GroupA_HW1

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Contents

CS - Chapter 1

Ex 1.1

Exponential random variable, $X \geq 0$, has p.d.f. $f(x) = \lambda \exp(-\lambda x)$.

1. *Find the c.d.f. and the quantile function for X.*
2. *Find Pr($X < \lambda$) and the median of X.*
3. *Find the mean and variance of X.*

Solution

1. C.D.F. and Quantile Function:

   The cumulative distribution function (c.d.f.) F(x) is:

   $$F(x) = \int_0^x \lambda e^{-\lambda t} dt = 1 - e^{-\lambda x}, \quad x \geq 0$$

   The quantile function Q(p) is the inverse of F(x):

   $$Q(p) = -\frac{1}{\lambda} \ln(1-p), \quad 0 \leq p < 1$$

2. Pr(X < λ) and Median:

   Pr(X < λ) = F(λ) = $1 - e^{-\lambda\lambda} = 1 - e^{-1} \approx 0.6321$

   For the median, we solve F(x) = 0.5:

   $$1 - e^{-\lambda x} = 0.5$$
   $$x = -\frac{1}{\lambda} \ln(0.5) = \frac{\ln(2)}{\lambda}$$

3. Mean and Variance:

   Mean: E[X] = $\int_0^\infty x\lambda e^{-\lambda x} dx = \frac{1}{\lambda}$

   Variance: Var(X) = E[X²] - (E[X])² = $\frac{2}{\lambda^2} - (\frac{1}{\lambda})^2 = \frac{1}{\lambda^2}$

Comments on the solution:

1. The exponential distribution is characterized by its rate parameter λ, which determines both its shape and scale.
2. Interestingly, Pr(X < λ) is always approximately 0.6321, regardless of the value of λ. This is a unique property of the exponential distribution.
3. The median of the distribution is $\frac{\ln(2)}{\lambda}$, which is always less than the mean ($\frac{1}{\lambda}$) due to the distribution's right-skewness.
4. The mean and variance are both functions of λ. As λ increases, both the mean and variance decrease, indicating that larger values of λ result in the distribution being more concentrated near zero.
5. The standard deviation of the distribution is equal to its mean, which is a distinctive feature of the exponential distribution.

Ex 1.6

Let X and Y be non-independent random variables, such that var(X) = σ_x^2, var(Y) = σ_y^2 and cov(X,Y) = σ_{xy}^2. Using the result from Section 1.6.2, find var(X + Y) and var(X - Y).

Solution

Using the formula for linear transformations of random vectors from Section 1.6.2:

$\mathbf{AX} \sim N(\mathbf{A}\mu, \mathbf{A}\ \mathbf{A^T})$

1. Define a random vector and its covariance matrix:
   $\mathbf{X} = \begin{pmatrix} X \\ Y \end{pmatrix}$
   $\Sigma = \begin{pmatrix} \sigma_x^2 & \sigma_{xy}^2 \\ \sigma_{xy}^2 & \sigma_y^2 \end{pmatrix}$
2. For var(X + Y): Let $\mathbf{A} = (1 \quad 1)$
   $\text{var}(X+Y) = \mathbf{A}\ \mathbf{A^T} = (1 \quad 1) \begin{pmatrix} \sigma_x^2 & \sigma_{xy}^2 \\ \sigma_{xy}^2 & \sigma_y^2 \end{pmatrix} \begin{pmatrix} 1 \\ 1 \end{pmatrix}$
   $= (1 \quad 1) \begin{pmatrix} \sigma_x^2 + \sigma_{xy}^2 \\ \sigma_{xy}^2 + \sigma_y^2 \end{pmatrix} = \sigma_x^2 + 2\sigma_{xy}^2 + \sigma_y^2$
3. For var(X - Y): Let $\mathbf{A} = (1 \quad -1)$
   $\text{var}(X-Y) = \mathbf{A}\ \mathbf{A^T} = (1 \quad -1) \begin{pmatrix} \sigma_x^2 & \sigma_{xy}^2 \\ \sigma_{xy}^2 & \sigma_y^2 \end{pmatrix} \begin{pmatrix} 1 \\ -1 \end{pmatrix}$
   $= (1 \quad -1) \begin{pmatrix} \sigma_x^2 - \sigma_{xy}^2 \\ -(\sigma_{xy}^2 - \sigma_y^2) \end{pmatrix} = \sigma_x^2 - 2\sigma_{xy}^2 + \sigma_y^2$

Therefore:

$\text{var}(X+Y) = \sigma_x^2 + 2\sigma_{xy}^2 + \sigma_y^2$

$\text{var}(X-Y) = \sigma_x^2 - 2\sigma_{xy}^2 + \sigma_y^2$

Comments on the solution:

1. For the sum (X + Y), the covariance term is added twice, potentially increasing the overall variance if X and Y are positively correlated.
2. For the difference (X - Y), the covariance term is subtracted twice, potentially decreasing the overall variance if X and Y are positively correlated.
3. If X and Y are independent (i.e., $\sigma_{xy}^2 = 0$), the variances of their sum and difference would both simplify to $\sigma_x^2 + \sigma_y^2$.

Ex 3.5

Consider solving the matrix equation $Ax = y$ for x, where y is a known n-vector and A is a known $n \times n$ matrix. The formal solution to the problem is $x = A^{-1}y$, but it is possible to solve the equation directly, without actually forming A^{-1}. This question explores this direct solution.

a. *First create an A, x and y satisfying $Ax = y$.*

```
set.seed(0)
n <- 1000
A <- matrix(runif(n*n), n, n)
x.true <- runif(n)
y <- A %*% x.true
```

The idea is to experiment with solving $Ax = y$ for x, but with a known truth to compare the answer to.

b. *Using solve, form the matrix $A-1$ explicitly and then form x1 = A^(-1)y. Note how long this takes. Also assess the mean absolute difference between x1 and x.true (the approximate mean absolute 'error' in the solution).*

c. *Now use solve to directly solve for x without forming A^(-1). Note how long this takes and assess the mean absolute error of the result.*

d. *What do you conclude?*

Solution

```
set.seed(0)
n <- 1000

# Part (a): Generate A, x.true, and y
A <- matrix(runif(n * n), n, n)
x.true <- runif(n)
y <- A %*% x.true

# Part (b): Solve by forming A^-1 explicitly
start_time_1 <- Sys.time()
A_inv <- solve(A)
x1 <- A_inv %*% y
end_time_1 <- Sys.time()

time_taken_1 <- end_time_1 - start_time_1
error_1 <- mean(abs(x1 - x.true))

# Part (c): Solve directly without forming A^-1
start_time_2 <- Sys.time()
x2 <- solve(A, y)
end_time_2 <- Sys.time()

time_taken_2 <- end_time_2 - start_time_2
error_2 <- mean(abs(x2 - x.true))

# Part (d): Print results and conclusions
cat("Results:\n")
```

```
## Results:
```

```
    cat("1. Using explicit inverse (A^-1 * y):\n")
```

```
## 1. Using explicit inverse (A^-1 * y):
```

```
    cat("   Time taken:", time_taken_1, "\n")
```

```
##    Time taken: 0.604563
```

```
    cat("   Mean absolute error:", error_1, "\n\n")
```

```
##    Mean absolute error: 2.956833e-11
```

```
    cat("2. Using direct solve (solve(A, y)):\n")
```

```
## 2. Using direct solve (solve(A, y)):
```

```
    cat("   Time taken:", time_taken_2, "\n")
```

```
##    Time taken: 0.1170411
```

Directly solving (solve(A, y)) is faster than forming the inverse and also has comparable accuracy.

Ex 3.6

The empirical cumulative distribution function (ECDF) for a set of measurements $x_i : i = 1, \dots, n$ *is*

$$\hat{F}(x) = \frac{\#\{x_i < x\}}{n}$$

where $\#\{x_i < x\}$ *denotes the number of* x_i *values that are less than* x*. When answering the following, try to ensure that your code is commented, clearly structured, and tested. To test your code, generate random samples using rnorm, runif, etc.*

a. *Write an R function that takes an unordered vector of observations* x *and returns the values of the empirical c.d.f. for each value, in the order corresponding to the original* x *vector. See ?sort.int.*

b. *Modify your function to take an extra argument plot.cdf, that when TRUE will cause the empirical c.d.f. to be plotted as a step function over a suitable* x *range.*

