Tugas Besar IF2220 - Probabilitas dan Statistika

Part 5: Two Samples Hypothesis

Anggota:
13521116 - Juan Christopher Santoso
13521162 - Antonio Natthan Krishna

All testing use significant of 5%

In [1]:
```
# Import Dataset
df <- read.csv("..\\test\\anggur.csv")

# Data Statistics
properties <- c("Rows", "Columns")
value <- c(nrow(df), ncol(df))
cbind(properties, value)

# List of Columns
columns_index <- c(1:ncol(df))
columns_name <- colnames(df)

# Display List
cbind(columns_index, columns_name)

# Significance
Significance <- 0.05
```

A matrix: 2 × 2 of type chr

properties	value
Rows	1000
Columns	12

A matrix: 12 × 2 of type chr

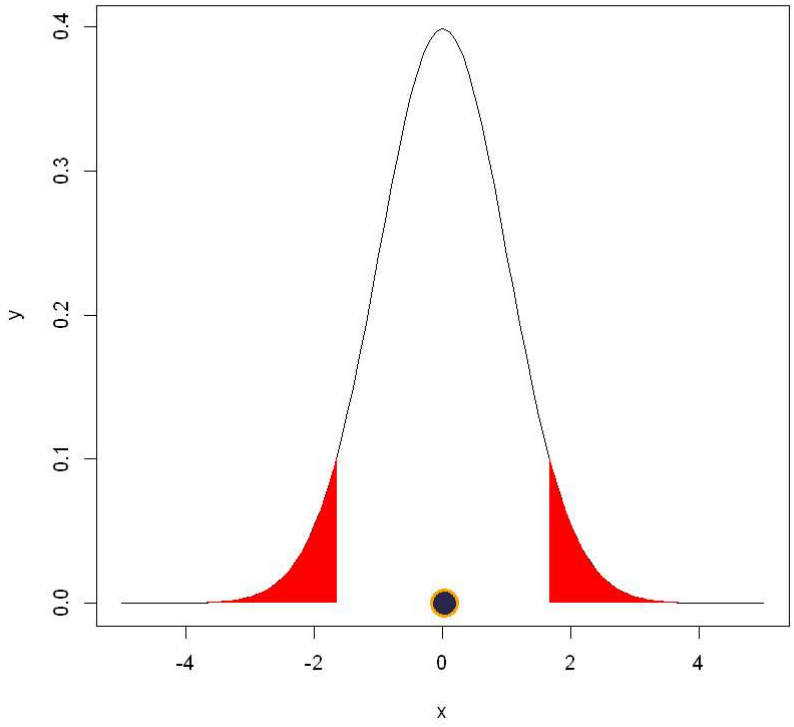
columns_index	columns_name
1	fixed.acidity
2	volatile.acidity
3	citric.acid
4	residual.sugar
5	chlorides
6	free.sulfur.dioxide
7	total.sulfur.dioxide
8	density
9	pH
10	sulphates
11	alcohol
12	quality

1. Data kolom fixed acidity dibagi 2 sama rata: bagian awal dan bagian akhir kolom. Benarkah rata-rata kedua bagian tersebut sama?

In [2]:
```
# Divide columns fixed acidity into 2 parts
numrow <- as.numeric(nrow(df)/2)
first_half <- df[1:numrow,]
second_half <- df[numrow+1:numrow,]

# Mean and Standard Deviation each part
first_half_mean <- mean(first_half,"fixed.acidity"])
second_half_mean <- mean(second_half,"fixed.acidity"])
first_half_sd <- sd(first_half,"fixed.acidity"])
second_half_sd <- sd(second_half,"fixed.acidity"])

T <- (first_half_mean - second_half_mean)/sqrt((first_half_sd^2)/numrow + (second_h
v <- round(((first_half_sd^2)/numrow + (second_half_sd^2)/numrow) ^ 2 / ((((first_h

t0low <- qt(0.05, v)
t0high <- qt(0.05, v, lower.tail = FALSE)

cat("T  :", T, "\n")
cat("v  :", v, "\n")
cat("t0 low :", t0low, "\n")
cat("t0 high :", t0high, "\n")
cat("P-value:", pt(T, v, lower.tail = FALSE))

# Plotting Critical Area
x <- seq(-5, 5, 0.1)
y <- dt(x, nrow(df))
```

```
plot(x, y, type = "l")

x2 <- seq(-5,t0low,0.01)
y2 <- dt(x2, nrow(df)-1)
x2 = c(-5,x2,t0low)
y2 = c(0,y2,0)
polygon(x2,y2, col="red", border=NA)

x3 <- seq(t0high,5,0.01)
y3 <- dt(x3, nrow(df)-1)
x3 = c(x3,5,t0high)
y3 = c(0,y3,0)
polygon(x3,y3, col="red", border=NA)

lines(T, 0, type = "o", pch=21, bg="#28284d", cex=3, lwd=3, col="orange")
```

```
T  : 0.02604107
v  : 998
t0 low : -1.646382
t0 high : 1.646382
P-value: 0.4896149
```



