Advanced Statistical Methods HW1

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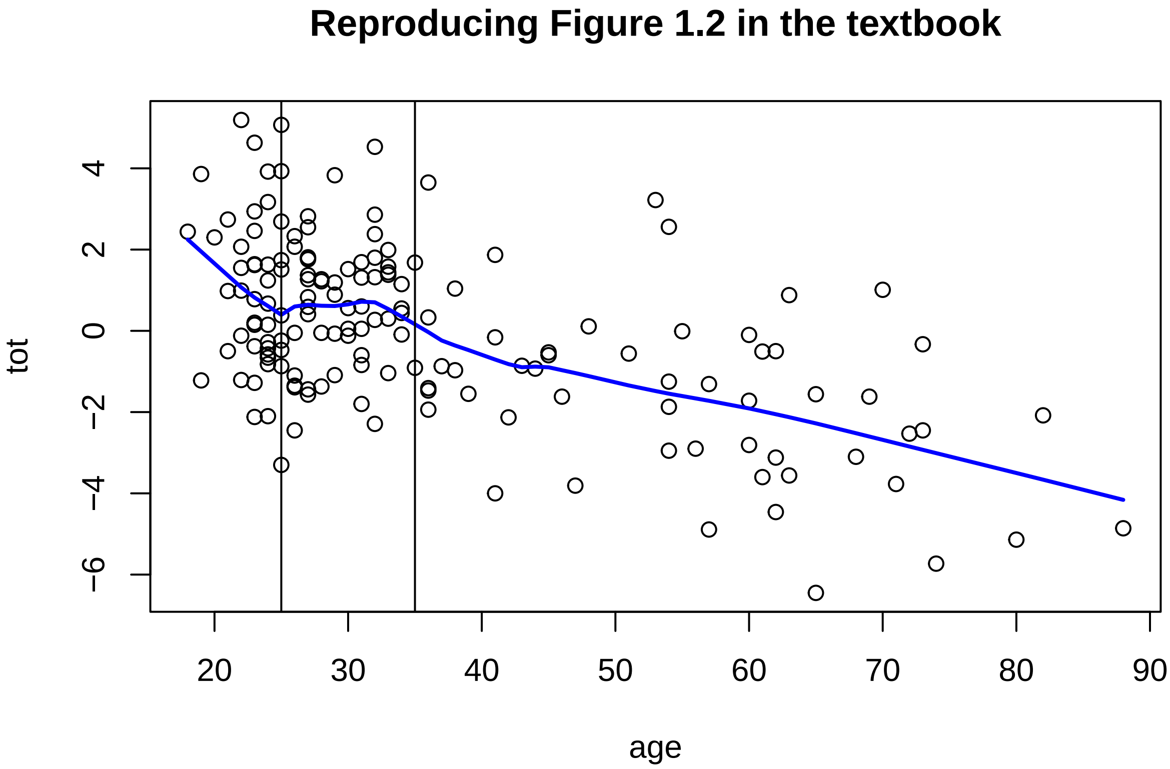
Exercise 1.2

2. The `lowess` curve in Figure 1.2 has a flat spot between ages 25 and 35. Discuss how one might use bootstrap replications like those in Figure 1.3 to suggest whether the flat spot is genuine or just a statistical artifact.

```
kidney <-
read.table('https://web.stanford.edu/~hastie/CASI_files/DATA/kidney.txt', header=T)

fit=lowess(kidney$age, kidney$tot, f=1/3)

plot(kidney, xlab='age', ylab='tot')
lines(fit, lwd=2, col='blue')
abline(v=c(25, 35))
title(main='Reproducing Figure 1.2 in the textbook')
```



Reproducing Figure 1.2 in the textbook

As we see in the plot above, which is almost same as figure 1.2, a flat spot of lowess fit curve between ages 25 and 35 is observed.
To inspect whether this is genuine or just a statistical artifact, we can suggest a method using bootstrap