Solution

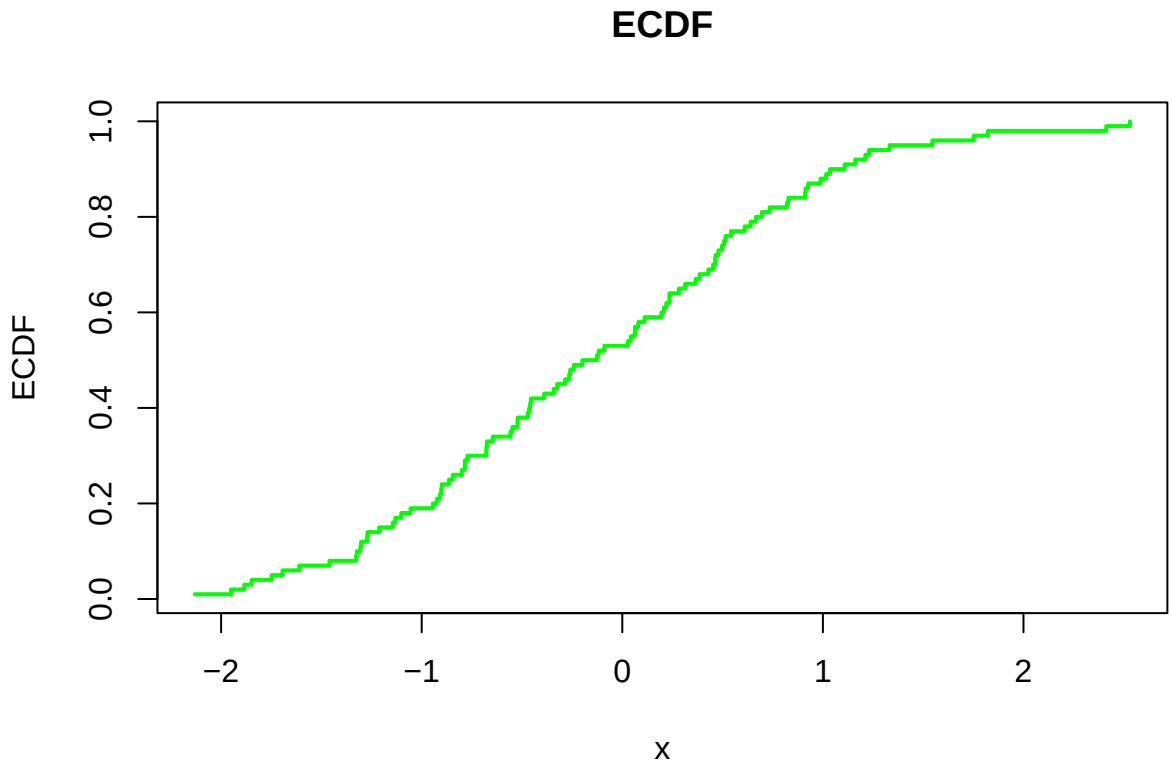
```
compute_ecdf <- function(x, plot.cdf = FALSE) {
  n <- length(x)
  sorted_x <- sort(x)
  ecdf_values <- cumsum(table(cut(x, breaks = c(-Inf, sorted_x)))) / n

  # Match ECDF values back to the original order of x
  ecdf_original_order <- ecdf_values[order(order(x))]
```

```r
  # Part (b)
  if (plot.cdf) {
    plot(sort(x), ecdf_values, type = "s", col = "green", lwd = 2, xlab = "x", ylab = "ECDF", main =
        }
  return(ecdf_original_order)
}

# Testing the function
set.seed(18)
x <- rnorm(100)

ecdf_values <- compute_ecdf(x)
print(ecdf_values)
```

```
##   (0.9138,0.9265]     (1.752,1.823]   (-1.694,-1.611] (-0.3246,-0.2851]
##              0.87              0.98              0.07              0.46
## (-0.3895,-0.3421]   (0.3135,0.3662]    (-1.46,-1.327]     (1.823,2.413]
##              0.44              0.67              0.09              0.99
##  (0.0624,0.06382]     (1.332,1.546]    (-1.95,-1.885]   (0.8279,0.9114]
##              0.57              0.96              0.03              0.85
##   (-1.324,-1.305] (0.02814,0.04207] (-0.7999,-0.7853]     (1.162,1.212]
##              0.11              0.55              0.28              0.93
## (-0.9446,-0.9245]  (-0.7721,-0.678]      (1.23,1.332]   (0.4522,0.4626]
##              0.21              0.31              0.95              0.71
##   (-1.305,-1.302]     (1.035,1.108] (-0.7848,-0.7721]  (-0.678,-0.6772]
##              0.12              0.91              0.30              0.32
##   (0.4626,0.4643]    (-2.131,-1.95]   (-1.102,-1.056] (-0.1265,-0.1178]
##              0.72              0.02              0.19              0.52
## (-0.2652,-0.2595]   (-1.848,-1.748] (-0.9245,-0.9089]   (0.1946,0.2069]
##              0.48              0.05              0.22              0.61
##   (0.2819,0.3135]     (1.108,1.162]   (-1.748,-1.694]     (1.016,1.035]
##              0.66              0.92              0.06              0.90
##     (0.64,0.6658]   (-1.302,-1.272]    (0.542,0.6096]    (0.7348,0.821]
##              0.80              0.13              0.78              0.83
##   (0.6658,0.6949]     (2.413,2.531]   (0.4289,0.4522]   (0.9265,0.9887]
##              0.81              1.00              0.70              0.88
## (-0.1992,-0.1265]   (0.5074,0.5149]    (0.821,0.8279]   (-1.327,-1.324]
##              0.51              0.76              0.84              0.10
## (-0.3421,-0.3246] (-0.6458,-0.5579] (-0.9089,-0.9026]   (-1.144,-1.132]
##              0.45              0.35              0.23              0.17
##   (0.4789,0.4971] (-0.5579,-0.5477] (-0.1178,-0.0894]     (-Inf,-2.131]
##              0.74              0.36              0.53              0.01
## (-0.9026,-0.9007]      (1.212,1.23] (0.06382,0.08006]   (0.3852,0.4289]
##              0.24              0.94              0.58              0.69
## (-0.8641,-0.8453]    (0.2197,0.235]    (-1.611,-1.46] (-0.0894,0.02814]
##              0.26              0.63              0.08              0.54
## (-0.6772,-0.6747]    (0.5149,0.542]   (-1.271,-1.212]     (0.6096,0.64]
##              0.33              0.77              0.15              0.79
##  (-0.5218,-0.471]   (0.1107,0.1946] (-0.5229,-0.5218] (-0.2421,-0.1992]
##              0.39              0.60              0.38              0.50
## (-0.5477,-0.5229]   (-1.272,-1.271] (-0.4558,-0.3895]   (0.2351,0.2819]
##              0.37              0.14              0.43              0.65
##   (0.3662,0.3852] (-0.8453,-0.7999]  (0.04207,0.0624]   (0.4971,0.5074]
```

```
##              0.68              0.27              0.56              0.75
##  (-0.459,-0.4558]   (-1.132,-1.102] (-0.7853,-0.7848]     (1.546,1.752]
##              0.42              0.18              0.29              0.97
##   (0.4643,0.4789]  (-0.471,-0.4645] (-0.2851,-0.2652]   (-1.885,-1.848]
##              0.73              0.40              0.47              0.04
##    (0.235,0.2351]   (0.6949,0.7348]  (0.08006,0.1107] (-0.9007,-0.8641]
##              0.64              0.82              0.59              0.25
##   (-1.212,-1.144]  (-0.4645,-0.459]   (0.2069,0.2197] (-0.6747,-0.6458]
##              0.16              0.41              0.62              0.34
##   (0.9114,0.9138]  (-1.056,-0.9446] (-0.2595,-0.2421]    (0.9887,1.016]
##              0.86              0.20              0.49              0.89
```

```r
# Compute the ECDF with plotting
compute_ecdf(x, plot.cdf = TRUE)
```




```
##   (0.9138,0.9265]     (1.752,1.823]   (-1.694,-1.611] (-0.3246,-0.2851]
##              0.87              0.98              0.07              0.46
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##              0.11              0.55              0.28              0.93
## (-0.9446,-0.9245]  (-0.7721,-0.678]      (1.23,1.332]   (0.4522,0.4626]
##              0.21              0.31              0.95              0.71
```

```
##   (-1.305,-1.302]     (1.035,1.108] (-0.7848,-0.7721]  (-0.678,-0.6772]
##              0.12              0.91              0.30              0.32
##   (0.4626,0.4643]    (-2.131,-1.95]   (-1.102,-1.056] (-0.1265,-0.1178]
##              0.72              0.02              0.19              0.52
## (-0.2652,-0.2595]   (-1.848,-1.748] (-0.9245,-0.9089]   (0.1946,0.2069]
##              0.48              0.05              0.22              0.61
##   (0.2819,0.3135]     (1.108,1.162]   (-1.748,-1.694]     (1.016,1.035]
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##     (0.64,0.6658]   (-1.302,-1.272]    (0.542,0.6096]    (0.7348,0.821]
##              0.80              0.13              0.78              0.83
##   (0.6658,0.6949]     (2.413,2.531]   (0.4289,0.4522]   (0.9265,0.9887]
##              0.81              1.00              0.70              0.88
## (-0.1992,-0.1265]   (0.5074,0.5149]    (0.821,0.8279]   (-1.327,-1.324]
##              0.51              0.76              0.84              0.10
## (-0.3421,-0.3246] (-0.6458,-0.5579] (-0.9089,-0.9026]   (-1.144,-1.132]
##              0.45              0.35              0.23              0.17
##   (0.4789,0.4971] (-0.5579,-0.5477] (-0.1178,-0.0894]     (-Inf,-2.131]
##              0.74              0.36              0.53              0.01
## (-0.9026,-0.9007]      (1.212,1.23] (0.06382,0.08006]   (0.3852,0.4289]
##              0.24              0.94              0.58              0.69
## (-0.8641,-0.8453]    (0.2197,0.235]    (-1.611,-1.46] (-0.0894,0.02814]
##              0.26              0.63              0.08              0.54
## (-0.6772,-0.6747]    (0.5149,0.542]   (-1.271,-1.212]     (0.6096,0.64]
##              0.33              0.77              0.15              0.79
##  (-0.5218,-0.471]   (0.1107,0.1946] (-0.5229,-0.5218] (-0.2421,-0.1992]
##              0.39              0.60              0.38              0.50
## (-0.5477,-0.5229]   (-1.272,-1.271] (-0.4558,-0.3895]   (0.2351,0.2819]
##              0.37              0.14              0.43              0.65
##   (0.3662,0.3852] (-0.8453,-0.7999]  (0.04207,0.0624]   (0.4971,0.5074]
##              0.68              0.27              0.56              0.75
##  (-0.459,-0.4558]   (-1.132,-1.102] (-0.7853,-0.7848]     (1.546,1.752]
##              0.42              0.18              0.29              0.97
##   (0.4643,0.4789]  (-0.471,-0.4645] (-0.2851,-0.2652]   (-1.885,-1.848]
##              0.73              0.40              0.47              0.04
##    (0.235,0.2351]   (0.6949,0.7348]  (0.08006,0.1107] (-0.9007,-0.8641]
##              0.64              0.82              0.59              0.25
##   (-1.212,-1.144]  (-0.4645,-0.459]   (0.2069,0.2197] (-0.6747,-0.6458]
##              0.16              0.41              0.62              0.34
##   (0.9114,0.9138]  (-1.056,-0.9446] (-0.2595,-0.2421]    (0.9887,1.016]
##              0.86              0.20              0.49              0.89
```

FSDS - Chapter 2

Ex 2.8

Each time a person shops at a grocery store, the event of catching a cold or some other virus from another shopper is independent from visit to visit and has a constant probability over the year, equal to 0.01.

(a) *In 100 trips to this store over the course of a year, the probability of catching a virus while shopping there is 100(0.01) = 1.0. What is wrong with this reasoning?*
(b) *Find the correct probability in (a).*

Solution

a)

The algorithm followed to compute the probability isn't correct. In fact, if we suppose to compute the same probability for 200 days, we will obtain a value of 2.0, but probability functions are defined in $\Omega \to [0, 1]$.

b)

The event of getting a cold at the supermarket in a single day can be described by a Bernoulli random variable:

$$X \sim \text{Be}(0.01)$$

The event of getting a cold at the supermarket over 100 days can be described by a Binomial random variable:

$$X \sim \text{Bin}(100, 0.01)$$

The probability of getting a virus, denoted P_v*, is given by:*

$$P_v = 1 - P(X = 0)$$

This can be calculated as:

$$P_v = 1 - P(X = 0) = 1 - \binom{100}{0} \cdot (0.01)^0 \cdot (1 - 0.01)^{100-0} \approx 0.6339677$$

Ex 2.16

Each day a hospital records the number of people who come to the emergency room for treatment.(a) In the first week, the observations from Sunday to Saturday are 10, 8, 14, 7, 21, 44, 60. Do you think that the Poisson distribution might describe the random variability of this phenomenon adequately. Why or why not?