a = mean first half
b = mean second half

H0 = (a == b)
H1 = (a != b)

Use the significance 0.05
Using t distribution with degree 998,

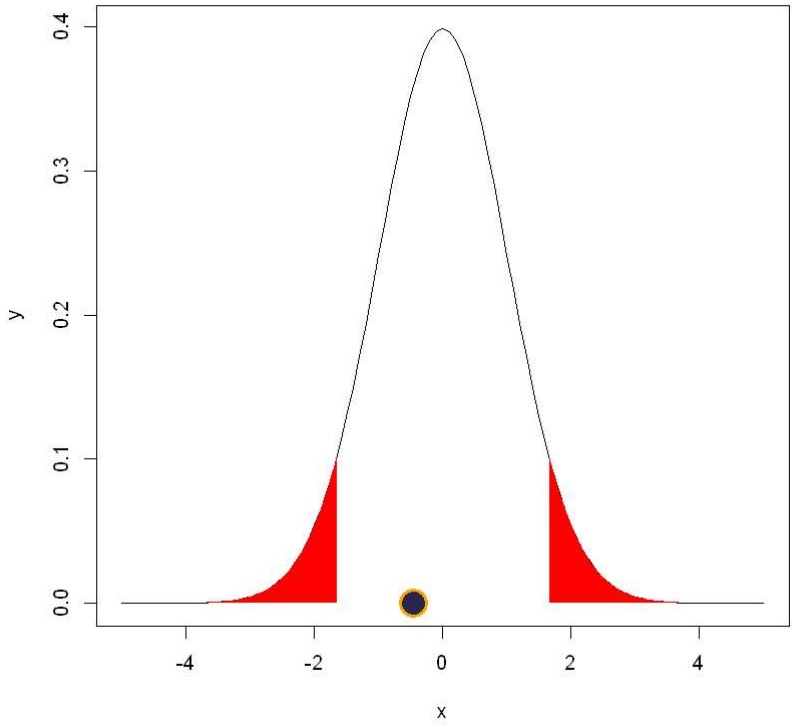
Critical area : t < t(-0.025), t > t(0.025)
Since t(-0.025) < t < t(0.025) (and p value > significance) which means t is NOT located in critical area. Hence, we accept H0.

Conclusion: mean first half is SAME as mean second half

2. Data kolom chlorides dibagi 2 sama rata: bagian awal dan bagian akhir kolom. Benarkah rata-rata bagian awal lebih besar daripada bagian akhir sebesar 0.001?

In [3]:
```
# Divide columns chlorides into 2 parts
numrow <- as.numeric(nrow(df)/2)
first_half <- df[1:numrow,]
second_half <- df[numrow+1:numrow,]

# Mean and Standard Deviation each part
first_half_mean <- mean(first_half[,"chlorides"])
second_half_mean <- mean(second_half[,"chlorides"])
first_half_sd <- sd(first_half[,"chlorides"])
second_half_sd <- sd(second_half[,"chlorides"])

T <- ((first_half_mean - second_half_mean)-0.001) / sqrt((first_half_sd^2)/numrow +
v <- round(((first_half_sd^2)/numrow + (second_half_sd^2)/numrow) ^ 2 / ((((first_h

t0low <- qt(0.05, v)
t0high <- qt(0.05, v, lower.tail = FALSE)

cat("T  :", T, "\n")
cat("v  :", v, "\n")
cat("t0 low :", t0low, "\n")
cat("t0 high :", t0high, "\n")
cat("P-value:", pt(T, v, lower.tail = FALSE))

# Plotting Critical Area
x <- seq(-5, 5, 0.1)
y <- dt(x, nrow(df))
plot(x, y, type = "l")

x2 <- seq(-5,t0low,0.01)
y2 <- dt(x2, nrow(df)-1)
x2 = c(-5,x2,t0low)
y2 = c(0,y2,0)
polygon(x2,y2, col="red", border=NA)

x3 <- seq(t0high,5,0.01)
y3 <- dt(x3, nrow(df)-1)
x3 = c(x3,5,t0high)
y3 = c(0,y3,0)
polygon(x3,y3, col="red", border=NA)

lines(T, 0, type = "o", pch=21, bg="#28284d", cex=3, lwd=3, col="orange")
```

```
T  : -0.4673171
v  : 998
t0 low : -1.646382
t0 high : 1.646382
P-value: 0.6798125
```



