

STAT 527 HW 3

Satoshi Ido (ID: 34788706)

5 February 2023

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 $100 \cdot i\%$ 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.

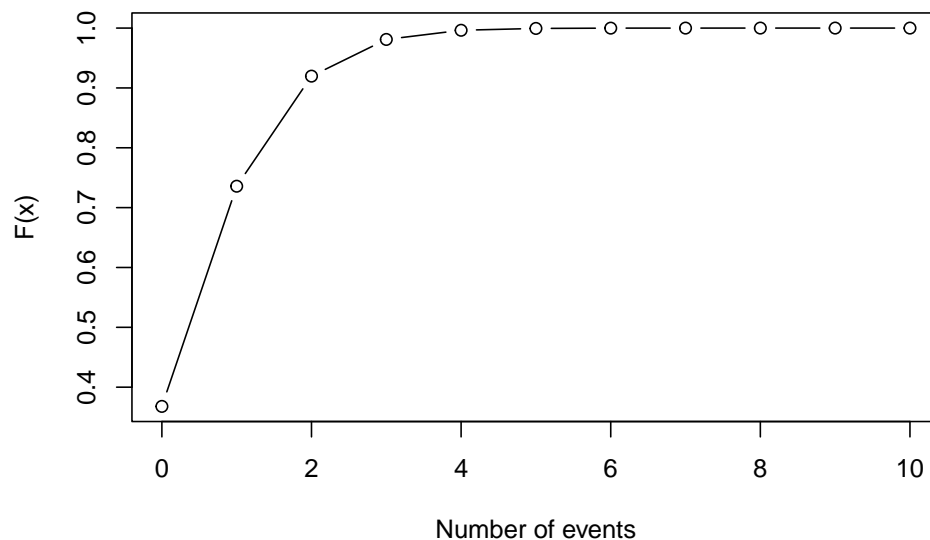
```
nt <- function(n0, i, t) {  
  out <- n0 * (1 + i)^t  
  return(out)  
}  
  
# This function seems work right  
nt(100, 0.05, 10)
```

```
## [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 $k \geq 0$. The cumulative distribution function (CDF) of Poisson distribution evaluated at $X = x$ is calculated as $\Pr(X \leq x)$. Write an R function that takes λ and x as inputs and returns the CDF value. Pick $\lambda=1$ and evaluate your function at $x = 0, 1, \dots, 10$. 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  
  out <- ppois(a, lambda)  
  return(out)  
}  
  
a <- 0:10  
plot(a, cdf(1, 10), xlab = "Number of events", ylab = "F(x)",  
     main = "The plot of CDF for Poisson distribution", type = "b")
```

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 p^2 , 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
```