
Online Appendix 16.A: Demonstration of Poisson sampling

Online Appendix 16.A.1: Code listing

```
#mainPoissonExample.R
rm(list = ls())
library(exactci)

K <- 10000
cat ("K = ", K,"lambdaP 1st reader = ", 1,"lambdaP 2nd reader = ", 2,"\n")
lambdaP <- c(1,2)
seed <- 1;set.seed(seed);samples1 <- rpois(K,lambda = lambdaP[1]);cat("obs. mean, reader 1 = ",
mean(samples1), "\n")
seed <- 1;set.seed(seed);samples2 <- rpois(K,lambda = lambdaP[2]);cat("obs. mean, reader 2 = ",
mean(samples2), "\n")

ret1 <- poisson.exact(sum(samples1),K)
ret2 <- poisson.exact(sum(samples2),K)

cat ("Rdr. 1: 95% CI = ", ret1$conf.int[1:2],"\n")
cat ("Rdr. 2: 95% CI = ", ret2$conf.int[1:2],"\n")
```

Note the usage of the **R** package **exactci**, for exact confidence intervals (these will generally be asymmetric and not include illegal values, like negative values for the Poisson parameter). If one gets a message like **there is no package called ‘exactci’**, it means the relevant package has not been loaded. Use the **Packages – Install** tabs in the lower right window of **RStudio** window to load the missing package.

Online Appendix 16.B: Demonstration of binomial sampling #1

Online Appendix 16.B.1: Code listing

```
#mainPoissonExample.R
rm(list = ls())
library(exactci)

K <- 10000
cat ("K = ", K,"lambdaP 1st reader = ", 1,"lambdaP 2nd reader = ", 2,"\n")
lambdaP <- c(1,2)
seed <- 1;set.seed(seed);samples1 <- rpois(K,lambda = lambdaP[1]);cat("obs. mean, reader 1 = ",
mean(samples1), "\n")
seed <- 1;set.seed(seed);samples2 <- rpois(K,lambda = lambdaP[2]);cat("obs. mean, reader 2 = ",
mean(samples2), "\n")

ret1 <- poisson.exact(sum(samples1),K)
ret2 <- poisson.exact(sum(samples2),K)

cat ("Rdr. 1: 95% CI = ", ret1$conf.int[1:2],"\n")
cat ("Rdr. 2: 95% CI = ", ret2$conf.int[1:2],"\n")
```

Online Appendix 16.C: Demonstration of binomial sampling #2

Online Appendix 16.C.1: Code listing

```
#mainBinomialExample2.R
rm(list = ls())
library(exactci)

K2 <- c(97,2,1);Lk <- c(1,2,3);nuP1 <- 0.5;nuP2 <- 0.9;
samples1 <- array(dim = c(sum(K2),length(K2)))
cat("K2[1] = ", K2[1],"K2[2] = ", K2[2],"K2[3] = ", K2[3], ", nuP1 = ", nuP1, ", nuP2 = ", nuP2,
"\n")
seed <- 1;set.seed(seed)
for (l in 1:length(K2)) {
  samples1[1:K2[l],l] <- rbinom(K2[l],Lk[l],nuP1)
}
```

```
cat("obsvd. mean, reader 1 = ", sum(samples1[!is.na(samples1)])/sum(K2*Lk), "\n")

samples2 <- array(dim = c(sum(K2),length(K2)))
seed <- 1;set.seed(seed)
for (l in 1:length(K2)) {
  samples2[1:K2[l],l] <- rbinom(K2[l],Lk[l],nuP2)
}
cat("obsvd. mean, reader 2 = ", sum(samples2[!is.na(samples2)])/sum(K2*Lk), "\n")

ret1 <- binom.exact(sum(samples1[!is.na(samples1)]),sum(K2*Lk))
ret2 <- binom.exact(sum(samples2[!is.na(samples2)]),sum(K2*Lk))

cat ("Rdr. 1: 95% CI = ", ret1$conf.int[1:2],"\n")
cat ("Rdr. 2: 95% CI = ", ret2$conf.int[1:2],"\n")
```