a = mean first half
b = mean second half

H0 = (a - b == 0.1)
H1 = (a - b != 0.1)

Use the significance 0.05
Using t distribution with degree 998,
Critical area : t < t(-0.025), t > t(0.025)
Since t(-0.025) < t < t(0.025) (and p value > significance) which means t is NOT located in critical area. Hence, we accept H0.

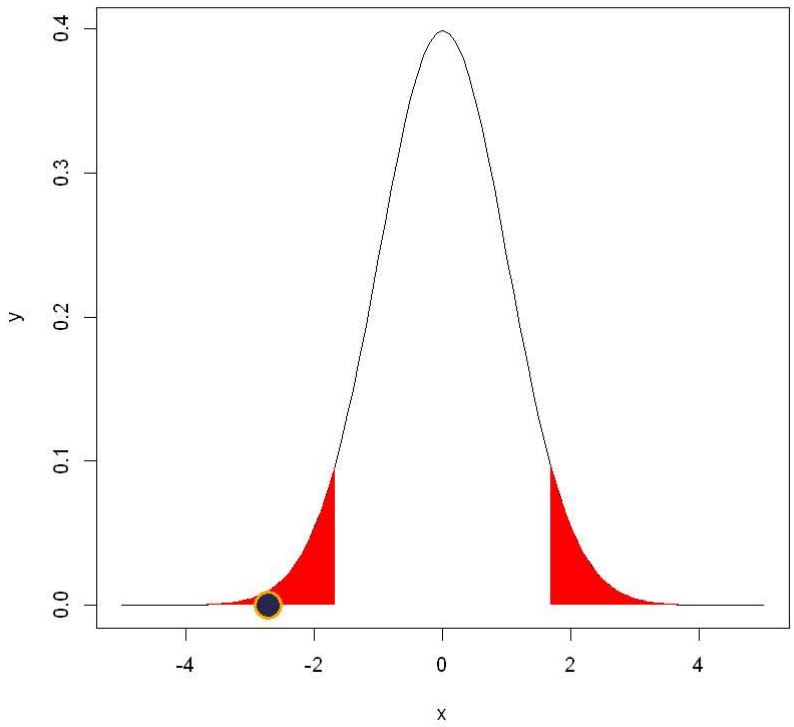
Conclusion: mean first half is GREATER than mean second half BY 0.001

3. Benarkah rata-rata sampel 25 baris pertama kolom Volatile Acidity sama dengan rata-rata 25 baris pertama kolom Sulphates ?

In [4]:
```
# Divide columns chlorides into 2 parts
numrow <- 25
first_25 <- df[1:25,]
```

```r
# Mean and Standard Deviation each part
volatile_acidity_mean <- mean(first_half[,"volatile.acidity"])
sulphates_mean <- mean(second_half[,"sulphates"])
volatile_acidity_sd <- sd(first_half[,"volatile.acidity"])
sulphates_sd <- sd(second_half[,"sulphates"])

T <- ((volatile_acidity_mean - sulphates_mean)-0.001) / sqrt((volatile_acidity_sd^2
v <- round(((volatile_acidity_sd^2)/numrow + (sulphates_sd^2)/numrow) ^ 2 / ((((vol

t0low <- qt(0.05, v)
t0high <- qt(0.05, v, lower.tail = FALSE)

cat("T  :", T, "\n")
cat("v  :", v, "\n")
cat("t0 low :", t0low, "\n")
cat("t0 high :", t0high, "\n")
cat("P-value:", pt(T, v, lower.tail = FALSE))

# Plotting Critical Area
x <- seq(-5, 5, 0.1)
y <- dt(x, nrow(df))
plot(x, y, type = "l")

x2 <- seq(-5,t0low,0.01)
y2 <- dt(x2, nrow(df)-1)
x2 = c(-5,x2,t0low)
y2 = c(0,y2,0)
polygon(x2,y2, col="red", border=NA)

x3 <- seq(t0high,5,0.01)
y3 <- dt(x3, nrow(df)-1)
x3 = c(x3,5,t0high)
y3 = c(0,y3,0)
polygon(x3,y3, col="red", border=NA)

lines(T, 0, type = "o", pch=21, bg="#28284d", cex=3, lwd=3, col="orange")
```

```
T  : -2.721924
v  : 48
t0 low : -1.677224
t0 high : 1.677224
P-value: 0.9954912
```