Solution To assess whether the Poisson distribution might adequately describe the random variability of emergency room visits, we'll examine the data and compare it to properties of the Poisson distribution.

```r
# Data
er_visits <- c(10, 8, 14, 7, 21, 44, 60)
days <- c("Sun", "Mon", "Tue", "Wed", "Thu", "Fri", "Sat")

# Basic statistics
mean_visits <- mean(er_visits)
var_visits <- var(er_visits)

# Print results
cat("Mean of visits:", round(mean_visits, 2), "\n")
```

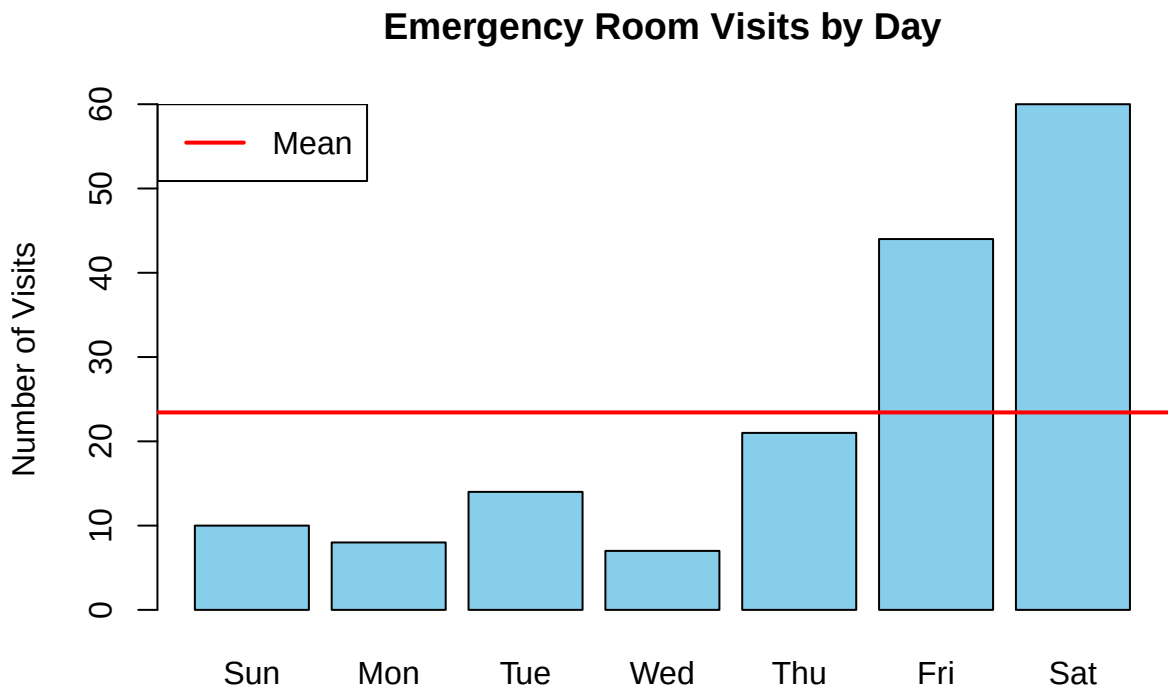
a)

```
## Mean of visits: 23.43
```

```r
cat("Variance of visits:", round(var_visits, 2), "\n")
```

```
## Variance of visits: 423.95
```

```r
# Plot the data
barplot(er_visits, names.arg = days, main = "Emergency Room Visits by Day",
        ylab = "Number of Visits", col = "skyblue")

# Add a line for the mean
abline(h = mean_visits, col = "red", lwd = 2)
legend("topleft", legend = "Mean", col = "red", lwd = 2)
```



1. The Poisson distribution has the property that its mean and variance are equal. In our data:
   - Mean: 23.4285714
   - Variance: 423.952381 The large difference between these values suggests that the Poisson distribution may not be appropriate.
2. The bar plot shows a clear increasing trend throughout the week, with a sharp increase on Friday and Saturday. This pattern is not consistent with the Poisson distribution, which assumes a constant rate of events.
3. The Poisson distribution assumes:
   - Events occur independently

- The average rate of occurrences is constant

In this case, the number of ER visits doesn't satisfy these assumptions:

- There may be dependencies (e.g., a local event affecting multiple people)
- The rate clearly varies by day of the week

4. The data shows overdispersion (variance much larger than the mean), which is not characteristic of the Poisson distribution.

Given these observations, we can conclude that the Poisson distribution does not adequately describe the random variability of emergency room visits in this hospital. A more complex model that accounts for day-of-week effects and overdispersion (such as a negative binomial distribution or a time series model) would likely be more appropriate.

b) Solution

Yes, we would expect the Poisson distribution to better describe the number of weekly admissions to the hospital for a rare disease.

1. **Rare events**: The Poisson distribution is particularly well-suited for modeling rare events. A rare disease, by definition, occurs infrequently.
2. **Independence**: Admissions for a rare disease are more likely to be independent of each other, especially if the disease is not contagious.
3. **Constant rate**: The occurrence of a rare disease is less likely to be affected by day-of-week patterns or other cyclical factors that we observed in general ER admissions.
4. **No simultaneous occurrences**: With rare diseases, the probability of two or more admissions occurring simultaneously is extremely low, which aligns with another assumption of the Poisson distribution.
5. **Lower variance**: Rare events typically have a lower variance, which is more likely to be closer to the mean.
6. **Small numbers**: The Poisson distribution is often used to model count data when the counts are small, which is likely the case for weekly admissions of a rare disease.

To illustrate this point, we can simulate weekly admissions for a hypothetical rare disease:

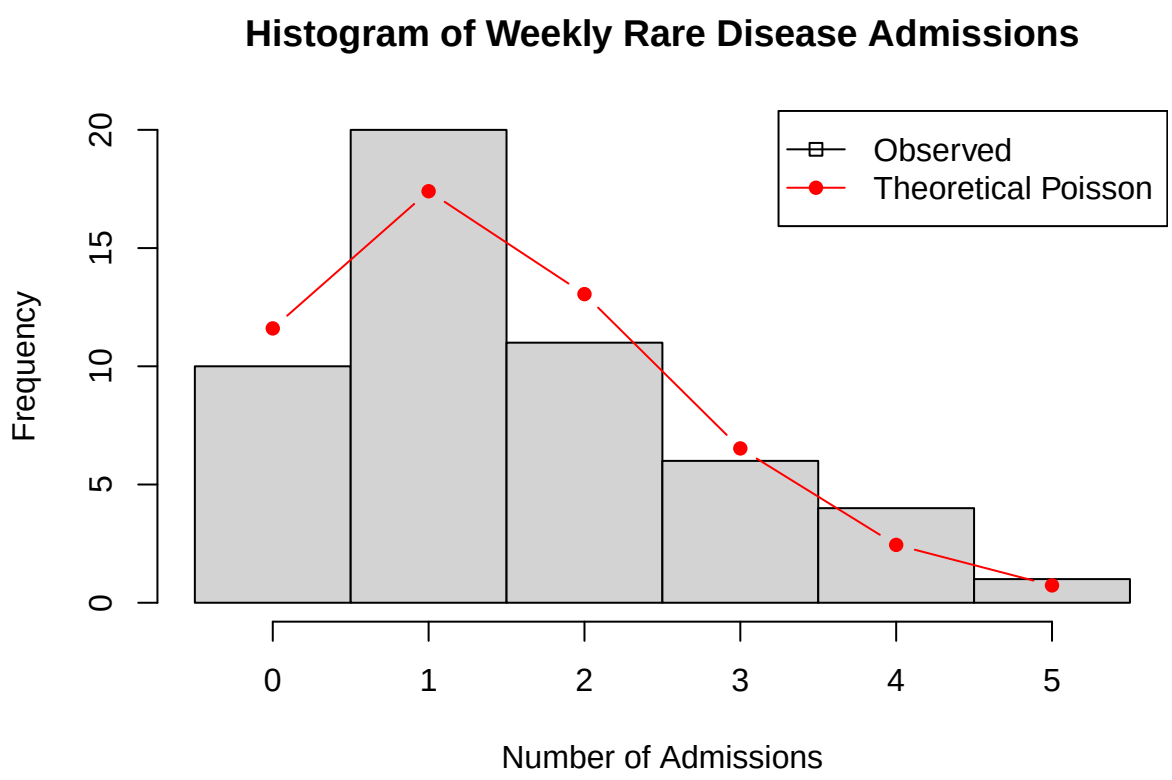
```
set.seed(123)
weeks <- 52
lambda <- 1.5  # Average 1.5 admissions per week for the rare disease
rare_disease_admissions <- rpois(weeks, lambda)

# Basic statistics
mean_admissions <- mean(rare_disease_admissions)
var_admissions <- var(rare_disease_admissions)

# Print results
cat("Mean of admissions:", round(mean_admissions, 2), "\n")
```

```
## Mean of admissions: 1.56
```

```r
cat("Variance of admissions:", round(var_admissions, 2), "\n")
```

```
## Variance of admissions: 1.58
```

```r
# Plot the data
hist(rare_disease_admissions, breaks = seq(-0.5, max(rare_disease_admissions) + 0.5, by = 1),
     main = "Histogram of Weekly Rare Disease Admissions",
     xlab = "Number of Admissions", ylab = "Frequency")

# Overlay Poisson distribution
x <- 0:max(rare_disease_admissions)
lines(x, dpois(x, lambda) * weeks, col = "red", type = "b", pch = 16)
legend("topright", legend = c("Observed", "Theoretical Poisson"),
       col = c("black", "red"), lty = 1, pch = c(22, 16))
```



Comments on Solution:

1. The mean (1.56) and variance (1.58) of the simulated data are much closer to each other, which is characteristic of the Poisson distribution.
2. The histogram of simulated admissions closely follows the theoretical Poisson distribution (red line), indicating a good fit.
3. The number of admissions per week is small and varies within a narrow range, which is typical for rare events and well-described by the Poisson distribution.