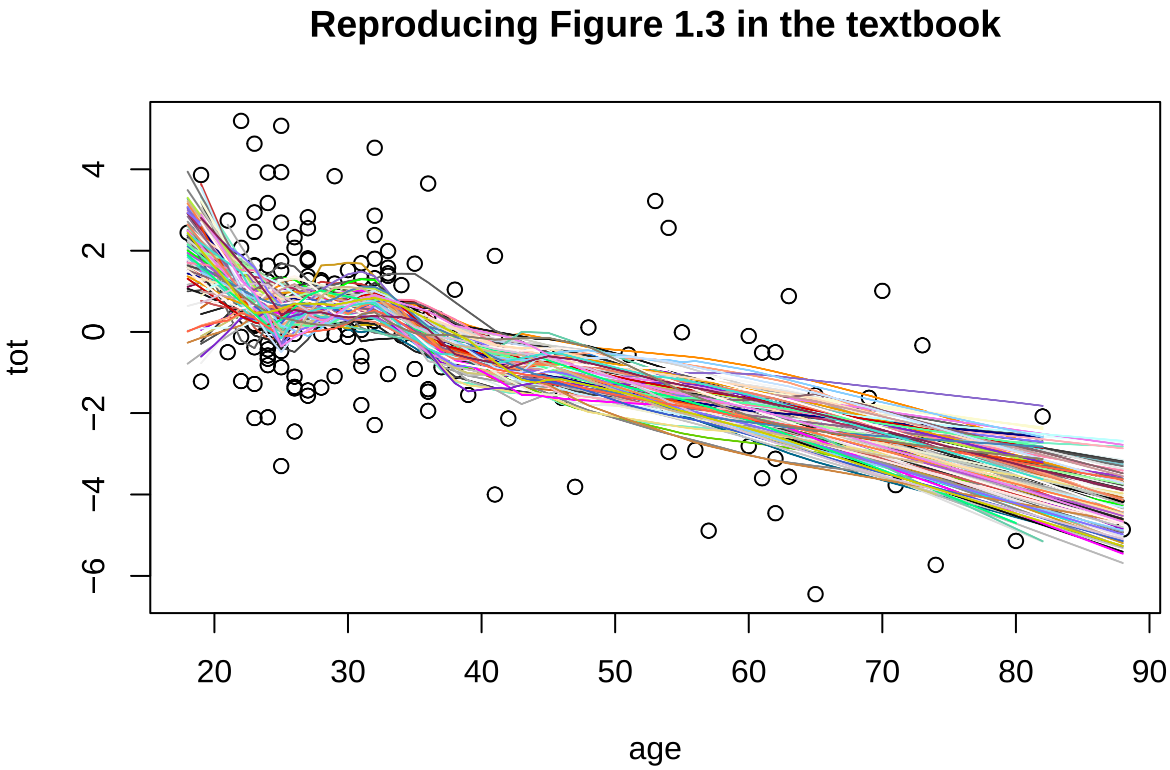
replications.
What we implement in the following code is

1. Produce 1000 bootstrap datasets by resampling 157 pairs of (x_i, y_i) from the original 157 with replacement.
2. To measure "how flat the region is", we suggest

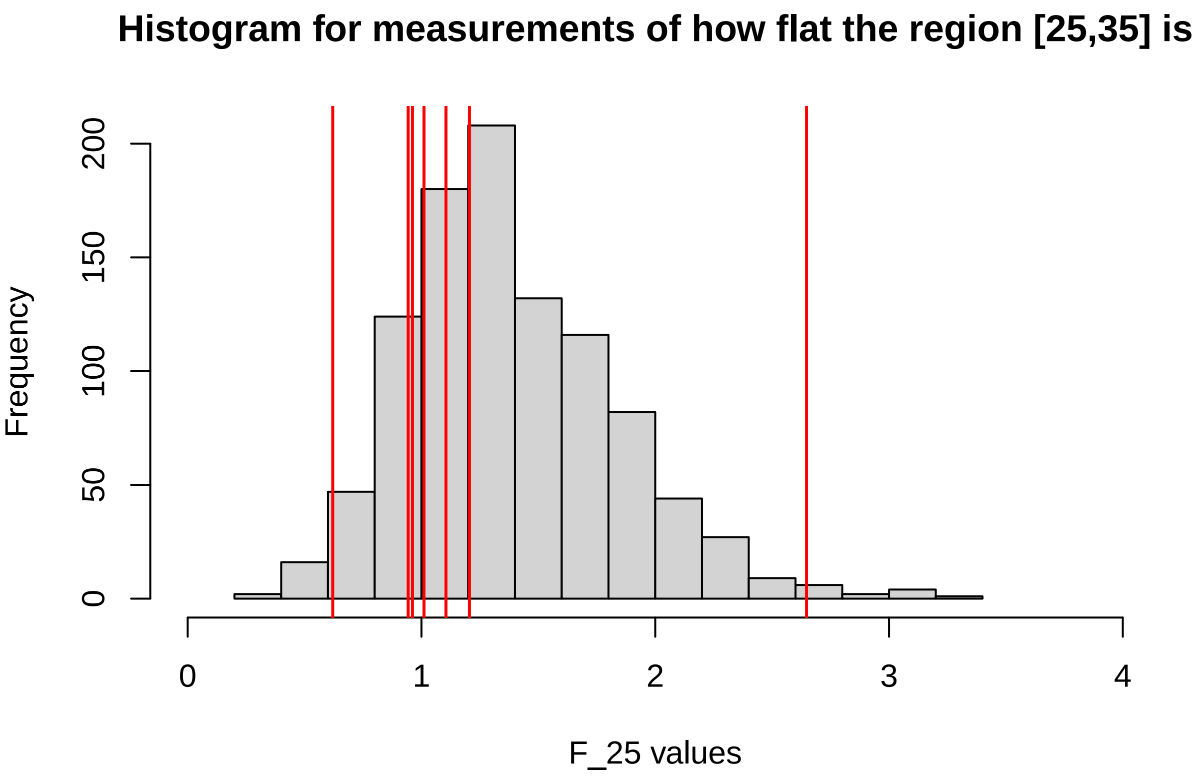
$$F_s = \sum_{i=0}^{9} |y^*_{i+s} - y^*_{i+s+1}|$$

