APPENDIX 3

Sequence of commands for spatial distribution of count data (Binomial Distribution).

Uniform pattern of number of taxa 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.

n<-length(Taxa)

n

#STEP 2) POPULATION PARAMETERS.

Mean<-mean(Taxa)

Mean

Variance<-var(Taxa)

Variance

#STEP 3) OBSERVED VALUES

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

table(Taxa)

#Observed values including full range of number of individuals.

Taxa1 <- factor(Taxa, levels = c(0:max(Taxa+1)))

table(Taxa1)

#Frequency of sampling units by counts of individuals.

TableCounts<-data.frame(table(Taxa1))

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(Taxa)/mean(Taxa)

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 lower than tabulated values the pattern is uniform (ID < 1)

#STEP 5) BINOMIAL FIT FOR UNIFORM PATTERN (ID < 1)

#The binomial distribution is determined by the equation:

# with

#To fit the data to the binomial distribution, first k is estimated: ,

#k is the maximum number of individuals can be found in a sampling unit, and a estimate of n.

k<-round(Mean^2/(Mean-Variance))

k

#The probability (p) of an event x occurs is calculated

p<-Mean/k

p

#and the probability of not occurrence of an event (q)

q<-1-p

q

#number of individuals

x<-0:max(Taxa+1)

x

# STEP 6) BINOMIAL DISTRIBUTION PROBABILITIES

#Probability of found an X number of individuals in a sampling unit.

binomialp<-dbinom(x, k, p)

#STEP 7) EXPECTED FREQUENCIES FOR A THEORETICAL BINOMIAL DISTRIBUTION

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

binomialfreq<-dbinom(x, k, p)\*n

# STEP 8) SUMMARY TABLE WITH OBSERVED AND EXPECTED VALUES

SummaryTable<-data.frame(x=TableCounts,binomialfreq,binomialp)

SummaryTable

#STEP 9) COMPARISON OF THE OBSERVED AND EXPECTED FREQUENCIES WITH A BARPLOT

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

both<-numeric(E)

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

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

labels<-character(E)

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

Fig<-barplot(both,col=rep(c("black","white"),max(Taxa+1)),names=labels,ylab="Frequency of samples",

xlab="Counts")

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

#STEP 10) GOODNESS OF FIT (G TEST):

#USING G TEST

#The null hypothesis is that observed values follow a binomial 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(Taxa+1))

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

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

#expected values for G test:

ef<-as.vector(tapply(SummaryTable$binomialfreq,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$binomialp,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) - 3 statistics (total, *p* and *k*) used to fit the binomial distribution.

gl<-sum(ef>0)-3

gl

#Theoretical values of G test (using chi-squared distribution).

qchisq(0.95,gl)

#probability of the null hypothesis.

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

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

#Conclusion: The data follows a binomial distribution.

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

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

q

Gadj<-G/q

Gadj

qchisq(0.95,gl)

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

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

#Conclusion: The data follows a binomial distribution.