Assessment02

STAT414

2024-12-14

```r
library(EnvStats)
```

```
##
## Attaching package: 'EnvStats'

## The following objects are masked from 'package:stats':
##
##     predict, predict.lm
```

```r
# Let X1, ..., Xn denote a random sample from a normal population distribution with an
# unknown value of sig. Assume that the population is well-approximated by a normal
# distribution with mean mu and variance sig^2
#A sample of size (=25) yielded mean 102 (102=Xbar) and standard deviation of 7 (s=7).

# (a) Test the null H0 : mu = 100 vs Ha : mu > 100 at level alpha = 0.05 and state your
# conclusions based on the above sample. Please clearly show all seven steps of the
# hypothesis testing procedure.

#1 - Parameter of interest is mu
n=25
#2-3 -  H0: mu = 100
#       HA: mu > 100
#alpha = .05, use t-test
alpha = .05

#4 - test statistic = xbar-mu / s/sqrt(n)
tvalue <- (102-100) / (7/sqrt(25))

#5-6 - pvalue/rejection region
pvalue <- pt(tvalue, n-1, lower.tail = FALSE)
rejection <- qt(1-alpha, n-1)
rejection_mean <- 100 + rejection*(7/sqrt(25))

#7 - Conclusion
pvalue
```

```
## [1] 0.08300679
```

```r
rejection_mean
```

```
## [1] 102.3952
```

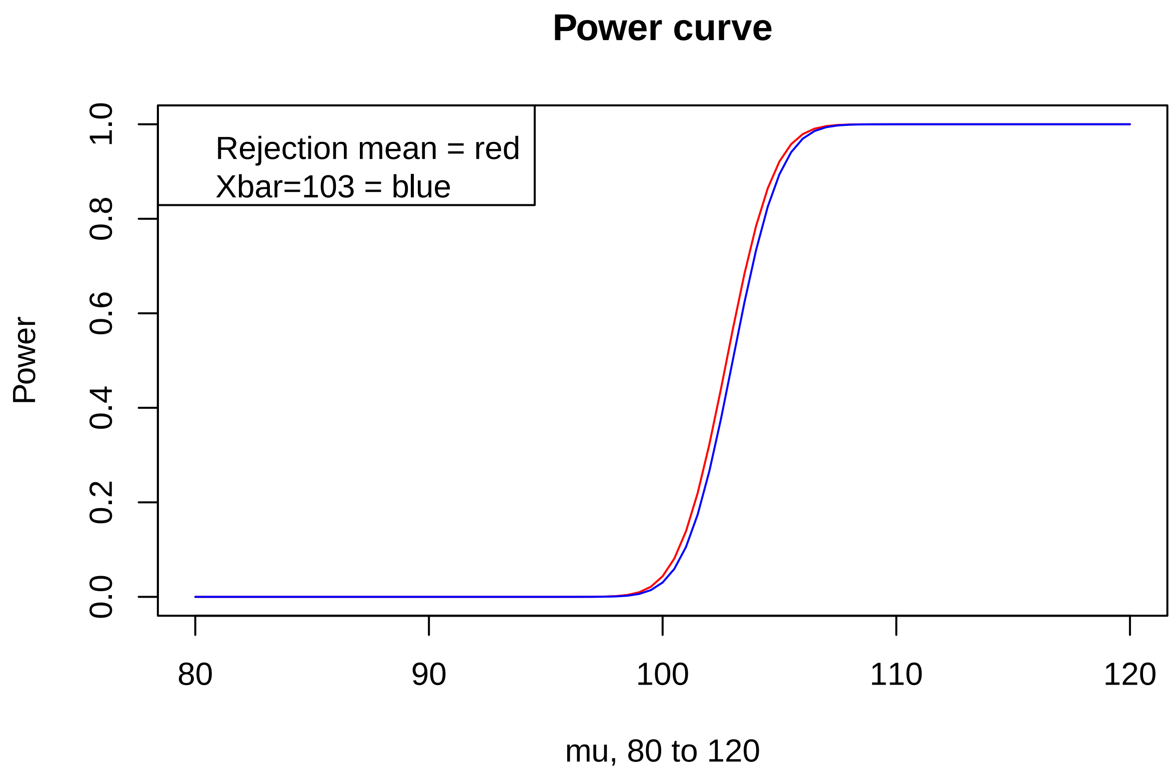
```r
cat("We reject H0 if the calculated pvalue is less than alpha or the sample mean
    Xbar is less than the rejection mean. The pvalue is", pvalue, "which is greater
    than alpha=.05, therefore we fail to reject the null hypothesis and conclude
    that the there is not enough evidence to support that the parameter of interest
    mu is greater than 100, statistical evidence shows support to the idea that mu
    is equal to 100.")
```

```
## We reject H0 if the calculated pvalue is less than alpha or the sample mean
##     Xbar is less than the rejection mean. The pvalue is 0.08300679 which is greater
##     than alpha=.05, therefore we fail to reject the null hypothesis and conclude
##     that the there is not enough evidence to support that the parameter of interest
##     mu is greater than 100, statistical evidence shows support to the idea that mu
##     is equal to 100.
```

