new object  
Factor<-as.factor(x[,vf])  
  
## Extracts the standard size variable to a new object  
vpadrao<-x[,vpd]  
##### NAs and Zeros #####  
  
## Creates a logical object to determinated the presence of NAs at any  
position of the data frame and stores the column of each one  
{Na<-sapply(x1,function(x)any(is.na(x)))  
## Creates a logical object to determinated the presence of zeros at any  
position of the data frame and stores the column of each one  
zero<-sapply(x1,function(x)any(x==0))  
  
## Conditional statement that uses logical evaluation for determination of  
NAs  
if(any(Na))  
  
## Conditional statement that stops the process and shows an error message  
indicating treatment of NAs  
{stop(paste("Please replace NA in column",paste(which(Na),collapse=",")))}  
  
## Conditional statement that uses logical evaluation for determination of  
zeros  
else if(any(zero))  
  
## Conditional statement that stops the process and shows an error message  
indicating treatment of zeros  
{stop(paste("Please replace Zeros in column",paste(which(zero),collapse=","  
")))}  
  
##### Growth Constant #####  
  
## Copies the data into a new object  
x2<-x
```

```
## Erase the standard body size variable from the data set
x2[,vpd]<-NULL

## Extract the numeric variables and store them into a new data frame,
reducing to n-1 variables (data set without the standard size variable)
x3<-x2[sapply(x2,is.numeric)]

## Creates a matrix of NAs to later include the regression coefficients
{abs<-matrix(NA,ncol=2,nrow=ncol(x3))}
## Creates a matrix of NAs to later include the growth constants
b<-rep(NA,ncol(x3))

## for-loop function that calculates the coefficients of each variable and
stores into a new object
for (i in 1:ncol(x3))

## Calculates the regression between variables and includes its coefficients
into the abs matrix
{abs[i,]<-coefficients(lm(log(vpadrao)~log(x3[,i])))}

## Calculates the exponential of each growth constant and include its value
into the object b
b[i]<-abs[i,2]}}

##### Transformation #####

## Creates an object with the total number of elements in the data set to be
scaled
{l<-nrow(x3)*ncol(x3)}

## Transform the data set into a matrix
n.m<-as.matrix(x3)

## Creates a matrix with the values of the growth constants, repeated by
columns.
n.b<-matrix(rep(b,rep(nrow(x3),ncol(x3))),ncol=ncol(x3))

## Creates a matrix with the values of the standard size variable, repeated
by columns.
y<-matrix(rep(vpadrao,ncol(x3)),ncol=ncol(x3))

## for-loop function that calculates the scaled value of each value of the
original matrix.
for(i in 1:l)

## Calculates the scaled value and include it in a new scaled matrix.
{n.m[i]<-n.m[i]*((mean(vpadrao)/y[i])^n.b[i])}
## Transform the scaled matrix into a data frame object
scaled<-as.data.frame(n.m)}

## Includes the standard size variable into the data set of scaled variables
```

```
scaled$VPD<-vpadrao

## Includes the factor into the data set of scaled variables
scaled$Factor<-Factor}

##### PCA #####

## Original Data ##

## Performs an analysis of principal components (using the covaration
matrix) on the original data (only the numeric variables)
{pca0rig<-prcomp(x1)

## Creates an object with the variances of each principal component (columns
in pca0rig$x)
vs<-apply(pca0rig$x,2,var)

## Creates an object with the Proportion of variation of each principal
component
povar<-vs/sum(vs)

## Saves the loadings of the principal components in a data frame
pcs<-as.data.frame(pca0rig$x)

## Includes the Factor variable into the data set of loadings of the
principal components of original data set
pcs$Factor<-Factor}

## Scaled Data ##

## Performs an analysis of principal components (using the covaration
matrix) on the scaled data (only the numeric variables)
{pcaScal<-prcomp(scaled[sapply(scaled,is.numeric)])

## Creates an object with the variances of each principal component (columns
in pcaScal$x)
vs2<-apply(pcaScal$x,2,var)

## Creates an object with the Proportion of variation of each principal
component
povar2<-vs2/sum(vs2)

## Saves the loadings of the principal components in a data frame
pcs2<-as.data.frame(pcaScal$x)

## Includes the Factor variable into the data set of loadings of the
principal components of scaled data set
pcs2$Factor<-Factor}
```

```
## Creates a graphic window to include two plots, arranged horizontally
par(mfrow=c(1,2))

## PCA Plots ##

## Plot the First Principal Component against the second, both from the
original data
{plot(pcaOrig$x,main="PCA of Original Data",xlab=paste("First Principal
Componet ",round((povar[1])*100,1),"%"),ylab=paste("Second Principal
Componet ",round((povar[2])*100,1),"%"),bty="l",type="n")
## Plot the points as the their respective factor names, for the original
variable
text(x=pcs[,1],y=pcs[,2],labels=pcs[,ncol(pcs)])

## Plot the First Principal Component against the second, both from the
scaled data
plot(pcaScal$x,main="PCA of Scaled Data",xlab=paste("First Principal
Componet ",round((povar2[1])*100,1),"%"),ylab=paste("Second Principal
Componet ",round((povar2[2])*100,1),"%"),bty="l",type="n")

## Plot the points as the their respective factor names, for the scaled
variable
text(x=pcs2[,1],y=pcs2[,2],labels=pcs2[,ncol(pcs2)])
}

##### MANOVA #####

## Performs a MANOVA with the original data
{manova.orig<-manova(as.matrix(x1)~Factor)
## Performs a MANOVA with the Scaled data
manova.scal<-manova(as.matrix(scaled[sapply(scaled,is.numeric)])~Factor)

## Prints a title previous to the summary of the Wilks MANOVA test for the
original data
cat("Wilks MANOVA test for Original Data\n")

## Prints the summary table of the Wilks MANOVA test for the original data
print(summary(manova.orig,test="Wilks"))

## Prints a paragraph line
cat("\n")

## Prints a title previous to the summary of the Wilks MANOVA test for the
Scaled data
cat("Wilks MANOVA test for Scaled Data\n")

## Prints the summary table of the Wilks MANOVA test for the Scaled data
print(summary(manova.scal,test="Wilks"))}

##### File #####
```

```
{  
  
## Saves a file in the working directory with the scaled data  
write.csv(scaled,"Data Scaled.csv",row.names=FALSE)  
  
## Explanatory text for the function and the arrangement of the columns in  
the scaled file  
cat("\nExplanation\n\nThe File -Data Scaled.csv- was saved in your  
working\ndirectory, and contains your scaled variables as a\nproduct of the  
transformation of your original data,\nfollowing the proposal of Lleonart et  
al., (2000)*.\nThe file contains an equal number of variables that\nyour  
original data; however, the variables of the\nstandard size (vpd) and factor  
(vf) were named as\n-VPD- and -Factor-, respectively, and moved to the\nend  
of the data set.\n\n* Lleonart J., J. Salat, & G. T. Torres. 2000.\nRemoving  
allometric effects of body size in morphological analysis.\nJournal of  
Theoretical Biology 205:85–93.\nhttp://dx.doi.org/10.1006/jtbi.2000.2043")  
}  
}
```

## Arquivos com os scripts

[size.free.R](#)

[example\\_size.free.R](#)

1)

Quaisquer variável que seja afetada por mudanças no crescimento alométrico de um indivíduo. Peso, Altura, comprimentos corporais, etc.

2)

Proposta de Lleonart et al (2000), que emprega uma modificação da equação do modelo de crescimento alométrico. Link com o PDF do artigo no final

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