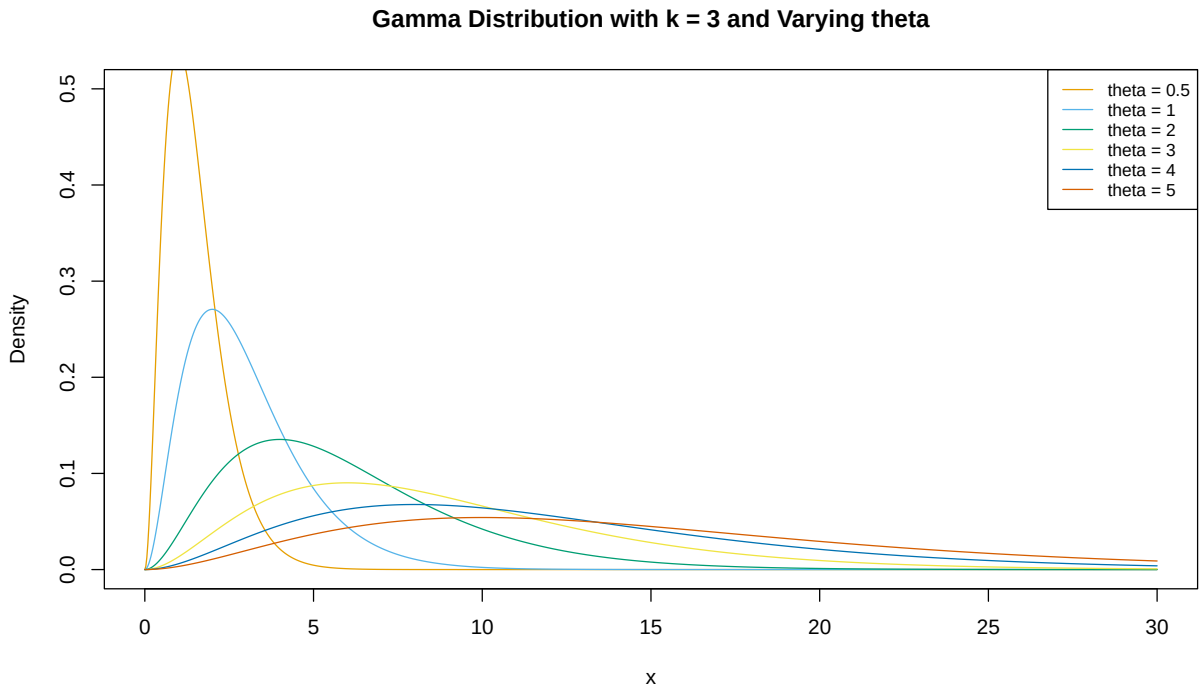
Ex 2.21

Plot the gamma distribution by fixing the shape parameter $k = 3$ and setting the scale parameter $\theta = 0.5$, 1, 2, 3, 4, 5. What is the effect of increasing the scale parameter? (See also Exercise 2.48.)

Solution

To visualize the effect of increasing the scale parameter on the gamma distribution, we'll create a plot showing multiple gamma distributions with a fixed shape parameter and varying scale parameters.

```r
# Set parameters
k <- 3  # Shape parameter
theta <- c(0.5, 1, 2, 3, 4, 5)  # Scale parameters
colors <- c("#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00")

# Create x values
x <- seq(0, 30, length.out = 1000)

# Plot
plot(x, dgamma(x, shape = k, scale = theta[1]), type = "l", col = colors[1],
     main = "Gamma Distribution with k = 3 and Varying theta",
     xlab = "x", ylab = "Density", ylim = c(0, 0.5))

# Add lines for other scale parameters
for (i in 2:length(theta)) {
  lines(x, dgamma(x, shape = k, scale = theta[i]), col = colors[i])
}

# Add legend
legend("topright", legend = paste("theta =", theta), col = colors, lty = 1, cex = 0.8)
```



Comments on the solution:

1. **Shape of the distribution**: As we increase the scale parameter θ, we observe:
   a. The peak of the distribution shifts to the right (towards larger x values).
   b. The height of the peak decreases.
   c. The distribution becomes wider.

2. **Interpretation**:
   - A larger scale parameter θ indicates greater variability and a shift in the distribution.
   - This can be explained by the relationship between the parameters of the gamma distribution:
     - The mean of the gamma distribution is $\mu = k\theta$
     - The variance is $\sigma^2 = k\theta^2$
   - As θ increases:
     - The mean increases linearly ($k\theta$)
     - The variance increases quadratically ($k\theta^2$)
   - This quadratic increase in variance relative to the mean explains the greater spread and variability we observe with larger θ values.

Ex 2.26

Refer to Table 2.4 cross classifying happiness with family income.

Solution A. the corelation coefficient is given by $\rho = \frac{COV(X,Y)}{\sigma_X \sigma_Y}$ therefore we have to compute the mean, variance and covariance in oreder to have the desired corelations.

since we are talking about a joint distribution function, if we have S_x and S_y set of scores of each variable, the mean for each variable will be given by $\mu_x = \sum_{x \in S_x} xP(X = x_i)$ where $P(X = x) = \sum_{y \in S_y} P(X = x, Y = y)$ which we already have in the table under "total"

the variance is similarly done: $\mu_x = \sum_{x \in S_x} (x - \mu_x)^2 P(X = x_i)$ once we have the means and the covariance is defined by $COV(X,Y) = \sum_{y \in S_y} \sum_{x \in S_x} (x - \mu_x)(y - mu_y)P(x,y)$ from this we apply the first formula we stated at the beginning and get the corelation ρ.

controlla se devo usare mu o E

```
library(knitr)
l=c(0.080, 0.198, 0.079, 0.357,0.043, 0.254, 0.143, 0.440,0.017, 0.105, 0.081, 0.203, 0.140, 0.557, 0.3

S_1<-c(1,2,3)
S_2<-c(1,4,5)
dim(l)<- c(4,4)
rownames(l)<-c("Below average","Average","Above average", "Total")
colnames(l)<-c("Not too happy", "Pretty happy","Very happy", "Total")

kable(l, row.names=T)
```

	Not too happy	Pretty happy	Very happy	Total
Below average	0.080	0.043	0.017	0.140
Average	0.198	0.254	0.105	0.557
Above average	0.079	0.143	0.081	0.303
Total	0.357	0.440	0.203	1.000

```
m<- c(0,0) #mean
for(i in 1:length(S_1)){
  m[1]<-m[1]+(S_1[i]*l[4,i])#x
  m[2]<-m[2]+(S_1[i]*l[i,4])#y
}
m
```

```
## [1] 1.846 2.163
```

```
v<- c(0,0) #variance
for(i in 1:length(S_1)){
 v[1]<-(S_1[i]-m[1])^2*l[4,i]#x
 v[2]<-(S_1[i]-m[2])^2*l[i,4]#y
}
v
```

```
## [1] 0.2703383 0.2122724
```

```
#covariance matrix
covariance=0
for(i in 1:length(S_1)){
  for(j in 1:length(S_1)){
    a<-(S_1[i]-m[1])*(S_1[j]-m[2])*l[j,i]
    covariance<-covariance+(S_1[i]-m[1])*(S_1[j]-m[2])*l[j,i]

  }
}
covariance
```

```
## [1] 0.090102
```

```
#corelation
r<-covariance/(sqrt(v[1])*sqrt(v[2]))
r
```

```
## [1] 0.3761264
```

```
#repeat with s_2 for the Y

m<- c(0,0) #mean
for(i in 1:length(S_1)){
  m[1]<-m[1]+(S_1[i]*l[4,i])
  m[2]<-m[2]+(S_2[i]*l[i,4])
}
m
```

```
## [1] 1.846 3.883
```

```
v<- c(0,0) #variance
for(i in 1:length(S_1)){
 v[1]<-(S_1[i]-m[1])^2*l[4,i]
 v[2]<-(S_2[i]-m[2])^2*l[i,4]
}
v
```

```
## [1] 0.2703383 0.3780498
```

```
#covariance matrix
covariance=0
for(i in 1:length(S_1)){
  for(j in 1:length(S_1)){
    covariance<-covariance+(S_1[i]-m[1])*(S_2[j]-m[2])*l[j,i]
  }
}
covariance
```

```
## [1] 0.172982
```

```
#corelation
r<-covariance/(sqrt(v[1])*sqrt(v[2]))
r
```

```
## [1] 0.5410939
```

B. to exhibit indipendence the joint distribution must have $P(x, y) = P(x)P(y)$ therefore each $P(x, y)$ will be easely computed

```
marginal_X<-c(0.357,0.440,0.203)
marginal_Y<-c(0.140,0.557,0.303)

indy_table<-matrix(0,length(marginal_X),length(marginal_Y))
rownames(indy_table)<-c("Below average","Average","Above average")
colnames(indy_table)<-c("Not too happy", "Pretty happy","Very happy")
for(i in 1:length(marginal_X)){
  for(j in 1:length(marginal_Y)){
    indy_table[j,i]<-marginal_X[j]*marginal_Y[i]
  }
}
indy_table
```

```
##               Not too happy Pretty happy Very happy
## Below average       0.04998     0.198849   0.108171
## Average             0.06160     0.245080   0.133320
## Above average       0.02842     0.113071   0.061509
```

Ex 2.52

The pdf f of a $N(\mu, \sigma^2)$ distribution can be derived from the standard normal pdf ϕ shown in equation (2.9). (a) Show that the normal cdf F relates to the standard normal cdf Φ by $F(y) = \Phi[(y-\mu)/\sigma]$. (b) From (a), show that $f(y) = (1/\sigma)\phi[(y-\mu)/\sigma]$, and show this is equation (2.8).

Solution

a) *The cdf F of a normal distribution $N(\mu, \sigma^2)$ is defined as:*

$$F(y) = P(Y \leq y) = \int_{-\infty}^{y} f(t)\, dt$$

where f is the pdf of $N(\mu, \sigma^2)$

To express $F(y)$ in terms of the standard normal cdf Φ, we can standardize the variable Y to convert it to the std normal form

$$Z = \frac{Y-\mu}{\sigma} \sim N(0,1)$$

$$F(y) = P(Y \leq y) = P\left(\frac{Y-\mu}{\sigma} \leq \frac{y-\mu}{\sigma}\right)$$

Since $Z = \frac{Y-\mu}{\sigma} \sim N(0,1)$, the probability $P(Z \leq \frac{y-\mu}{\sigma})$, is the definition of the std normal cdf Φ

$$F(y) = \Phi\left(\frac{y-\mu}{\sigma}\right)$$

b) *The pdf $f(y)$ is the derivative of the cdf $F(y)$*

$$f(y) = \frac{d}{dy} F(y)$$

From (a) we know

$$F(y) = \Phi\left(\frac{y-\mu}{\sigma}\right)$$

Differentiate $F(y)$ with respect to y

$$f(y) = \frac{d}{dy}\Phi\left(\frac{y-\mu}{\sigma}\right) = \Phi'\left(\frac{y-\mu}{\sigma}\right)\frac{1}{\sigma}$$

Sixnce $\Phi'(z) = \phi(z)$, where $\phi(z)$ is the std normal pdf, we have:

$$f(y) = \phi\left(\frac{y-\mu}{\sigma}\right)\frac{1}{\sigma}$$

Ex 2.53

If Y is a standard normal random variable, with cdf Φ, what is the probability distribution of $X = \Phi(Y)$? Illustrate by randomly generating a million standard normal random variables, applying the cdf function $\Phi()$ to each, and plotting histograms of the (a) y values, (b) x values.