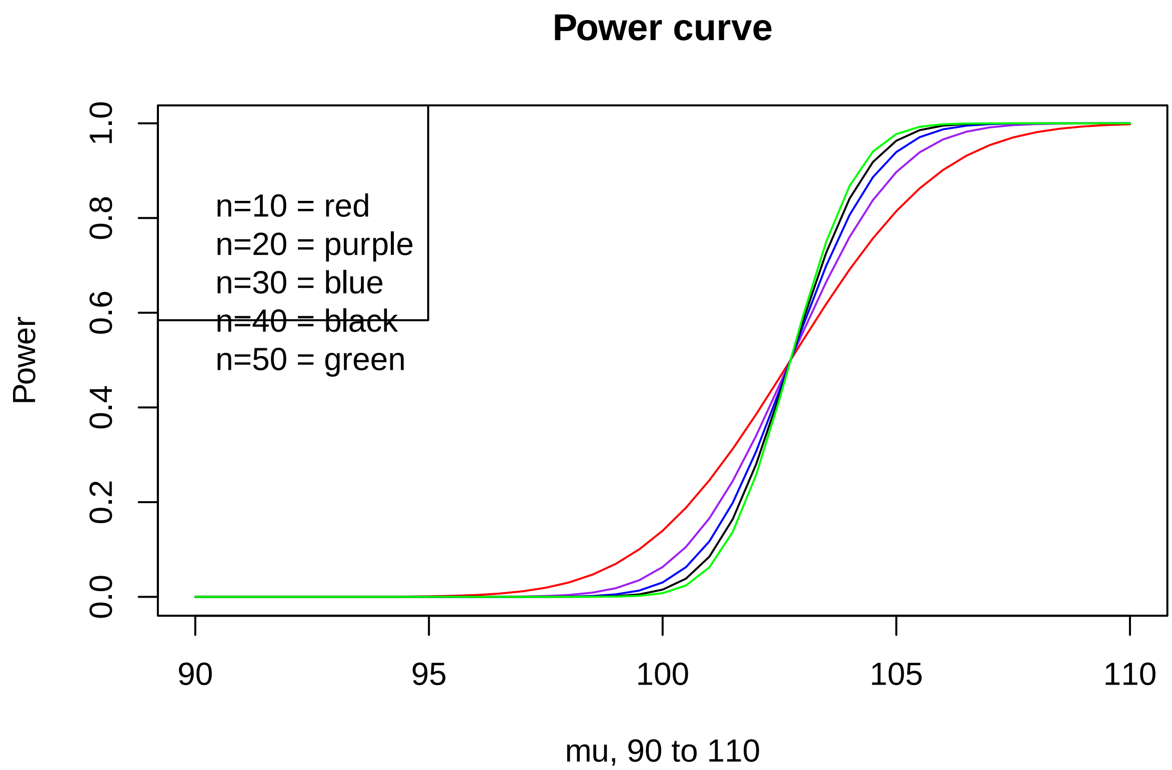
```r
# (b) Use tTestPower function of EnvStats, and compute the power curve of the above
# test procedure assuming that the standard deviation of the population (sig is 8.

# Plot the power curve of this test procedure. Suppose the data had yielded a
# sample mean Xbar = 103, what would the power curve look like?

tvalue <- (103-100) / (8/sqrt(25))
rejection <- qt(1-alpha, n-1)
rejection_mean <- 100 + rejection*(8/sqrt(25))
rejection_mean
```

```
## [1] 102.7374
```

```r
mu <- seq(80,120,.5)
plot(mu,1 - pnorm(rejection_mean, mu, sd = 8/sqrt(25)), type="l",
     ylab="Power", xlab="mu, 80 to 120", main="Power curve", col="red")
lines(mu,1 - pnorm(103, mu, sd = 8/sqrt(25)), type="l", col="blue")
legend("topleft", legend = ("Rejection mean = red
Xbar=103 = blue"))
```



