STAT 8010 R Lab 8: Confidence Intervals and Hypothesis Testing

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Average Height Example

We measure the heights of 40 randomly chosen men, and get a mean height of 5'9" ($\sim$ 175cm). Suppose we know the standard deviation of men's heights is 4" ($\sim$ 10cm). Find the 95% confidence interval of the true mean height of ALL men.

```r
xbar = 5 * 12 + 9
sd = 4
# 95% CI
alpha = 0.05
n = 40
ME <- qnorm(1 - alpha / 2) * (sd / sqrt(n))
CI <- c(xbar - ME, xbar + ME)
CI
```

```
## [1] 67.76041 70.23959
```

```r
n = 400
ME <- qnorm(1 - alpha / 2) * (sd / sqrt(n))
CI <- c(xbar - ME, xbar + ME)
CI
```

```
## [1] 68.60801 69.39199
```

```r
alpha = 0.01
ME <- qnorm(1 - alpha / 2) * (sd / sqrt(n))
CI <- c(xbar - ME, xbar + ME)
CI
```

```
## [1] 68.48483 69.51517
```

```r
sd = 6
ME <- qnorm(1 - alpha / 2) * (sd / sqrt(n))
CI <- c(xbar - ME, xbar + ME)
CI
```

```
## [1] 68.22725 69.77275
```

Sample Size Calculation

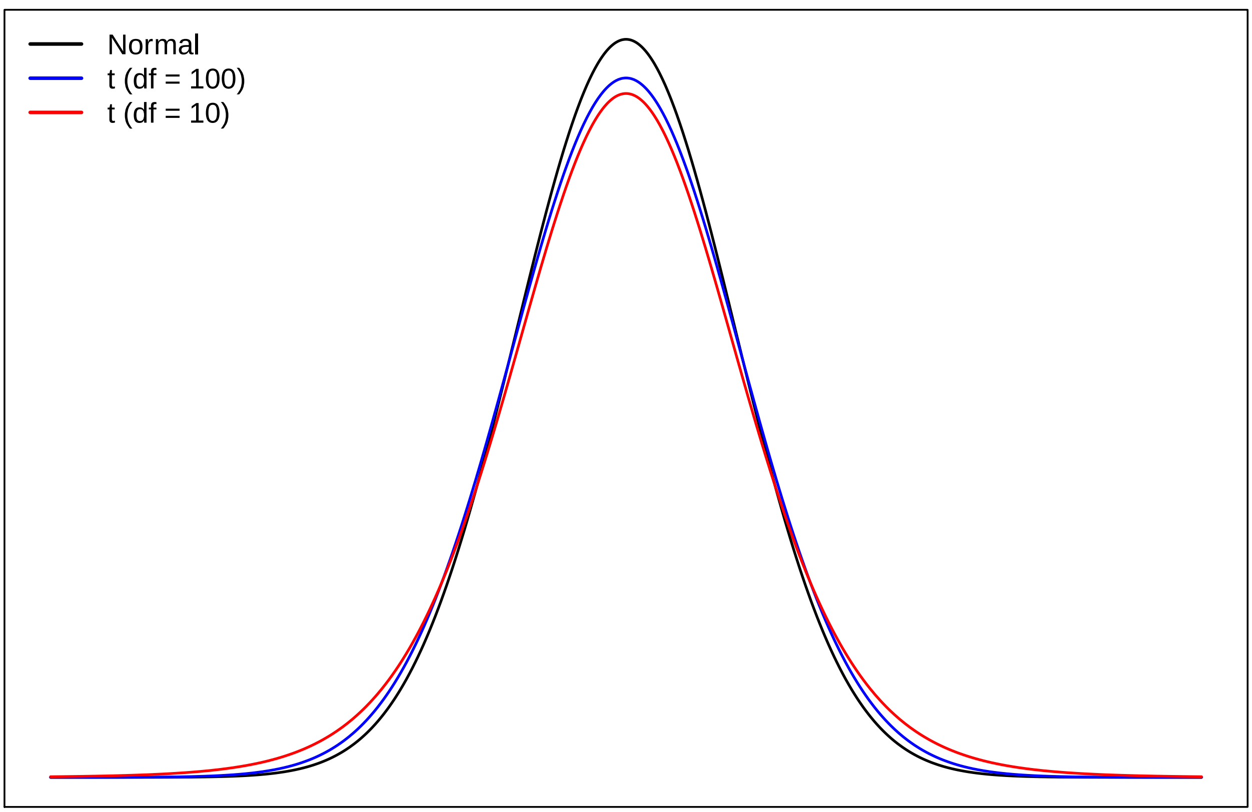
Compute the sample size needed in order to estimate the true mean height of All men such that the 95% CI to be 0.5 inches in width

```
sd = 4; alpha = 0.05; ME = 0.5 / 2
n = (qnorm(1 - alpha / 2) * 4 / ME)^2
n
```

```
## [1] 983.4135
```