Solution

Y is a standard normal variable, $Y \sim N(0,1)$ The cdf of a standard normal variable, $\Phi(y) = P(Y \leq y)$, gives the probability that Y takes on a value less than or equal to y By defininig $X = \Phi(Y)$, we're transforming Y by it's own cdf, so X take values in [0,1] Since Y is std normal, and so is a continuos random variable

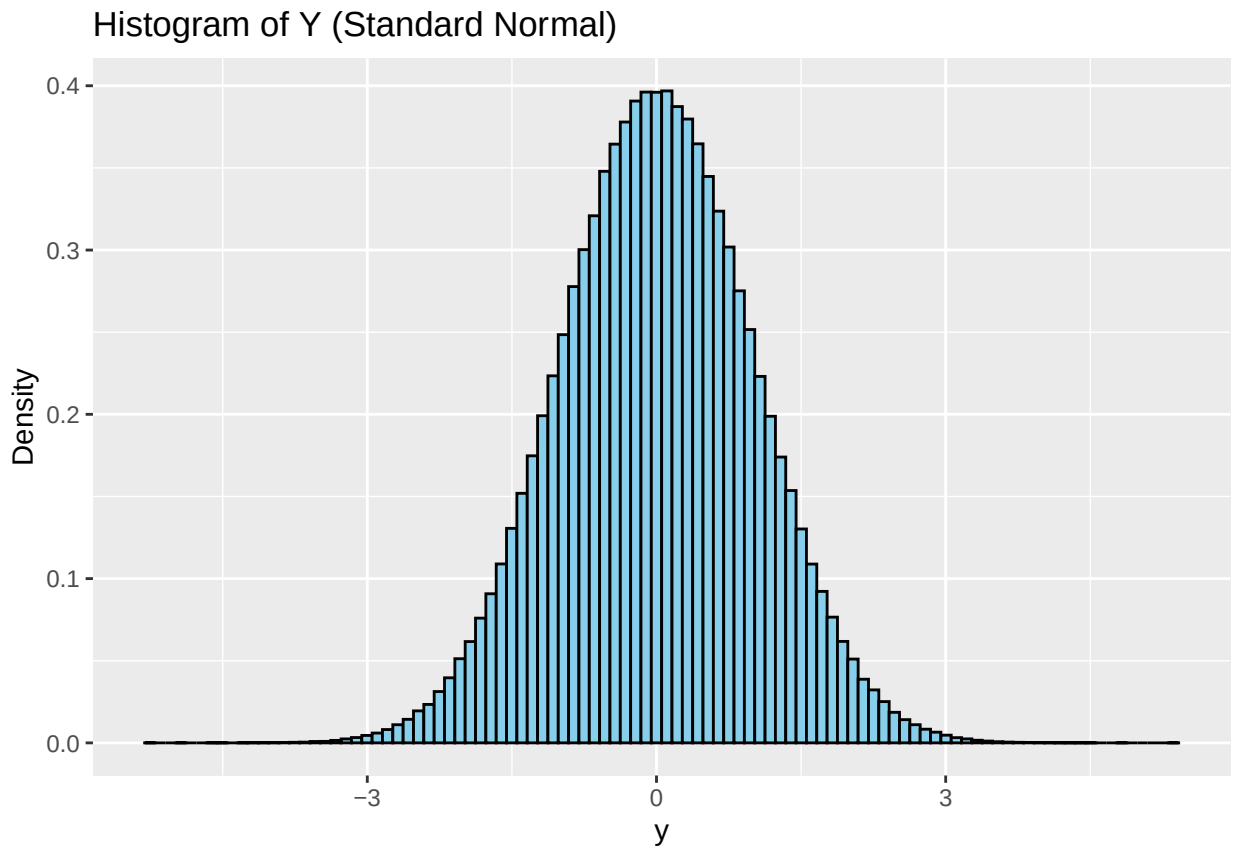
$$F_X = P(X \leq x) = P(F_Y(Y) \leq x)$$

We have to notice that $F_Y(Y) \leq x$ iff $Y \leq F_Y^{-1}(x)$, thus

$$F_X = P(Y \leq F_Y^{-1}(x)) = F_Y(F_Y^{-1}(x)) = x$$

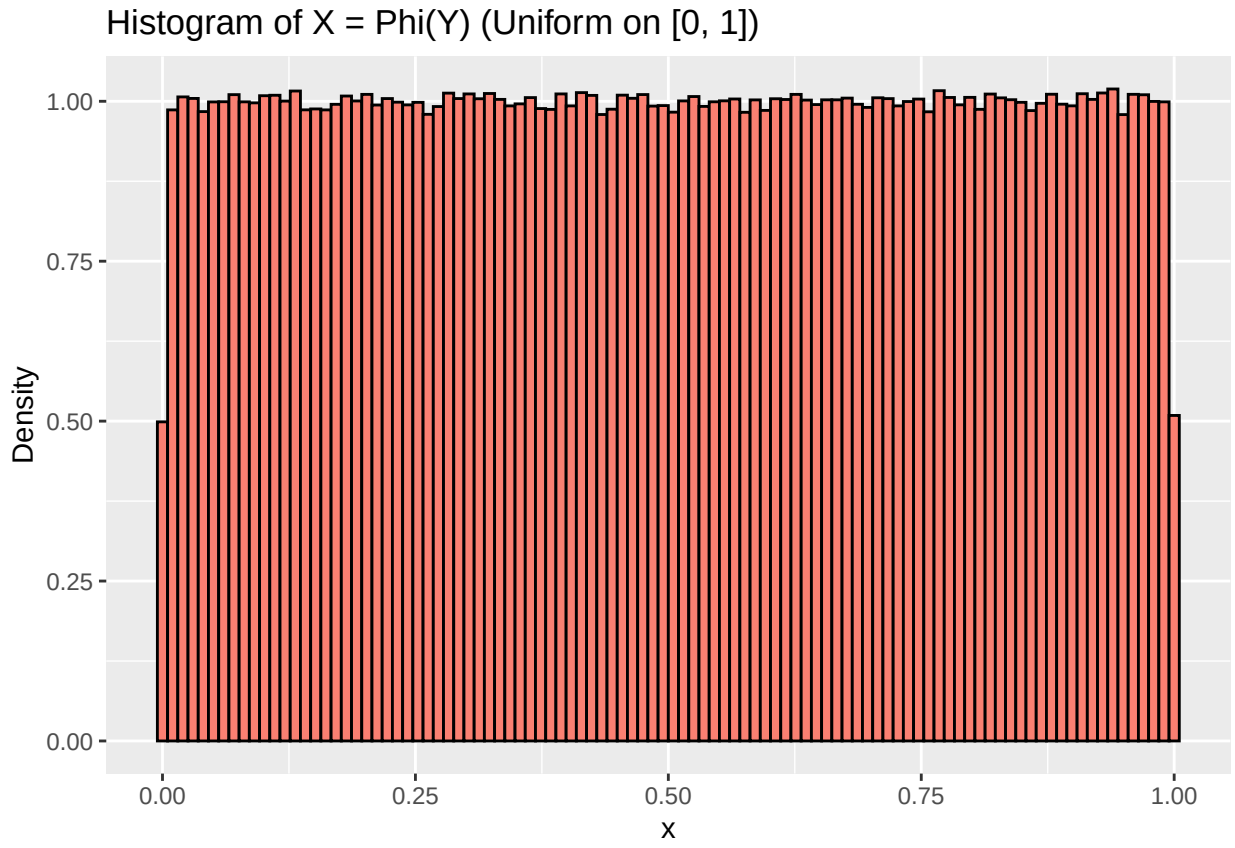
This shows that the cdf of X is $F_X(x) = x$, which is the cdf of a $U(0, 1)$

```
set.seed(18)
n_samples <- 1e6
Y <- rnorm(n_samples)

X <- pnorm(Y)

if (!requireNamespace("ggplot2", quietly = TRUE)) {
  install.packages("ggplot2")
}
library(ggplot2)

ggplot(data.frame(Y), aes(x = Y)) +
  geom_histogram(aes(y = after_stat(density)), bins = 100, fill = "skyblue", color = "black") +
  ggtitle("Histogram of Y (Standard Normal)") +
  xlab("y") +
  ylab("Density")
```




```
ggplot(data.frame(X), aes(x = X)) +
  geom_histogram(aes(y = after_stat(density)), bins = 100, fill = "salmon", color = "black") +
```

```
  ggtitle("Histogram of X = Phi(Y) (Uniform on [0, 1])") +
  xlab("x") +
  ylab("Density")
```



Ex 2.70

The beta distribution is a probability distribution over (0, 1) that is often used in applications for which the random variable is a proportion. The beta pdf is

$$f(y;\alpha,\beta) = \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} y^{\alpha-1}(1-y)^{\beta-1}, 0 \le y \le 1,$$

for parameters α and β, where $\Gamma()$ denotes the gamma function.

(a) Show that the uniform distribution is the special case $\alpha = \beta = 1$

(b) show that $\mu = E(Y) = \alpha/\alpha + \beta$

(c) Find $E(Y^2)$. Show that $var(Y) = \alpha\beta/(\alpha+\beta)^2(\alpha+\beta+1) = \mu(1-\mu)/(\alpha+\beta+1)$. For fixed $\alpha+\beta$, note that $var(Y)$ decreases as μ approaches 0 or 1.

(d) Using a function such as dbeta in R, plot the beta pdf for (i) $\alpha = \beta = 0.5, 1.0, 10, 100$,(ii) some values of $\alpha > \beta$ and some values of $\alpha < \beta$. Describe the impact of and on the shape and spread.

