

## 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  $\lambda$

##( $\lambda$  = mean = variance):

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

```
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 contingency for G test:
```

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

```
ContingenceTable<-data.frame(of,ef,p)
```

```
ContingenceTable
```

```
#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.