   where s is a starting index and y^*_j is a lowess fit value of y corresponding to $x = j$ in each bootstrap replication. Our main target region is $[25, 35]$, so we will focus on the case of $s = 25$
3. When calculating F_s, if there is no datapoint satisfying $x = j$ in bootstrap replication for some $j \in \{s, s+1, \cdots, s+10\}$, then we calculate average instead of sum and then multiply 10.
4. Aggregate 1000 values of F_s with $s = 25$ from each bootstrap replication.
5. Draw a histogram of those 1000 values and compare it to other F_s values for another region as $[15, 25], [35, 45], [40, 50], [45, 55], [55, 65], [60.70]$ which are calculated from the original dataset.

```r
# Plotting scatter plot and lowess fit from original data
plot(kidney, xlab='age', ylab='tot')
lines(fit, lwd=2)

# "Results" variable will store 1000 values of F_{s=25} values
results=0
set.seed(123)
for(i in 1:1000){
  # bootstrap resampling
  bootindex=sample(1:157, 157, replace=T)
  bootdat=kidney[bootindex,]
  bootfit<-lowess(bootdat$age, bootdat$tot, f=1/3)
  # drawing a lowess fit from bootstrap resampling data
  # reproducing a figure 1.3 in the textbook
  lines(bootfit, col=colors()[5*i])

  # Calculating F_{s=25} value for each bootstrap replication.
  target=NULL
  for(j in seq(25, 35, by=1)){
    if(j %in% bootfit$x) {
    target=append(target, bootfit$y[match(j, bootfit$x)])
    }
  }
  result = mean(abs(diff(target)))*10
  results[i]=result
}
title(main='Reproducing Figure 1.3 in the textbook')
```

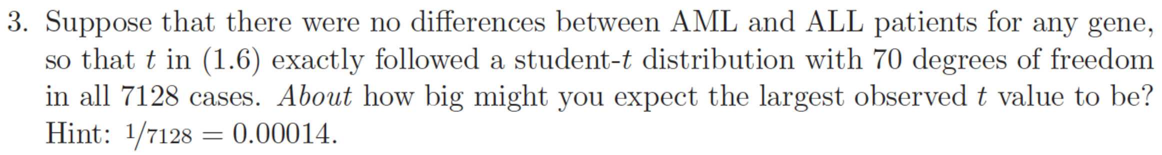


```
#Drawing histograms for 1000 values of F_{s=25}
hist(results, breaks=20, xlim=c(0,4),
     main='Histogram for measurements of how flat the region [25,35] is',
     xlab='F_25 values')

# To compare with other regions, calculate F_s for different s values.
# This calculation is implemented only from the original dataset.
compare = NULL

for(i in c(15, 35, 40, 45, 50, 55, 60)){
  target=NULL
  for(j in i:(i+10)){
    if(j %in% fit$x){
      target=append(target, fit$y[match(j, fit$x)])
      result= mean(abs(diff(target)))*10
    }
  }
  compare=append(compare, result)

}

# Draw vertical lines of those F_s values of other regions over the histogram.
abline(v=compare, col='red', lwd=1.5)
```



From the design of F_s, the small value of F_s implies that the region $[s, s+10]$ is flat. If a flat spot between ages 25 and 35 was genuine then those F values would be much smaller than F values corresponding to other regions. But as we can see from the histogram above, more than half of 1000 bootstrap replications yield F values for the region $[25, 35]$ bigger than F values for the other regions except only one region (which is $[18, 28]$). Observing this result, we can suggest that the flat spot between ages 25 and 35 is not quite genuine.