Solution

a) *The assumption will be proof by the moment generating function* $E(e^{tx}) = \int_0^1 e^{tx} f(x;\alpha,\beta)dx$

$$f(y;1,1) = \frac{\Gamma(2)}{\Gamma(1)\Gamma(1)} y^0(1-y)^0 = 1$$

$$E(e^{tx}) = \int_0^1 e^{tx} f(x;1,1)dx = \frac{e^t - 1}{t} = \frac{e^{tb} - e^{ta}}{t(b-a)}, b = 1, a = 0$$

But $\frac{e^{tb}-e^{ta}}{t(b-a)}$ *is the mgf of a* $U(0,1)$

b)

$$\mu = E(Y) = \int_{-\infty}^{+\infty} y \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} y^{\alpha-1}(1-y)^{\beta-1}dy = \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} \int_{-\infty}^{+\infty} y^{\alpha}(1-y)^{\beta-1}dy =$$

We can notice that the solution of the integral is as a combination of Gamma function

$$= \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} \frac{\Gamma(\alpha+1)\Gamma(\beta)}{\Gamma(\alpha+\beta+1)} =$$

Remembering that $\Gamma(\alpha+1) = \alpha\Gamma(\alpha)$

$$= \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)} \frac{\alpha\Gamma(\alpha)}{(\alpha+\beta)\Gamma(\alpha+\beta)} = \frac{\alpha}{\alpha+\beta}$$

c) *We start computing* $E(Y^2)$

$$E(Y^2) = \int_{-\infty}^{+\infty} y^2 \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} y^{\alpha-1}(1-y)^{\beta-1}dy = \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} \int_{-\infty}^{+\infty} y^{\alpha+1}(1-y)^{\beta-1}dy =$$

$$= \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} \frac{\Gamma(\alpha+2)\Gamma(\beta)}{\Gamma(\alpha+\beta+2)} = \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)} \frac{\alpha(\alpha+1)\Gamma(\alpha)}{(\alpha+\beta)(\alpha+\beta+1)\Gamma(\alpha+\beta)} =$$

$$= \frac{\alpha(\alpha+1)}{(\alpha+\beta)(\alpha+\beta+1)}$$

Using the equality $var(Y) = E(Y^2) - E(Y)^2$

$$E(Y^2) - E(Y)^2 = \frac{\alpha(\alpha+1)}{(\alpha+\beta)(\alpha+\beta+1)} \left(\frac{\alpha}{\alpha+\beta}\right)^2 =$$

$$= \frac{(\alpha^2+\alpha)(\alpha+\beta) - \alpha^2(\alpha+\beta+1)}{(\alpha+\beta)^2(\alpha+\beta+1)} =$$

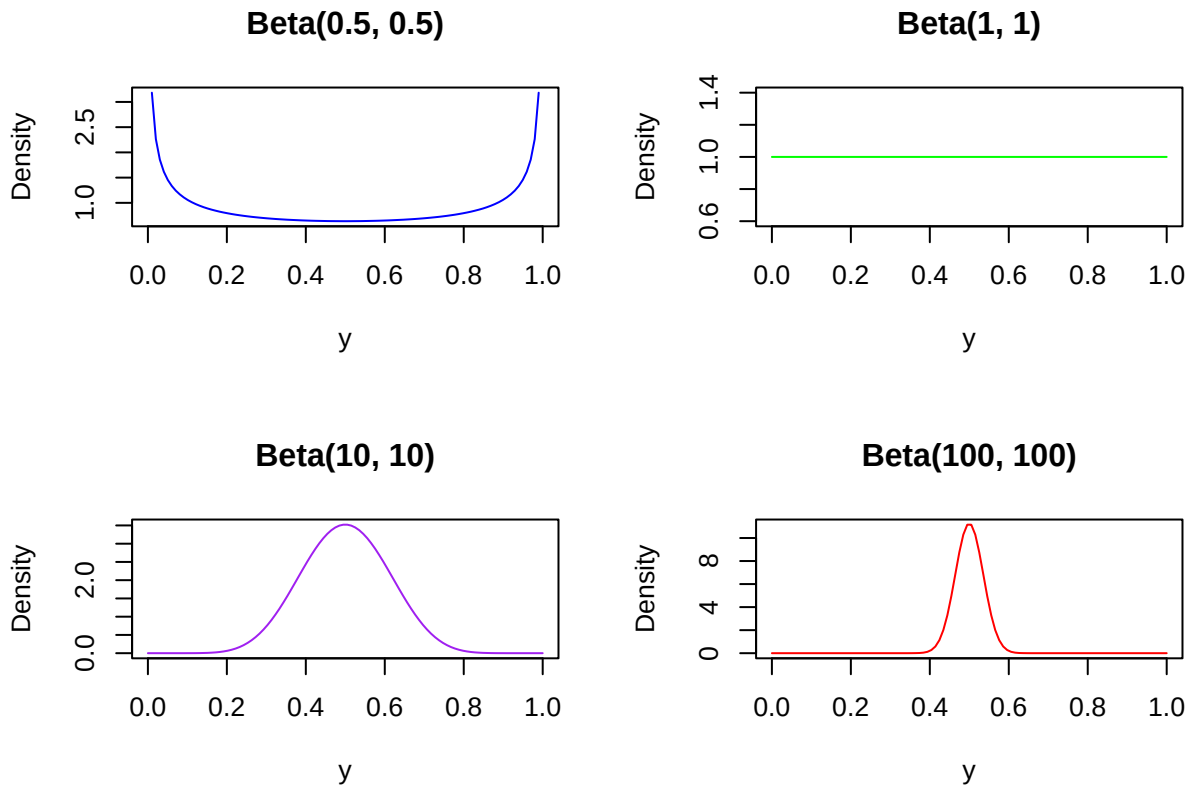
$$= \frac{\alpha^3 + \alpha^2\beta + \alpha^2 + \alpha\beta - \alpha^3 - \alpha^2\beta - \alpha^2}{(\alpha+\beta)^2(\alpha+\beta+1)} =$$

$$= \frac{\alpha\beta}{(\alpha+\beta)^2(\alpha+\beta+1)}$$

We can write this result as $\frac{\alpha}{\alpha+\beta}\left(1 - \frac{\alpha}{\alpha+\beta}\right)\frac{1}{(\alpha+\beta+1)} = \frac{\alpha}{\alpha+\beta}\frac{\beta}{\alpha+\beta}\frac{1}{(\alpha+\beta+1)}$

Then, $var(Y) = \frac{\mu(1-\mu)}{(\alpha+\beta)^2(\alpha+\beta+1)}$

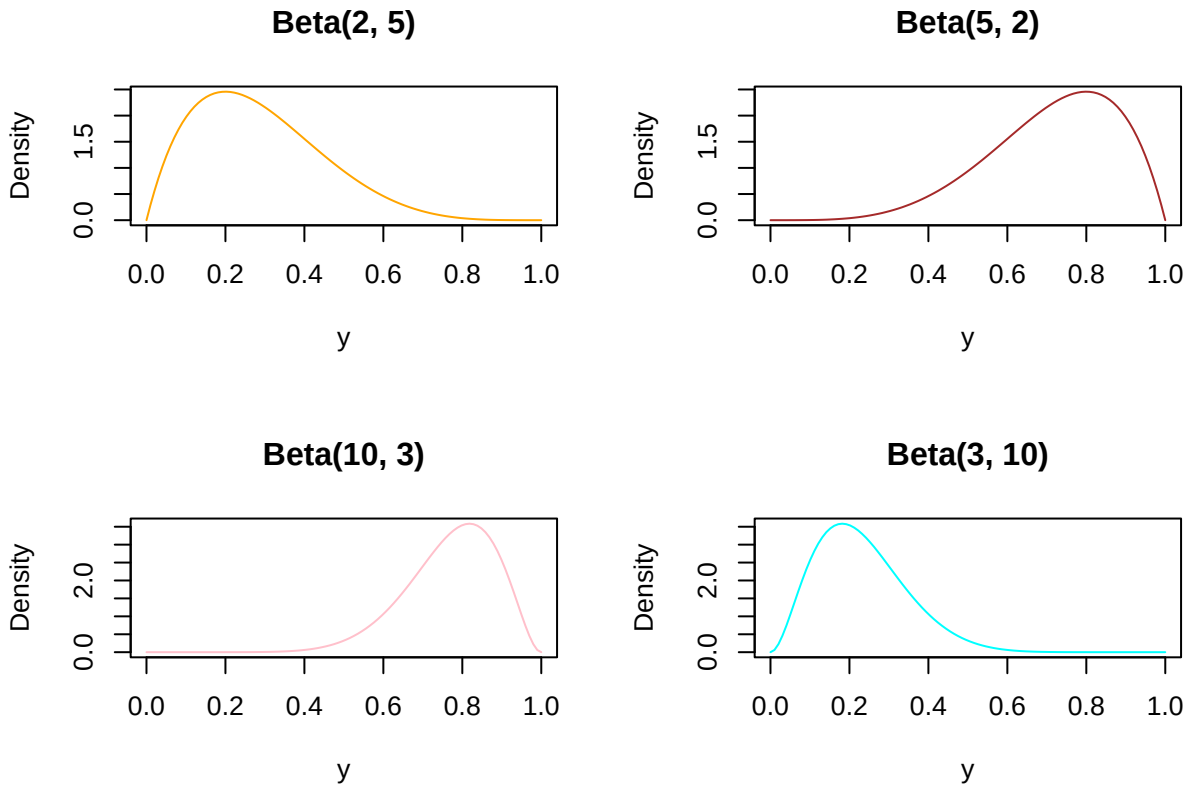
```r
par(mfrow = c(2, 2))
y <- seq(0, 1, length.out = 100)


plot(y, dbeta(y, 0.5, 0.5), type = "l", col = "blue", main = "Beta(0.5, 0.5)",
     ylab = "Density", xlab = "y")

plot(y, dbeta(y, 1, 1), type = "l", col = "green", main = "Beta(1, 1)",
     ylab = "Density", xlab = "y")

plot(y, dbeta(y, 10, 10), type = "l", col = "purple", main = "Beta(10, 10)",
     ylab = "Density", xlab = "y")

plot(y, dbeta(y, 100, 100), type = "l", col = "red", main = "Beta(100, 100)",
     ylab = "Density", xlab = "y")
```



d)

```r
par(mfrow = c(2, 2))

plot(y, dbeta(y, 2, 5), type = "l", col = "orange", main = "Beta(2, 5)",
     ylab = "Density", xlab = "y")

plot(y, dbeta(y, 5, 2), type = "l", col = "brown", main = "Beta(5, 2)",
     ylab = "Density", xlab = "y")
```

```r
plot(y, dbeta(y, 10, 3), type = "l", col = "pink", main = "Beta(10, 3)",
     ylab = "Density", xlab = "y")

plot(y, dbeta(y, 3, 10), type = "l", col = "cyan", main = "Beta(3, 10)",
     ylab = "Density", xlab = "y")
```



Interpretation of the coefficients:

- $\alpha = \beta = 0.5$ *the distribution has a U-shape, with higher density near 0 and 1*
- $\alpha = \beta = 1$ *is the Uniform distribution*
- $\alpha = \beta > 1$ *the distribution becomes more peaked around the center*
- $\alpha > \beta$ *the distribution skews toward 1, with higher density on the right side of the interval*
- $\alpha < \beta$ *the distribution skews toward 0, with higher density on the left side of the interval*

FSDS - Chapter 3

Ex 3.18

Sunshine City, which attracts primarily retired people, has 90,000 residents with a mean age of 72 years and a standard deviation of 12 years. The age distribution is skewed to the left. A random sample of 100 residents of Sunshine City has $y = 70$ and $s = 11$.

(a) Describe the center and spread of the (i) population distribution, (ii) sample data distribution. What shape does the sample data distribution probably have? Why?

Solution the center of spread of the distribution is $\mu = 72$ and the spread is equal to the standard deviation $\sigma = 12$ while for the sample it's $\widehat{Y} = 70$ and spread $\widehat{S} = 11$ the sample data distribution probably have the shape of a normal distribution, since with the sample size of 100 we can apply the central limit theorem to approximate it.