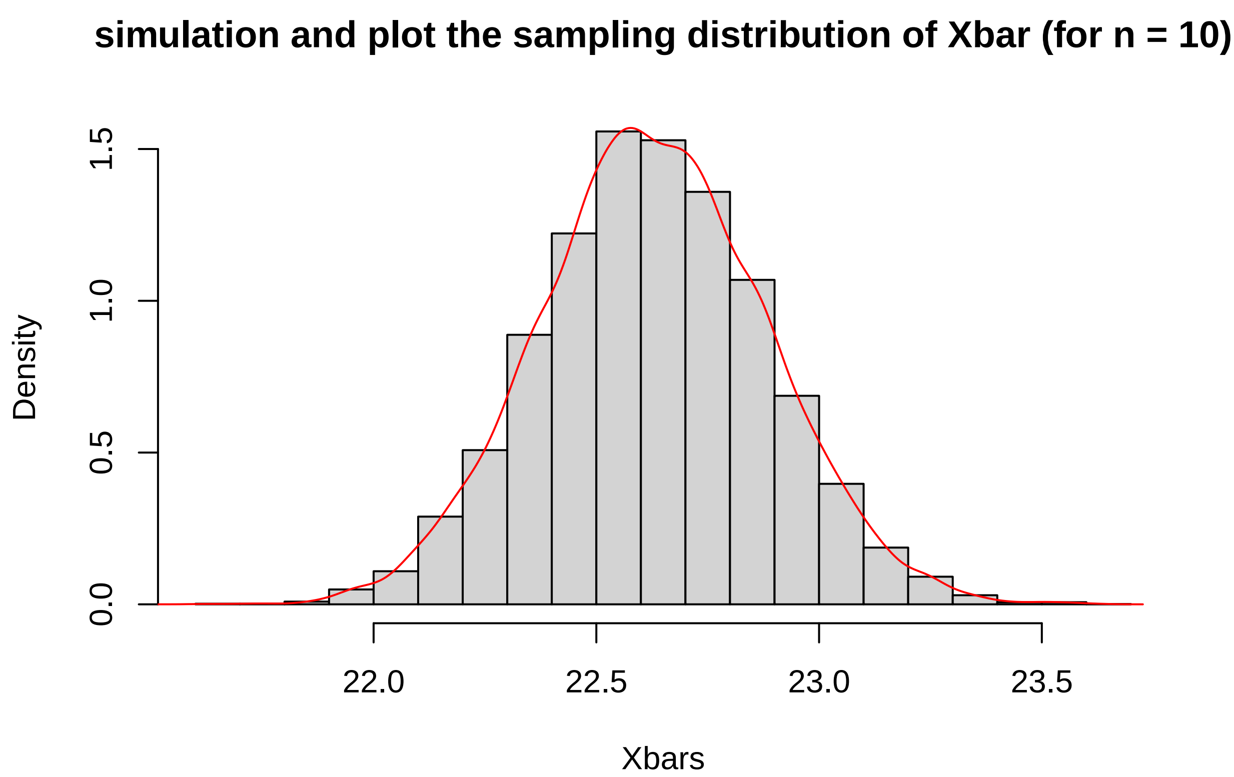

```r
# (c) Plot the power curve of this test for values of mu ranging from 90 to 110 for sample
# sizes n = 10, 20, 30, 40, 50. Plot all these curves on the same plot. Add a legend
# to your plot.
mu <- seq(90,110,.5)
plot(mu,1 - pnorm(rejection_mean, mu, sd = 8/sqrt(10)), type="l",
     ylab="Power", xlab="mu, 90 to 110", main="Power curve", col="red")
lines(mu,1 - pnorm(rejection_mean, mu, sd = 8/sqrt(20)), col="purple")
lines(mu,1 - pnorm(rejection_mean, mu, sd = 8/sqrt(30)), col="blue")
lines(mu,1 - pnorm(rejection_mean, mu, sd = 8/sqrt(40)), col="black")
lines(mu,1 - pnorm(rejection_mean, mu, sd = 8/sqrt(50)), col="green")
legend("topleft", legend = ("n=10 = red
n=20 = purple
n=30 = blue
n=40 = black
n=50 = green"))
```




```
# 2. Suppose the investigator had mistakenly thought that the population is Normal. In
# reality it is a Gamma, with shape alpha and scale beta.

# (a) Use simulation and plot the sampling distribution of Xbar (for n = 10) when the
# null hypothesis is true and the population standard deviation (sig) is 8.

#null hypothesis is true implies mu = 100, sig given as 8
n = 10
mu = 100
sig = 8

#shape = k * theta = mu * sig
alpha <- mu * sig

#scale = k / sqrt(theta) = mu / sqrt(sig)
beta <- mu / sqrt(sig)

set.seed(1)
Xbars <- c()

#10000 simulations of xbar(mean) of rgamma for n=10, for shape=alpha, scale=beta
for(i in 1:10000){
  simu <- rgamma(10,alpha, beta)
  Xbars[i] <- mean(simu)
}
```

```r
hist(Xbars, probability="TRUE", main = "simulation and plot the sampling distribution of Xbar (for n = 
lines(density(Xbars), add=TRUE, col="red")
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): "add" is not a graphical
## parameter
```




```r
#curve(dgamma(x, shape=(mean(Xbars)*sd(Xbars)), scale=(mean(Xbars)/sd(Xbars))), add=TRUE, col="blue")

# (b) Suppose the mu = 102 and standard deviation (sig) is 8. Compute the true power of
# the test and compare it to the power under the [wrong] assumption of Normality
# as in #1.

xbar <- mean(Xbars)
xbar
```

```
## [1] 22.62771
```

```r
mu = 102
sig = 8

tvalue <- (xbar-mu) / (sig/sqrt(n))
rejection <- qt(1-.05, n-1)
rejection_mean <- mu + rejection*(sig/sqrt(n))
rejection_mean
```

```
## [1] 106.6374
```

```r
#True power = 1 - beta = 1 - P(type II error)
power <- 1 - pnorm(rejection_mean, mean=mu, sd = sig/sqrt(n))
cat("True power is:", power)
```

```
## True power is: 0.03339289
```