

```

#1
score=c(90,95,89,71,73,96,87,95,107,89,96,80,97,95,102,97,93,101,82,
83,74,91,83,98,95,111,99, 120,93,84)
#a sample mean
mean(score)
#b
No, because it is a sample data. so we don't know it is equal to
parameter.
#c
se=sd(score)/sqrt(30)
se
#d
it is a difference with population mean. 95% of the random samples
the interval include the population mean
#e
92.2-qt(0.975,29)*se
92.2+qt(0.975,29)*se
t.test(score)
#f
population mean belongs to 91.49271 and 92.90729 section by 95% C.I

```

```

#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)
#H0: male cholesterol mean= female cholesterol mean
#H1: not a H0
t.test(male,female, alternative="two.sided", var.equal=TRUE)
#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

```

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#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
#e True

```

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#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")
#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)
#=3.02765
#and, standard error is
sd(r)/sqrt(5)
#=1.439213
```