(b) Find the center and spread of the sampling distribution of Y for n = 100. What shape does it have and what does it describe?

Solution by the central limit theorem we can assume that the center of the sample distribution is going to be $\mu_{\widehat{Y}} = \mu = 72$. and the spread is going to be $\sigma_{\widehat{Y}} = \frac{\sigma}{\sqrt{n}} = 12/10 = 1.2$, the shape, as stated before, is going to be approximately that of a normal distribution and it tell us the likely range of sample means of a sampling of 100 citizens.

(c) Explain why it would not be unusual to sample a person of age 60 in Sunshine City, but it would be highly unusual for the sample mean to be 60, for a random sample of 100 residents.

Solution this is due to the difference in spread of the two distributions, with a standard deviation of 12 and a mean of 72 it's easy to see that a person of age 60 can be easly drawn, while the sample mean distribution has a much smaller standard deviation resulting in having a sample mean that stays very close to $\widehat{\mu}$.

(d) Describe the sampling distribution of Y : (i) for a random sample of size n = 1; (ii) if you sample all 90,000 residents.

Solution the sample distribution will keep $\mu_{\widehat{Y}} = 72$ in both cases, what is going to change is the standard deviation, in the first case the standard deviation is going to be $\sigma_{\widehat{Y}} = \frac{\sigma}{\sqrt{n}} = 12/1 = 12$ while in the second case it's going to be $\sigma_{\widehat{Y}} = \frac{\sigma}{\sqrt{n}} = 12/300 = 0,04$ which basically means that if you sampled the whole city you would get the exact mean for the original distribution every time.

Ex 3.28

A survey is planned to estimate the population proportion π supporting more government action to address global warming. For a simple random sample, if π may be near 0.50, how large should n be so that the standard error of the sample proportion is 0.04?

Solution we know that we want a $SE = 0.04$, the formula for the standard error for a proportion is $SE(p) = \sqrt{\frac{pi(1-pi)}{n}}$ and by substituting π we get $0,04 = \sqrt{\frac{0,25}{n}}$ therefore $n = \frac{0.25}{0,04^2} = 156.25 \approx 157$

Ex 3.24 (use R)

Construct a population distribution that is plausible for Y = number of alcoholic drinks in the past day. Use the following steps: (a) Simulate a single random sample of size n = 1000 from this population to reflect results of a typical sample survey. Summarize how the sample mean and standard deviation resemble those for the population. (Alternatively, you can do this and part **Solution** I find this solution plausible because a person is more likely to not drink in a day then to drink, and the higher the number the less likely a person is to drink another drink, we could have also used a poisson distribution but it would have not given the high differce that there is between 0 and 1 or more drinks

in the following, the theoretical mean and variance, the sample mean and sample variance are calculated. the sample mean is an estimate of the population mean and should be close to the theoretical mean of the distribution based on the population proportions and the sample variance

```r
set.seed(123)
n=1000
values <- c(0, 1, 2, 3, 4)
probs <- c(0.55, 0.24, 0.15, 0.05, 0.01)
mu=0
sigmasq=0
for(i in 1:5)
{
  mu=mu+values[i]*probs[i]
}
for(i in 1:5)
{
  sigmasq=sigmasq+((values[i]-mu)^2*probs[i])
}
mu
```

```
## [1] 0.73
```

```r
sqrt(sigmasq)
```

```
## [1] 0.9576534
```

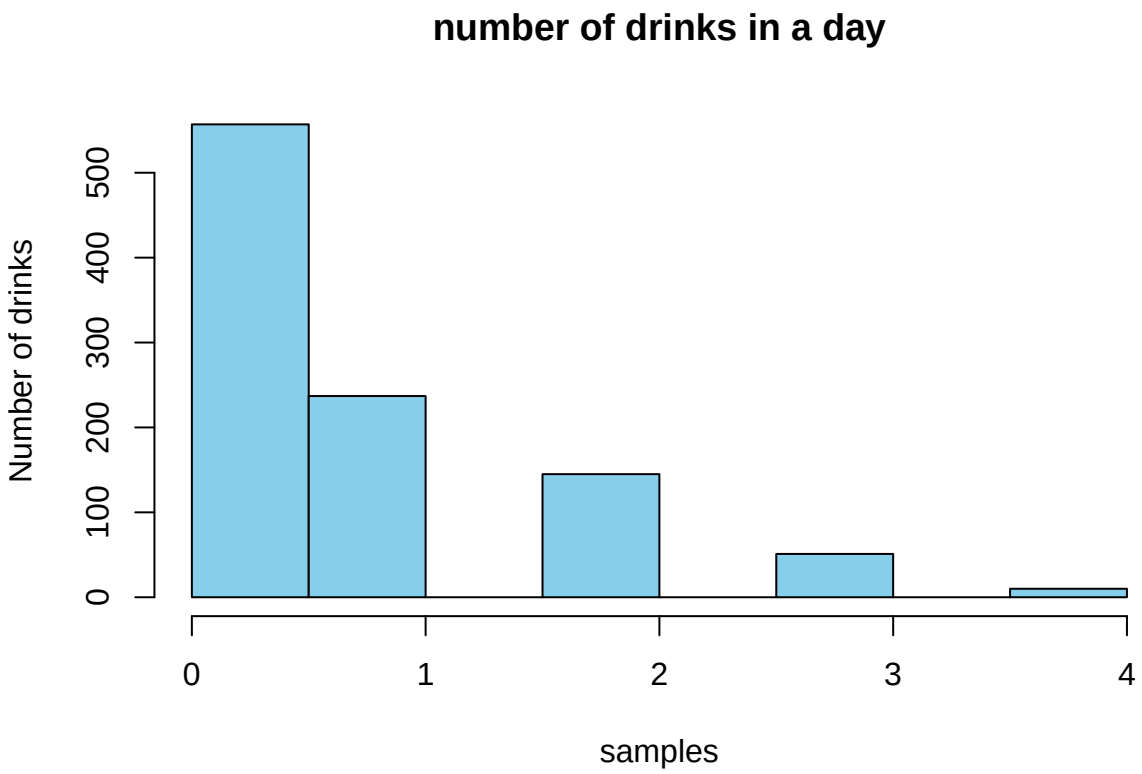
```r
samples <- sample(values, size = 1000, replace = TRUE, prob = probs)

smean =mean(samples)
svar=var(samples)

smean
```

```
## [1] 0.72
```

```r
svar
```

```
## [1] 0.9185185
```

```r
hist(samples, main = "number of drinks in a day",
        ylab = "Number of drinks", col = "skyblue")
```



Now draw 10,000 random samples of size 1000 each, to approximate the sampling distribution of Y . Report the mean and standard deviation of this simulated sampling distribution, and compare to the theoretical values. Explain what this sampling distribution represents.

solution

```
set.seed(123)
n=1000
m=10000
values <- c(0, 1, 2, 3, 4)
probs <- c(0.55, 0.24, 0.15, 0.05, 0.01)


means= array(0,dim=10000)
for(i in 1:10000)
{
  multisamples=sample(values, size = 1000, replace = TRUE, prob = probs)
  means[i]=mean(multisamples)
}

meanofmeans=mean(means)
varianceofmeans=var(means)
meanofmeans
```

```
## [1] 0.7298131
```

```r
sqrt(varianceofmeans)
```

```
## [1] 0.03012794
```

this distribution represents the distribution of sample means you would expect if you repeatedly took random samples of size 1,000 from this population which brings the mean of this distribution close to the original due to the law of large numbers. the standard deviation will be extremely small since it represents how well the distribution gets every time it gets sampled to the means, this means that every time we extract a sample mean it will be extremely close to the theoretical one.## FSDS - Chapter 4

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Ex 4.14

Using the Students data file, for the corresponding population, construct a 95% confidence interval:

(a) *for the mean weekly number of hours spent watching TV.*
(b) *to compare females and males on the mean weekly number of hours spent watching TV.*

In each case, state assumptions, including the practical importance of each, and interpret results.

Solution

(a) 95% Confidence Interval for Mean Weekly Hours of TV Watching Let:

$$\bar{X} = \text{sample mean of weekly hours spent watching TV},$$

$$s = \text{sample standard deviation of weekly hours},$$

$$n = \text{sample size}.$$

The standard error of the mean is:

$$\text{SE} = \frac{s}{\sqrt{n}}.$$

The 95% confidence interval is:

$$\bar{X} \pm t_{\alpha/2,\, n-1} \times \text{SE}$$

where $t_{\alpha/2,\, n-1}$ is the critical value from the t-distribution with $n-1$ degrees of freedom.

Assumptions: The data is randomly sampled, and either normally distributed or sufficiently large for the Central Limit Theorem to apply.

Interpretation: This interval provides a range within which the true mean weekly hours of TV watching is expected to fall with 95% confidence.

(b) 95% Confidence Interval for the Difference in Mean Weekly Hours Between Females and Males Let:

$$\bar{X}_f = \text{mean weekly hours for females}, \quad s_f = \text{standard deviation for females},$$
$$\bar{X}_m = \text{mean weekly hours for males}, \quad s_m = \text{standard deviation for males},$$
$$n_f = \text{sample size for females}, \quad n_m = \text{sample size for males}.$$

The pooled standard error is:

$$\text{SE}_{\text{pooled}} = \sqrt{\frac{s_f^2}{n_f} + \frac{s_m^2}{n_m}}.$$

The 95% confidence interval for the difference in means $(\mu_f - \mu_m)$ is:

$$(\bar{X}_f - \bar{X}_m) \pm t_{\alpha/2,\, df} \times \text{SE}_{\text{pooled}}$$

where $t_{\alpha/2,\, df}$ is the critical t-value with degrees of freedom df (calculated as $\min(n_f - 1, n_m - 1)$ or using the Satterthwaite approximation if variances are unequal).

Assumptions: Samples are independent and randomly selected. We assume normality or large sample sizes, and equal variances for females and males (if not, use Welch's t-test).

Interpretation: This interval gives a range for the true difference in mean weekly hours between females and males. If the interval includes 0, it suggests no significant difference in weekly hours spent watching TV by gender.

Ex 4.16

The Substance data file shows a contingency table formed from a survey that asked a sample of high school students whether they have ever used alcohol, cigarettes, and marijuana. Construct a 95% Wald confidence interval to compare those who have used or not used alcohol on whether they have used marijuana, using:

(a) *formula (4.13);*
(b) *software.*

State assumptions for your analysis, and interpret results.

Solution

Contingency Table Information Let: - n_{11} = number of students who have used both alcohol and marijuana, - n_{10} = number of students who have used alcohol but not marijuana, - n_{01} = number of students who have not used alcohol but have used marijuana, - n_{00} = number of students who have not used either alcohol or marijuana.