Exercise 1.3



3. Suppose that there were no differences between AML and ALL patients for any gene, so that t in (1.6) exactly followed a student-t distribution with 70 degrees of freedom in all 7128 cases. *About* how big might you expect the largest observed t value to be? Hint: $1/7128 = 0.00014$.

For the given problem, we have 7128 t_i's, which are identically distributed as t-distribution with 70 degrees of freedom. If we asssume additionally those 7128 genes are independent, then we can expect that $P(T > t_{(N)}) \cong \frac{1}{N+1}$ where $t_{(1)} < t_{(2)} < \cdots < t_{(i)} < \cdots < t_{(N)}$ with $N = 7128$ and $T \sim t(70)$. Indeed, the idea is that all the regions $(-\infty, t_{(1)}), (t_{(1)}, t_{(2)}), \cdots, (t_{(i)}, t_{(i+1)}), \cdots, (t_{(N-1)}, t_{(N)})$ and $(t_{(N)}, \infty)$ should have equal probability i.e. for any interval I among those N+1 number of $(t_{(i)}, t_{(i+1)})$'s, $P(T \in I)$ should be similar to $\frac{1}{N+1}$

```
N=7128
qt(1/(N+1), df=70, lower.tail=F)
```

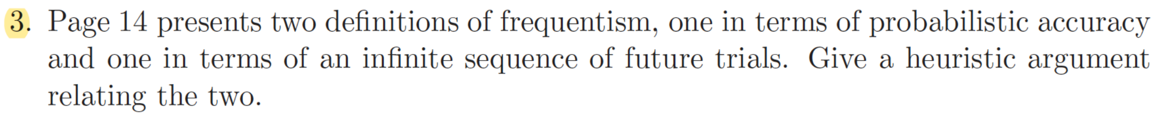
```
## [1] 3.825479
```

```
qnorm(1/(N+1), lower.tail=F)
```

```
## [1] 3.632633
```

Calculating $\frac{1}{N+1}$-quantile of t-distribution with 70 d.f., we expect that the value of $t_{(N)}$, which is the largest observed t value, is similar to 3.825. For a just comparison, if every t_i's were distributed as $N(0, 1)$ rather than t distribution, then we might expect that the value of $t_{(N)}$ is similar to 3.633. This difference is due to heavy tail of t-distribution compared to standard normal.

Exercise 2.3



3. Page 14 presents two definitions of frequentism, one in terms of probabilistic accuracy and one in terms of an infinite sequence of future trials. Give a heuristic argument relating the two.

