



Chi-square tests:

```
data.chisq<-read.table("clipboard")           #Reading data from Excel
chisq.test(data.chisq)                       #Chi Square test
```

Manly selection ratios and Likelihood-ratio test (both analysis are performed with the same function):

```
library(adehabitatHS)
snake.used<-c(10,37,7,6)
snake.avail<-c(21,16,22,1)
names(snake.used)<-c("Mature forest","Early Succession","Late Succession","Human
infrastructure")
BothropsSR<-widesl(snake.used,snake.avail,avknown=TRUE,alpha=0.05)
#Manly Selection ratios and Likelihood-ratio test
BothropsSR
```

MANOVA and Discriminant Function Analysis:

```
library(mvnormttest)
library(biotools)
library(MVN)
library(MASS)
datas <- read_csv(C:\Users\Danie\Downloads\MANOVA_DFA)
manova.datas<-
manova(cbind(SC,CC,DNBW,DNFL,DNT)~Type_of_observation,data=datas,test="Wilks")
#MANOVA Test for microhabitat values of snakes locations vs random points
summary(manova.datas)
lda.data<-lda(Type_of_observation~SC+CC+DNBW+DNFL+DNT,data=datas)
#Discriminant Function Analysis for snakes locations vs random points
lda.data
manova.datas2<-manova(cbind(SC,CC,DNBW,DNFL,DNT)~Season,data=datas,test="Wilks")
#MANOVA Test for microhabitat values between diferrent seasons
summary(manova.datas2)
manova.datas3<-
manova(cbind(SC,CC,DNBW,DNFL,DNT)~Age_class,data=datas,test="Wilks") #MANOVA
Test for microhabitat values between diferrent age classes
summary(manova.datas3)
manova.datas4<-manova(cbind(SC,CC,DNBW,DNFL,DNT)~Behavior,data=datas,test="Wilks")
#MANOVA Test for microhabitat values between diferrent behaviors
summary(manova.datas4)
lda.data2<-lda(Behavior~SC+CC+DNBW+DNFL+DNT,data=datas) #Discriminant
Function Analysis for different behaviors
lda.data2
```

Poisson regression:

```
library(msm)
library(Rtools)
dataPR <- read_csv(C:\Users\Daniel\Downloads\Poisson_regression)
summary(dataPR)
glm.data<-glm(Num_snakes ~ Num_amphi, family="poisson", data=dataPR)      #Poisson
regression
summary(glm.data)
exp(cbind(IR = coef(glm.data), confint(glm.data)))      #Incidence rates ratios
with(glm.data, cbind(res.deviance = deviance, df = df.residual, p = pchisq(deviance, df.residual,
lower.tail=FALSE)))      #Deviance goodness of fit test
```

Mann Whitney U tests were performed in STATISTICA.