APPENDIX 1

Sequence of commands for spatial distribution of count data (Poisson Distribution). Random distribution of isopod individuals in a sandy beach on the Caribbean, Costa Rica.

#The data file is called beach.fauna in format .csv, and it is available at : <http://www.kerwa.ucr.ac.cr/handle/10669/29428>

#Commands based in Krebs (1999) and Crawley (2007)

attach(beach\_fauna)

#STEP 1) SAMPLE SIZE.

Isopoda<-Cirolana+Ancinus

n<-length(Isopoda)

n

#STEP 2) POPULATION PARAMETERS.

Mean<-mean(Isopoda)

Mean

Variance<-var(Isopoda)

Variance

#STEP 3) OBSERVED VALUES

#Table of observed values = first row: number of individuals, and second row: number of sampling units.

table(Isopoda)

#Observed values including the full range of number of individuals.

Isopoda1 <- factor(Isopoda, levels = c(0:max(Isopoda+1)))

table(Isopoda1)

#Frequency of sampling units by counts of individuals.

TableCounts<-data.frame(table(Isopoda1))

freq<- c(TableCounts$Freq)

freq

#STEP 4) INDEX OF DISPERSION:

#random pattern (ID = 1), uniform pattern (ID < 1), and clumped pattern (ID > 1).

ID<-var(Isopoda)/mean(Isopoda)

ID

#Index of dispersion test, based in a chi-squared.

CHI<-ID\*(n-1)

CHI

#if chi-squared value is between tabular values the null hypothesis of random pattern (ID = 1) is not rejected.

qchisq(0.975,(n-1), lower.tail = FALSE) #tabular value of chi-squared 0.975

qchisq(0.025,(n-1), lower.tail = FALSE) #tabular value of chi-squared 0.025

#In this case, If the value of the index of dispersion is between the tabulated values the pattern is random (ID = 1)

#STEP 5) POISSON FIT FOR RANDOM PATTERN (ID = 1). AGGREGATION PROBABILITIES.

#The probability of obtaining X individuals in a sample follows a random pattern modeled by the Poisson distribution.

#density function to obtain the probability of found an *x* number of individuals in a sampling unit, with a parameter λ

#(λ = mean = variance):

$$p(x) =\left(e\right)^{- λ}\left(\frac{λ^{x}}{x!}\right)$$

poisp<-dpois(0:max(Isopoda+1), Mean)

#STEP 6) EXPECTED FREQUENCIES FOR A THEORETICAL POISSON DISTRIBUTION

#The Poisson probabilities can be expressed as frequencies by multiplying each by the sample size (n)

poisfreq<-dpois(0:max(Isopoda+1), Mean)\*n

#STEP 7) SUMMARY TABLE WITH OBSERVED AND EXPECTED VALUES

SummaryTable<-data.frame(x=TableCounts,poisfreq, poisp)

SummaryTable

#STEP 8) COMPARISON OF THE OBSERVED AND EXPECTED FREQUENCIES WITH A BARPLOT

par(mfrow=c(1,1), pch=22)

E<-(max(Isopoda+1)+1)\*2

both<-numeric(E)

both[1:E %% 2 != 0]<-freq

both[1:E %% 2 == 0]<-poisfreq

labels<-character(E)

labels[1:E %% 2 == 0]<-as.character(0:max(Isopoda+1))

barplot(both,col=rep(c("black","white"),max(Isopoda)),names=labels,ylab="Frequency of samples",

 xlab="Counts")

legend(x = "topright",c("observed","expected"),fill=c("black","white"))

#STEP 9) GOODNESS OF FIT (G TEST):

#The null hypothesis is that observed values follow a Poisson distribution

#To follow the assumption of all expected values should be 1 or more, the last observations need be pooled (Krebs, 1999):

cs<-factor(0:max(Isopoda+1))

a<-max(which(SummaryTable$poisfreq>1))

a

levels(cs)[a:max(Isopoda+a)]<-"+"

levels(cs)

#expected values for G test:

ef<-as.vector(tapply(SummaryTable$poisfreq,cs,sum))

#observed values for G test:

of<-as.vector(tapply(SummaryTable$x.Freq,cs,sum))

#Table of contingence for G test:

p<-as.vector(tapply(SummaryTable$poisp,cs,sum))

ContigenceTable<-data.frame(of,ef,p)

ContigenceTable

#G test:

G<-2\*sum((of)\*log(of/ef))

G

#Degrees of freedom = Frequency classes (counts) - 2 statistics (total and mean) used to fit the Poisson distribution.

df<-sum(ef>0)-2

df

qchisq(0.95,df)

pchisq(G,df, lower.tail = FALSE)

#In this case p>0.05, and null hypothesis can not be rejected.

#Conclusion: The data follows a Poisson distribution.

#G test adjusted by Williams' correction for continuity for small samples (n < 200)(Krebs, 1999).

q<-1+((a+1)/(6\*sum(of)\*df))

q

Gadj<-G/q

Gadj

qchisq(0.95,df)

pchisq(Gadj,df, lower.tail = FALSE)

#In this case p > 0.05, and null hypothesis can not be rejected.

#Conclusion: The data follows a Poisson distribution.