Two definitions of frequentism suggested in the textbook are

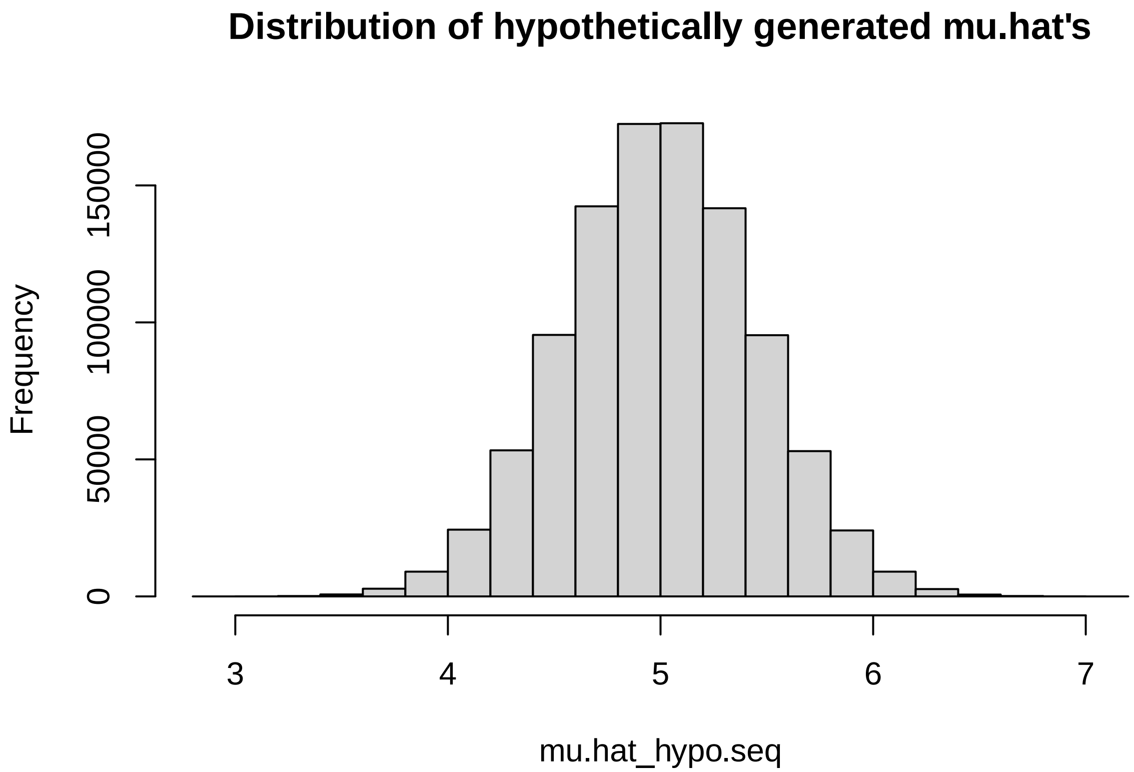
1. The accuracy of an observed estimate $\hat{\theta} = t(x)$ is the probabilistic accuracy of $\hat{\Theta} = t(X)$ as an estimator of θ
2. Imagine hypothetical data sets $X^{(1)}, X^{(2)}, X^{(3)}, \cdots$ generated by the same mechanism as x providing corresponding values $\hat{\Theta}^{(1)}, \hat{\Theta}^{(2)}, \hat{\Theta}^{(3)}, \cdot$s where $\hat{\Theta}^{(k)} = t(X^{(k)})$

What we have is a dataset X and observed value x of X. Our goal is to estimate target parameter θ. We use estimate $\hat{\theta} = t(x)$ to fulfill our goal. The problem is that we want to know the accuracy of our estimate value $\hat{\theta}$. Note that $X = x$ is observed this time, but in another experiment, observed value of X might be different according to probabilistic property of X. This logic applies same to $\hat{\Theta} = t(X)$ and $\theta = t(x)$. $\theta = t(x)$ is observed in this time, but $\hat{\Theta} = t(X)$ can be observed as different values according to its probabilistic property in another experiment.
In the view of frequentism, we can measure the accuracy of $\hat{\theta} = t(x)$ which is from our given data, by calculating probabilistic accuracy of $\hat{\Theta} = t(X)$ which is not from our given data. Typically, the probabilistic accuracy of $\hat{\Theta} = t(X)$ is measured by a standard error.

$$SE(\hat{\Theta}) = \sqrt{Var(\hat{\Theta})}$$

Probabilistic properties like standard error can be understood as the statistics (in this case, a standard deviation) of infinitely many $\hat{\Theta}$ values yielded from hypothetical inifinite sequence of future experiments.
As an example, consider a situation where we observe an $i.i.d$ sample X of size 20 which is distributed as $N(5, 4)$. Our target parameter is normal mean $\mu = 5$ which is assumed to be unknown as well as normal variance $\sigma^2 = 4$. What we can observe is one set of given sample $X = x$ and the observed estimate sample mean $\hat{\mu} = \overline{X}$. But for calculating accuracy of this observed estimate, we use hypothetical infinite sequence of datasets which are generated same way as X and corresponding estimate $\hat{\mu}$. Standard error of our $\hat{\mu}$ is measured by standard deviation of inifinitely many $\hat{\mu}$'s generated from inifinite sequence of hypothetical experiments.

```r
set.seed(100)

n=20
x=rnorm(n, mean=5, sd=2)  # Observed sample.
mu.hat=mean(x)  # Our estimate for target parameter mu.

# This vector will store infinitely many hypothetical mu.hat's
mu.hat_hypo.seq=0

# Since we cannot use the Infinite number, replace it by one million.
N=1000000
for(i in 1:N){
  x_hypo=rnorm(n, mean=5, sd=2)
  mu.hat_hypo=mean(x_hypo)
  mu.hat_hypo.seq[i]=mu.hat_hypo
}

hist(mu.hat_hypo.seq, main='Distribution of hypothetically generated mu.hat\'s')
```



