STAT 527 HW 3

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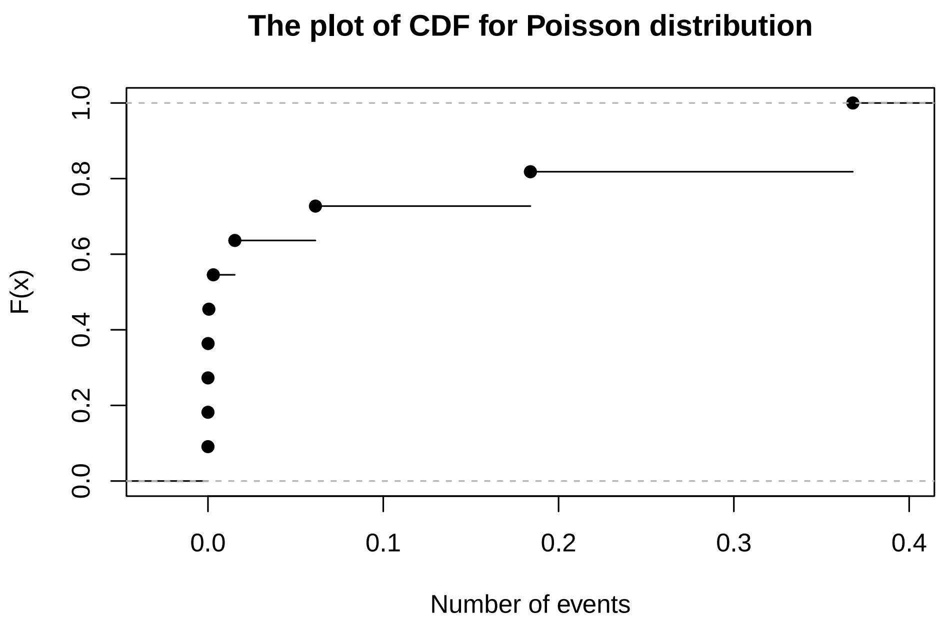
1
(10 points) Money growth. Write an R function to calculate the amount of money, nt, in a fixed interest investment at any time t in the future, starting with n0 dollars at 100 · i% per year interest.
The equation is nt =n0(1+i)t.
Besides n0 and i, the function should take as an argument a whole vector of times and return a whole vector of corresponding dollar amounts. Evaluate your function with appropriate experimental inputs.

```
nt <- function(n0, i, t) {
    out <- n0 * (1 + i)^t
    return(out)

}

# This function seems work right
nt(100, 0.05, 10)
```

```
## [1] 162.8895
```

2 (10 points) Poisson distribution. A discrete random variable X is said to have a Poisson distribution, with parameter lambda > 0, if it has a probability mass function given by: f(k;lambda) = Pr(X = k) = (lambda * k * e^ - lambda)/k! where k >= 0. The cumulative distribution function (CDF) of Poisson distribution evaluated at X = x is calculated as Pr(X =< x). Write an R function that takes lambda and x as inputs and returns the CDF value. Pick lambda=1 and evaluate your function at x = 0, 1, . . . , 10. Plot your results and set an appropriate title for your plot. Hint: you may find the R functions exp() and factorial() being useful.

```
cdf <- function(lambda, x) {
    a <- 0:x
    pmf <- lambda ^ a * exp(lambda * (-1)) / factorial(a)
    out <- unlist(ecdf(pmf))
    # out2 <- ppois(a, lambda)
    return(out)
}
a <- 0:10
plot(cdf(1, 10), xlab = "Number of events", ylab = "F(x)",
    main = "The plot of CDF for Poisson distribution")
```



3

(10 points) Hardy-Weinberg frequencies. Remember from basic genetics that in humans and many animals a gene inherited from the mother and a gene inherited from the father combine to determine a trait inherited by an offspring. If there are two variants of a gene, labeled, say, A and B, in a population, then the possible genotypes of individuals in the population are AA, AB, or BB. Suppose we model the formation of a new generation as follows. Males and females put all their gametes or sex cells, each of which carries either an A gene or a B gene, into a big urn, and new individuals are made by drawing out two gametes at random. Suppose the proportion (or fraction) of gametes with A genes in the urn was p, and so the proportion of gametes with B genes was 1 - p. These two fractions are called the gene frequencies of A and B in the population. Draw out two gametes at random. The probability of drawing two As and forming an AA genotype individual is p2, the probability of an AB individual is 2p(1 - p) (an AB individual can be formed by drawing AB or BA), and the probability of a BB individual is (1 - p)2. These genotype frequencies, produced theoretically by "random mating," are called the Hardy-Weinberg frequencies. Write an R function to take any gene frequency for gene A (where the frequency is between 0 and 1) and calculate the Hardy-Weinberg genotype frequencies. The function should take as an argument a single number and return a vector of three quantities. Evaluate your function with appropriate experimental inputs.

```
gene <- function(p) {
    AA <- p^2
    AB <- 2 * p * (1 - p)
    BB <- (1 - p)^2
    return(c(AA, AB, BB))
}

# I suppose the proportion (or fraction) of gametes with A genes in the urn (p) is 0.2
gene(0.2)
```

```
## [1] 0.04 0.32 0.64
```