Student's t-distribution

```
curve(dnorm(x, sd = 0.95),
      from = -5, to = 5,
      xlab = "", ylab = "",
      lwd = 1.5, n = 1001,
      xaxt = "n", yaxt = "n")
curve(dt(x, 100), from = -5, to = 5, n = 1001, lwd = 1.5, add = T, col = "blue")
curve(dt(x, 10), from = -5, to = 5, n = 1001, lwd = 1.5, add = T, col = "red")
legend("topleft", legend = c("Normal", "t (df = 100)", "t (df = 10)"), col = c("black", "blue", "red"),
```



Average Height Example Revisited

We measure the heights of 40 randomly chosen men, and get a mean height of 5'9" ($\sim$ 175cm), and a standard deviation of 4.5" ($\sim$ 11.4cm). Find the 95% confidence interval of the true mean height of ALL men.

```
n = 40; alpha = 0.05; sdEst = 4.5; xbar = 69

ME <- qt(1 - alpha / 2, n - 1) * (sdEst / sqrt(n))
```

```
CI <- c(xbar - ME, xbar + ME)
CI
```

```
## [1] 67.56083 70.43917
```

Cereal Weight Example

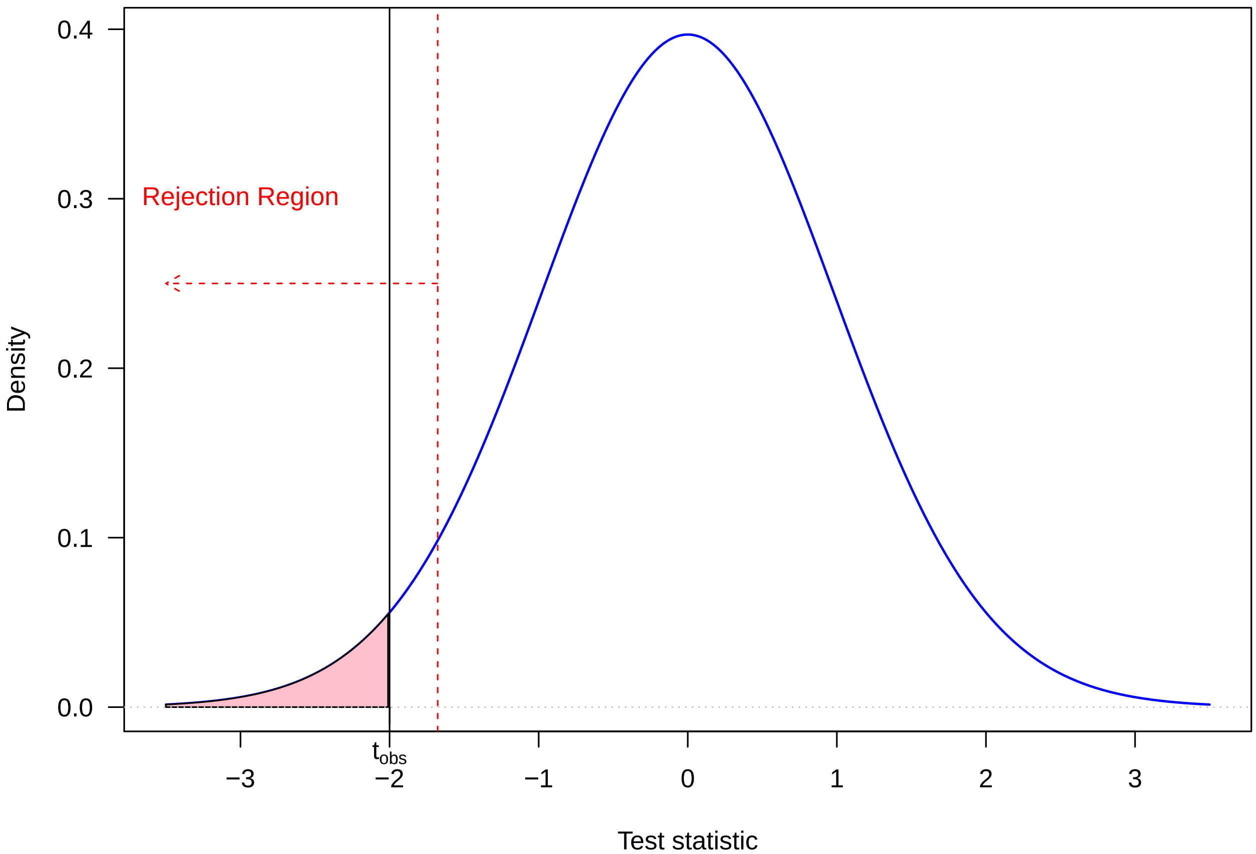
New Age Granola Inc claims that average weight of its cereal boxes is 16 oz. The Genuine Grocery Corporation will send back a shipment if the average weight is any less. Suppose Genuine Grocery Corporation takes a random sample of 49 boxes, weight each one, and compute the sample mean $\bar{X} = 15.9$ oz and sample standard deviation $s = 0.35$ oz. Perform a hypothesis test at 0.05 significant level to determine if they would reject H_0, and therefore, this shipment