Define:

$$n_1 = n_{11} + n_{10} \quad \text{(total who have used alcohol)}$$
$$n_0 = n_{01} + n_{00} \quad \text{(total who have not used alcohol)}$$
$$p_1 = \frac{n_{11}}{n_1} \quad \text{(proportion of alcohol users who have used marijuana)}$$
$$p_0 = \frac{n_{01}}{n_0} \quad \text{(proportion of non-alcohol users who have used marijuana)}$$

The difference in proportions is:

$$\hat{p} = p_1 - p_0.$$

(a) 95% Wald Confidence Interval using Formula (4.13) The formula for the 95% Wald confidence interval for the difference between two proportions is given by:

$$\hat{p} \pm z_{\alpha/2}\sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_0(1-p_0)}{n_0}}$$

where $z_{\alpha/2}$ is the critical value from the standard normal distribution for a 95% confidence level (approximately 1.96).

Substitute p_1, p_0, n_1, and n_0 from the data to calculate the interval.

Assumptions: - Random sampling: The sample of high school students should be representative of the population. - Independence: The responses of individual students are independent of each other. - Normal approximation: Sample sizes n_1 and n_0 should be large enough for the normal approximation to hold (usually $n \times p \geq 5$ and $n \times (1-p) \geq 5$ for each group).

Interpretation: The confidence interval provides a range for the difference in proportions between alcohol users and non-users in terms of marijuana usage. If the interval includes 0, it suggests no significant difference in marijuana use between those who have and have not used alcohol.

(b) 95% Confidence Interval using Software To compute this confidence interval using software as R, calculating confidence intervals for two proportions. For example, in R:

Ex 4.48

For a simple random sample of n subjects, explain why it is about 95% likely that the sample proportion has error no more than $\frac{1}{\sqrt{n}}$ in estimating the population proportion. (Hint: To show this "$\frac{1}{\sqrt{n}}$" rule, find two standard errors when $\pi = 0.50$, and explain how this compares to two standard errors at other values of π.) Using this result, show that $n = \frac{1}{M^2}$ is a safe sample size for estimating a proportion to within M with 95% confidence.

Solution

Let:

$$\hat{p} = \text{sample proportion},$$

$$\pi = \text{population proportion}.$$

The standard error of the sample proportion $\hat{p}$ is given by:

$$\text{SE}(\hat{p}) = \sqrt{\frac{\pi(1-\pi)}{n}}.$$

To construct a 95% confidence interval, we use approximately two standard errors (since 95% of the standard normal distribution falls within ± 1.96 standard deviations of the mean). Therefore, the margin of error E at the 95% confidence level is:

$$E \approx 2 \times \text{SE}(\hat{p}) = 2\sqrt{\frac{\pi(1-\pi)}{n}}.$$

The $\frac{1}{\sqrt{n}}$ Rule To illustrate the $\frac{1}{\sqrt{n}}$ rule, consider the case where $\pi = 0.50$, which maximizes the product $\pi(1-\pi)$ and hence gives the largest possible standard error.

When $\pi = 0.50$, the standard error is:

$$\text{SE}(\hat{p}) = \sqrt{\frac{0.5 \times 0.5}{n}} = \frac{1}{2\sqrt{n}}.$$

Thus, the margin of error at the 95% confidence level becomes:

$$E \approx 2 \times \frac{1}{2\sqrt{n}} = \frac{1}{\sqrt{n}}.$$

This shows that, for a population proportion near 0.5, it is about 95% likely that the sample proportion $\hat{p}$ will be within $\frac{1}{\sqrt{n}}$ of the population proportion π. For other values of π, the standard error $\sqrt{\pi(1-\pi)/n}$ will be smaller, making $\frac{1}{\sqrt{n}}$ a conservative, safe upper bound on the margin of error.

Deriving the Sample Size Formula $n = \frac{1}{M^2}$ To ensure the margin of error $E \leq M$ with 95% confidence, we set the margin of error to M:

$$\frac{1}{\sqrt{n}} \leq M.$$

Solving for n, we get:

$$\sqrt{n} \geq \frac{1}{M},$$
$$n \geq \frac{1}{M^2}.$$

Thus, $n = \frac{1}{M^2}$ is a safe sample size for estimating the population proportion within a margin of error M with 95% confidence.

Conclusion: This result provides a guideline for determining sample size when estimating a population proportion. For a desired margin of error M at the 95% confidence level, a sample size of $n = \frac{1}{M^2}$ is sufficient to ensure that the sample proportion $\hat{p}$ will likely be within M of the population proportion π.

FSDS - Chapter 5

Ex 5.2

When a government does not have enough money to pay for the services that it provides, it can raise taxes or it can reduce services. When the Florida Poll asked a random sample of 1200 Floridians which they preferred, 52% (624 of the 1200) chose raise taxes and 48% chose reduce services. Let π denote the population proportion of Floridians who would choose raising taxes. Analyze whether this is a minority of the population ($\pi < 0.50$) or a majority ($\pi > 0.50$) by testing $H_0 : \pi = 0.50$ against $H_a : \pi \neq 0.50$. Interpret the P-value. Is it appropriate to "accept" H_0 ? Why or why not?

Solution

- $H_0 : \pi = 0.50$ (the population proportion is 50%, suggesting no majority preference for raising taxes).
- $H_a : \pi \neq 0.50$ (the population proportion is different from 50%).
- Sample size $(n) = 1200$
- Sample proportion $(\hat{p}) = 624 \ / \ 1200 = 0.52$
- Significance level $(\alpha) = 0.05$

```r
# Given data
n <- 1200                      # Sample size
p_hat <- 0.52                  # Sample proportion
mu <- 0.50                    # Hypothesized proportion

# Standard error for the proportion
standard_error <- sqrt((mu * (1 - mu)) / n)

# p-value for a two-tailed test
p_value <- 2 * (1 - pnorm(abs((p_hat - mu) / standard_error)))

# Display the p-value
p_value
```

```
## [1] 0.1658567
```

The P-value is greater than $\alpha = 0.05$, so we can't reject the null hypotesis. For definition, we can't "accept" H_0 but from this hypotesis testing we don't have any evidence against it.

Ex 5.12

The example in Section 3.1.4 described an experiment to estimate the mean sales with a proposed menu for a new restaurant. In a revised experiment to compare two menus, on Tuesday of the opening week the owner gives customers menu A and on Wednesday she gives them menu B. The bills average \$22.30 for the 43 customers on Tuesday ($s = 6.88$) and \$25.91 for the 50 customers on Wednesday ($s = 8.01$). Under the strong assumption that her customers each night are comparable to a random sample from the conceptual population of potential customers, show how to compare the mean sales for the two menus based on (a) the P-value of a significance test, (b) a 95% confidence interval. Which is more informative, and why? (When used in an experiment to compare two treatments to determine which works better, a two-sample test is often called an A/B test.).

Solution

We have two groups of customers who were given different menus, A and B, on consecutive days. The objective is to compare the average sales between these two menus.

- **Menu A** (Tuesday): Mean = 22.30, n = 43, Standard Deviation = 6.88
- **Menu B** (Wednesday): Mean = 25.91, n = 50, Standard Deviation = 8.01

Assuming these samples are representative of the population, we will conduct a two-sample t-test to determine if there is a statistically significant difference between the two menu sales averages.

Hypothesis:
- H_0: There is no difference in mean sales between the two menus $\mu_A = \mu_B$. - H_1: There is a difference in mean sales $\mu_A \neq \mu_B$.

Significance Level: We will use a 5% significance level or $\alpha = 0.05$.

```r
mean_A <- 22.30
sd_A <- 6.88
n_A <- 43

mean_B <- 25.91
```

```r
sd_B <- 8.01
n_B <- 50

# Pooled standard deviation
s_p <- sqrt(((n_A - 1) * sd_A^2 + (n_B - 1) * sd_B^2) / (n_A + n_B - 2))

# Degrees of freedom
df <- n_A + n_B - 2

# Test statistic
t_statistic <- (mean_A - mean_B) / (s_p * sqrt(1 / n_A + 1 / n_B))

# P-value for a two-tailed test
p_value <- 2 * pt(-abs(t_statistic), df)

# 95% Confidence Interval
alpha <- 0.05
t_critical <- qt(1 - alpha/2, df)
margin_of_error <- t_critical * s_p * sqrt(1 / n_A + 1 / n_B)
confidence_interval <- c((mean_A - mean_B) - margin_of_error,
                         (mean_A - mean_B) + margin_of_error)



t_statistic
```

```
## [1] -2.311357
```

```r
df
```

```
## [1] 91
```

```r
p_value
```

```
## [1] 0.02307139
```

```r
confidence_interval
```

```
## [1] -6.7124295 -0.5075705
```

The confidence interval is more informative because:

- The P-value in this specific case is smaller than the tipical α significance level, so we can reject the null hypotesis, so we at least know that the sale price will influence the sales. If it was greater we simply don't know anything about the problem, because by definition we can't accept H_0, but just fail to reject it.
- A 95% confidence intervalgives us a range of plausible values for the difference in mean sales between the two menus. So, it not only tells us whether there's a difference but also gives a range for how much difference to expect.

Ex 5.50

A random sample of size 40 has $\bar{y} = 120$. *The P-value for testing* $H_0 : \mu = 100$ *against* $H_a : \mu \neq 100$ *is 0.057. Explain what is incorrect about each of the following interpretations of this P-value, and provide a proper interpretation.*

(a) *The probability that* H_0 *is correct equals 0.057.*

(b) *The probability that* $\bar{y} = 120$ *if* H_0 *is true equals 0.057.*

(c) *The probability of Type I error equals 0.057.*

(d) *We can accept* H_0 *at the* $\alpha = 0.05$ *level.*

Solution

a) The probability that H_0 is correct equals 0.057. *0.057 is the P-value, but it is not the probability that* H_0 *is true. The p-value represents the probability of obtaining a result as extreme as, or more extreme than, the observed result, assuming that* H_0 *is true.*

b) The probability that $\bar{y} = 120$ if H_0 is true equals 0.057. *This interpretation is incorrect because the P-value does not reflect the probability of observing exactly* $\bar{y} = 120$ *if* H_0 *is true.Instead, it measures the probability of observing a value as extreme, or more extreme than* $\bar{y} = 120$

c) The probability of Type I error equals 0.057. *It's incorrect because the Type I error is equals to the significance level* α *and not to the P-value. So, if we choose* $\alpha = 0.05$ *like in the next point, the probability of a Type I error would be 0.05 or 5% and not 0.057 or 5.7%*

d) We can accept H_0 at the $\alpha = 0.05$ level. *In the hypothesis testing, you never can accept* H_0. *You can only "reject it" if your p-value is smaller than your significance level (*α*) or "fail to reject it" if your p-value is greater or equal to it. In this specific case, the p-value is greater, so, for now, we failed to reject it.*