```
>
> #1
score = c(90.95.89.71.73.96.87.95.107.89.96.80.97.95.102.97.93.101.82.83.74.91.83.98.95.11
1,99, 120,93,84)
> #a sample mean
> mean(score)
[1] 92.2
> #b
> No, because it is a sample data. so we don't know it is equal to parameter.
에러: 예기치 않은 ','입니다 in "No,"
> #c
> se=sd(score)/sqrt(30)
[1] 1.976529
> #d
> it is a difference with population mean
에러: 예기치 않은 심볼입니다 in "it is"
> #e
> 92.2-qt(0.975,29)*se
[1] 88.15754
> 92.2+qt(0.975,29)*se
[1] 96.24246
> t.test(score)
        One Sample t-test
data: score
t = 46.6474, df = 29, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 88.15754 96.24246
sample estimates:
mean of x
    92.2
> #f
> population mean belongs to 88.15754 and 96.24246 section by 95% C.I
에러: 예기치 않은 심볼입니다 in "population mean"
>
```

```
> #2.
> male=c(220.1,218.6,229.6,228.8,222.0,224.1,226.5)
> female=c(223.4,221.5,230.2,224.3,223.8,230.8)
> #HO: male cholesterol mean= female cholesterol mean
> #H1: not a H0
> #look at the data first
> par(mfrow=c(1,2))
> hist(male)
> hist(female)
> t.test(male,female, alternative="two.sided", var.equal=TRUE)
       Two Sample t-test
data: male and female
t = -0.6268, df = 11, p-value = 0.5436
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-6.423378 3.575759
sample estimates:
mean of x mean of y
224.2429 225.6667
> #t=-0.6268, df=11, p-value is 0.5436, so we can not reject H0, So male and
female cholesterol mean is not the same at the significant level 0.05
> #95 percent confidence interval:
> #-6.423378 3.575759
> #3
> #a False, it has a effect, but we do not know it is small or big.
> #b True
> #c False, type 1 error is fixed at 0.05
> #d False, bete is the type 2 error
> #e True
```

```
> #4
> #H0: 1.5 times the personA's median=personB's median
> #H1: not a H0
> personA =c(248,236,269,254,249,251,260,245,239,255)
> personAA=1.5*personA
> personB = c(380,391,377,392,398,374)
> wilcox.test(personAA, personB , alternative="two.sided")
       Wilcoxon rank sum test
data: personAA and personB
W = 16, p-value = 0.1471
alternative hypothesis: true location shift is not equal to 0
> #W=16, p-value is 0.1471, so we can not reject H0, so personB are not 1.5
times the volume of person A
> #5
> #standard error of mean is when we do not know the population parameter, we
estimate standard error and use this instead of standard deviation.
> #In contrast, we know the population parameter, we can calculate standard
deviation.
> #If, population data is
> p=c(1,2,3,4,5,6,7,8,9,10)
> #and random sample is
> r=c(2.4,7,8,10)
> #then, standard deviation is
> sd(p)
[1] 3.02765
> #=3.02765
> #and, standard error is
> sd(r)/sqrt(5)
[1] 1.439213
> #=1.439213
```