a = mean first 25 volatile acidity
b = mean first 25 sulphates

H0 = (a == b)
H1 = (a != b)

Use the significance 0.05
Using t distribution with degree 998,
Critical area : t < t(-0.025), t > t(0.025)
Since t < t(-0.025) (and p value < significance/2) which means t is located in critical area.
Hence, we reject H0.

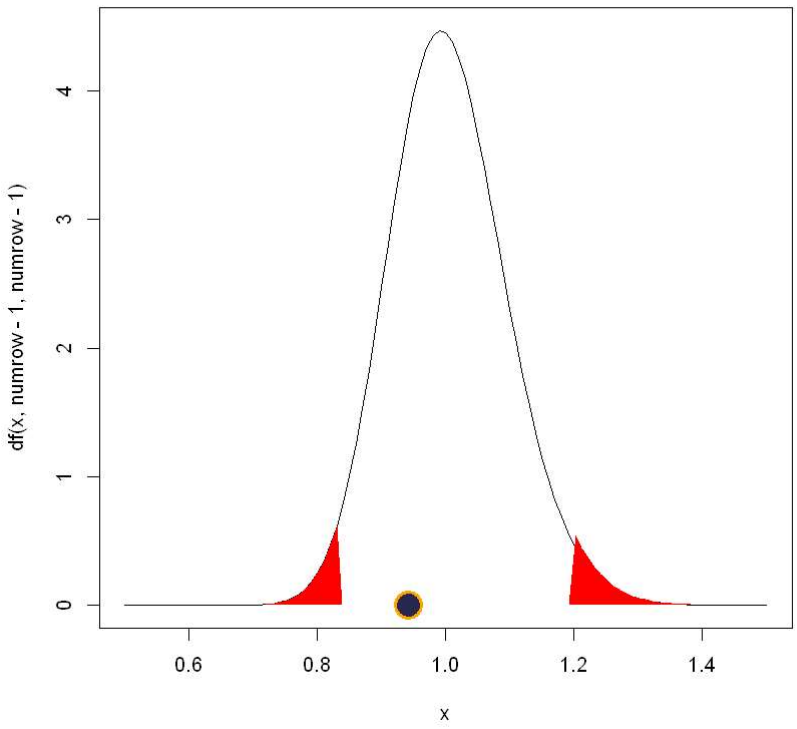
Conclusion: mean first 25 volatile acidity is NOT SAME as mean first 25 sulphates

4. Bagian awal kolom residual sugar memiliki variansi yang sama dengan bagian akhirnya?

In [5]:
```
numrow <- as.numeric(nrow(df)/2)
first_half <- df[1:numrow,]
second_half <- df[numrow+1:numrow,]

f <- sd(first_half[,"residual.sugar"])^2 / sd(second_half[,"residual.sugar"])^2
f0low <- qf(0.025, numrow-1, numrow-1)
f0high <- qf(0.025, numrow-1, numrow-1, lower.tail = FALSE)

cat("T  :", f, "\n")
cat("f0 low :", f0low, "\n")
```

```r
cat("f0 high :", f0high, "\n")
cat("P-value:", pf(f, numrow-1, numrow-1))

# Plotting Critical Area
x <- seq(0.5, 2, 0.01)
y <- df(x, numrow-1, numrow-1)
curve(df(x, numrow-1, numrow-1), 0.5, 1.5)

x2 <- seq(0.5,f0low,0.01)
y2 <- df(x2, numrow-1, numrow-1)
x2 = c(0.5,x2,f0low)
y2 = c(0,y2,0)
polygon(x2,y2, col="red", border=NA)

x3 <- seq(f0high,1.5,0.01)
y3 <- df(x3, numrow-1, numrow-1)
x3 = c(x3,1.5,f0high)
y3 = c(0,y3,0)
polygon(x3,y3, col="red", border=NA)

lines(f, 0, type = "o", pch=21, bg="#28284d", cex=3, lwd=3, col="orange")
```

```
T  : 0.9420041
f0 low : 0.8388858
f0 high : 1.192057
P-value: 0.2524102
```



a = variances first half

b = variances second half

H0 = (a == b)
H1 = (a != b)