1. $H_0 : \mu = 16$ vs. $H_a : \mu < 16$
2. Test Statistic: $t_{obs} = \frac{15.9-16}{0.35/\sqrt{49}} = -2$
3. Rejection Region Method: $-t_{0.05,48} = -1.68 \Rightarrow$ Rejection Region is $(-\infty, -1.68]$. Since t_{obs} is in rejection region, we reject H_0
4. P-Value Method: $\mathbb{P}(t^* \leq -2) = 0.0256 < \alpha = 0.05 \Rightarrow$ reject H_0
5. Draw a Conclusion: We do have enough statistical evidence to conclude that the average weight is less than 16 oz at 0.05 significant level

```
# P-value
pt(-2, 48)
```

```
## [1] 0.02558797
```

```
curve(dt(x, 48), from = -3.5, to = 3.5, n = 1001, lwd = 1.5, col = "blue",
      xlab = "Test statistic",
      ylab = "Density", las = 1)
abline(v = -2)
x_grid <- seq(-3.5, 3.5, 0.01)
y_grid <- dt(x_grid, 48)
polygon(c(x_grid[x_grid < -2], rev(x_grid[x_grid < -2])),
        c(y_grid[x_grid < -2], rep(0, length(y_grid[x_grid < -2]))), col = "pink")
abline(h = 0, lty = 3, col = "gray")
axis(1, at = -2, labels = expression(t["obs"]),
     line = -0.75)
abline(v = -qt(0.95, 48), lty = 2, col = "red")
arrows(-1.68, 0.25, x1 = -3.5, length = 0.1,
       lty = 2, col = "red")
text(-3, 0.3, "Rejection Region", col = "red")
```