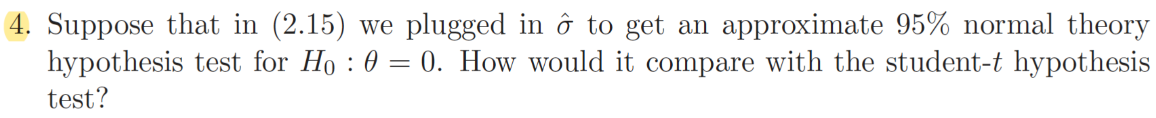
```
# If N is truly infinite, then this is understood as standard error of mu.hat
sd(mu.hat_hypo.seq)
```

```
## [1] 0.4472634
```

```
# Since we know true standard error of mu.hat, compare it with above
(true.se=2/sqrt(n))
```

```
## [1] 0.4472136
```

Exercise 2.4



4. Suppose that in (2.15) we plugged in $\hat{\sigma}$ to get an approximate 95% normal theory hypothesis test for $H_0 : \theta = 0$. How would it compare with the student-t hypothesis test?

What we get in (2.15) is that under H_0,

$$\hat{\theta} \sim N\Big(0, \sigma^2(\frac{1}{n_1} + \frac{1}{n_2})\Big)$$

The unbiased estimate of σ^2 is pooled sample variance $\hat{\sigma}^2$
Hence, under H_0,

$$t = \frac{\overline{x}_2 - \overline{x}_1}{\widehat{sd}} \sim t(n_1 + n_2 - 2) \quad where \quad \widehat{sd} = \hat{\sigma}\Big(\frac{1}{n_1} + \frac{1}{n_2}\Big)$$

Note that this is the exact distribution, not the approximate one. On the other hand, if we plug in $\sigma^2 = \hat{\sigma}^2$ in (2.15) then we get approximate distribution of $\hat{\theta}$, which is

$$\hat{\theta} \approx N\Big(0, \hat{\sigma}^2(\frac{1}{n_1} + \frac{1}{n_2})\Big)$$

By scaling, what we get is under H_0,

$$t = \frac{\overline{x}_2 - \overline{x}_1}{\widehat{sd}} \approx N(0,1)$$

Note that this is not the exact distribution but the approximate one. Since those two tests (t-test and normal z-test using approximate distribution) have same test statistic t, the only difference is the distribution ; $t(n_1 + n_2 - 2)$ vs $N(0,1)$. It is known that t-distribution has heavier tail than standard normal, so for the same observed data, t-test would yield larger p.value than z-test. This means that z-test using approximate distribution could reject the null hypothesis while t-test does not reject. Since t-test use the exact distribution while z-test uses approximate one, we can say t-test is more "correct" than z-test. Hence, in the situation I've just mentioned above, using z-test can cause claiming the significant difference between two groups where in fact, difference between two groups is not statistically significant.

```r
library(dplyr)
gr1 = sleep %>% filter(group==1) ;gr1 <- gr1[,1]    # First group observed
gr2 = sleep %>% filter(group==2) ; gr2<- gr2[,1]    # Second group observed
n1=length(gr1) ; n2=length(gr2)

xbar1<-mean(gr1)
xbar2<-mean(gr2)
# our estimate for theta
theta.hat<-xbar2-xbar1
# square root of pooled sample variance is estimate of sigma
sigma.hat<-sqrt(((n1-1)*var(gr1)+(n2-1)*var(gr2))/(n1+n2-2))
# our test statistic
tstat=theta.hat/(sigma.hat*sqrt(1/n1+1/n2))
```

```r
(pvalue_ttest<-2*pt(tstat, df=n1+n2-2, lower.tail=F))
```

```
## [1] 0.07918671
```

```r
(pvalue_ztest<-2*pnorm(tstat, lower.tail=F))
```

```
## [1] 0.06277052
```

From the simple example above, we can see that pvalue produced from z-test is smaller than t-test. Hence z-test using approximate normal distribution may bring about rejection of null hypothesis even when there is no significant difference between two groups.