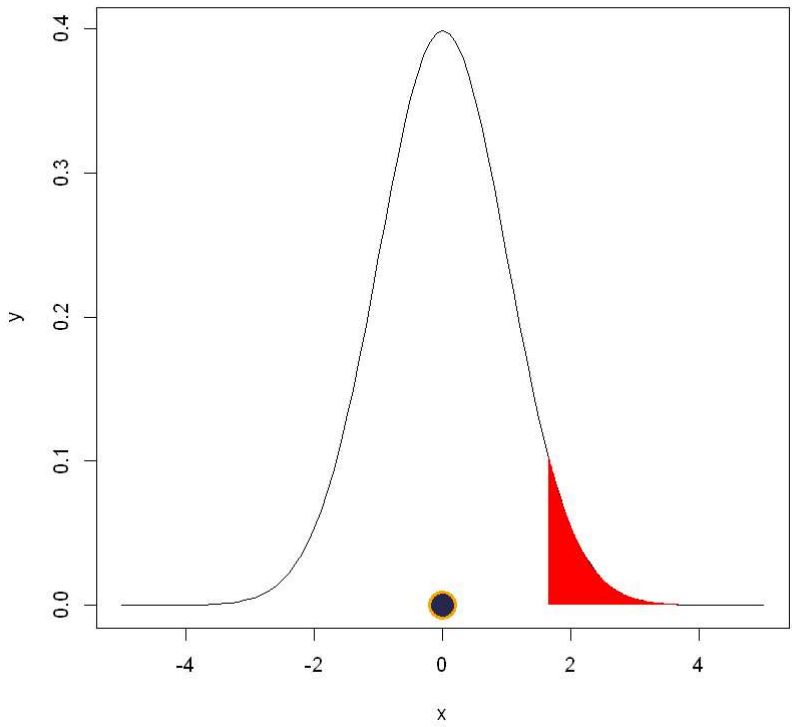
Use the significance 0.05
Using t distribution with degree 499 (first_half) and 499 (second_half)
Critical area : f < f(-0.025), f > f(0.025)
Since f(-0.025) < f < f(-0.025) (and p value > significance/2) which means f is NOT located in critical area. Hence, we accept H0.

Conclusion: variances first half is EQUAL to variances second half

5. Proporsi nilai setengah bagian awal alcohol yang lebih dari 7, adalah lebih besar daripada, proporsi nilai yang sama di setengah bagian akhir alcohol?

In [6]:
```
numrow <- as.numeric(nrow(df)/2)
first_half <- df[1:numrow,]
second_half <- df[numrow+1:numrow,]

proportion_first_half <- nrow(first_half[first_half$"alcohol" > 7,]) / numrow
proportion_second_half <- nrow(second_half[second_half$"alcohol" > 7,]) / numrow

z <- (proportion_first_half - proportion_second_half) / sqrt(proportion_first_half*
z0 <- qnorm(0.05, lower.tail = FALSE)

cat("z  :", z, "\n")
cat("z0 low :", z0, "\n")
cat("P-value:", 1-pnorm(z))

# Plotting Critical Area
x <- seq(-5, 5, 0.1)
y <- dnorm(x)
plot(x, y, type = "l")

x3 <- seq(z0,5,0.01)
y3 <- dnorm(x3)
x3 = c(x3,5,z0)
y3 = c(0,y3,0)
polygon(x3,y3, col="red", border=NA)

lines(z, 0, type = "o", pch=21, bg="#28284d", cex=3, lwd=3, col="orange")
```

```
z  : 0
z0 low : 1.644854
P-value: 0.5
```



a = proportion of first half alchohol which greater than 7
b = proportion of second half alcohol which greater than 7

H0 = (a == b)
H1 = (a > b)

Use the significance 0.05
Critical area : z > z(0.005)
Since z < z(0.005) (and p value > significance) which means z is NOT located in critical area.
Hence, we accept H0.

Conclusion: proportion first half alcohol which greater than 7 is NOT GREATER than proportion second half alcohol which greater than 7