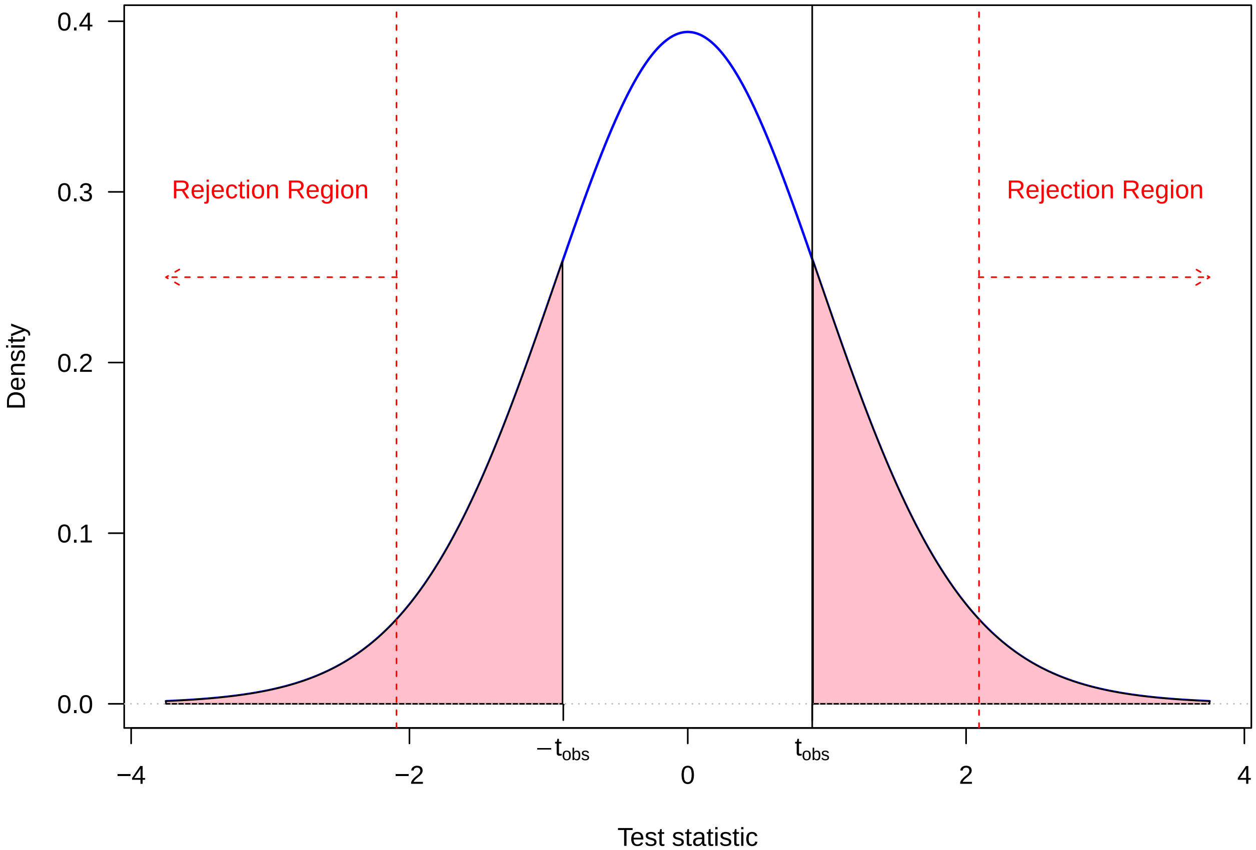
Blood Test Example

A series of blood tests were run on a particular patient over five days. It is of interest to determine if the mean blood protein for this patient differs from 7.25, the value for healthy adults. Suppose the sample mean ($n = 20$) is 7.35 and sample standard deviation is 0.5. Perform a hypothesis test using significance level of 0.05

1. $H_0 : \mu = 7.25$ vs. $H_a : \mu \neq 7.25$
2. $t_{obs} = \frac{7.35-7.25}{0.5/\sqrt{20}} = 0.8944$
3. P-value: $2 \times \mathbb{P}(t^* \geq 0.8944) = 0.3823 > 0.05$
4. We do not have enough statistical evidence to conclude that the mean blood protein is different from 7.25 at 5% significant level

```
curve(dt(x, 19), from = -3.75, to = 3.75, n = 1001, lwd = 1.5, col = "blue",
      xlab = "Test statistic",
      ylab = "Density", las = 1)
x_grid <- seq(-3.75, 3.75, 0.01)
y_grid <- dt(x_grid, 19)
t_star = 0.8944
polygon(c(x_grid[x_grid < -t_star], rev(x_grid[x_grid < -t_star])),
        c(y_grid[x_grid < -t_star], rep(0, length(y_grid[x_grid < -t_star]))), col = "pink")
polygon(c(x_grid[x_grid > t_star], rev(x_grid[x_grid > t_star])),
        c(y_grid[x_grid > t_star], rep(0, length(y_grid[x_grid > t_star]))), col = "pink")
abline(h = 0, lty = 3, col = "gray")
axis(1, at = 0.8944, labels = expression(t["obs"]), line = -0.75)
```

```
axis(1, at = -0.8944, labels = expression(-t["obs"]), line = -0.75)
abline(v = -qt(0.975, 19), lty = 2, col = "red")
abline(v = qt(0.975, 19), lty = 2, col = "red")
abline(v = 0.8944)
arrows(-2.09, 0.25, x1 = -3.75, length = 0.1,
       lty = 2, col = "red")
arrows(2.09, 0.25, x1 = 3.75, length = 0.1,
       lty = 2, col = "red")
text(-3, 0.3, "Rejection Region", col = "red")
text(3, 0.3, "Rejection Region", col = "red")
```



Type I and Type II Errors

```
library(scales)
curve(dnorm(x), from = -3.75, to = 6.75, n = 1001, lwd = 1.5, col = "gray",
      xlab = "",
      ylab = "", las = 1,
      xaxt = "n", yaxt = "n")
abline(v = 1.96, lty = 2, col = "blue")
x_grid <- seq(-3.75, 6.75, 0.01)
y_grid <- dnorm(x_grid)
polygon(c(x_grid[x_grid > 1.96], rev(x_grid[x_grid > 1.96])),
        c(y_grid[x_grid > 1.96], rep(0, length(y_grid[x_grid > 1.96]))), col = alpha("pink", 0.2))
curve(dnorm(x, mean = 3), from = -3.75, to = 6.75, n = 1001, lwd = 1.5, add = T,
      xlab = "",
```

```r
      ylab = "", las = 1)
x_grid <- seq(-3.75, 6.75, 0.01)
y_grid <- dnorm(x_grid, mean = 3)
polygon(c(x_grid[x_grid < 1.96], rev(x_grid[x_grid < 1.96])),
        c(y_grid[x_grid < 1.96], rep(0, length(y_grid[x_grid < 1.96]))), col = alpha("lightblue", 0.2))
abline(v = 0, lty = 2, col = "gray")
abline(v = 3, lty = 2)
axis(1, at = 0, labels = expression(mu[0]))
axis(1, at = 3, labels = expression(mu[a]))
text(2.2, 0.02, expression(alpha), col = "red")
text(1.6, 0.02, expression(beta), col = "blue")
```