

t.test

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```
HW6 <- read.csv(file.choose(),header=T)
attach(HW6)
View(HW6)
```

Normality test :

```
library(moments)
skewness(heamoglobin)
```

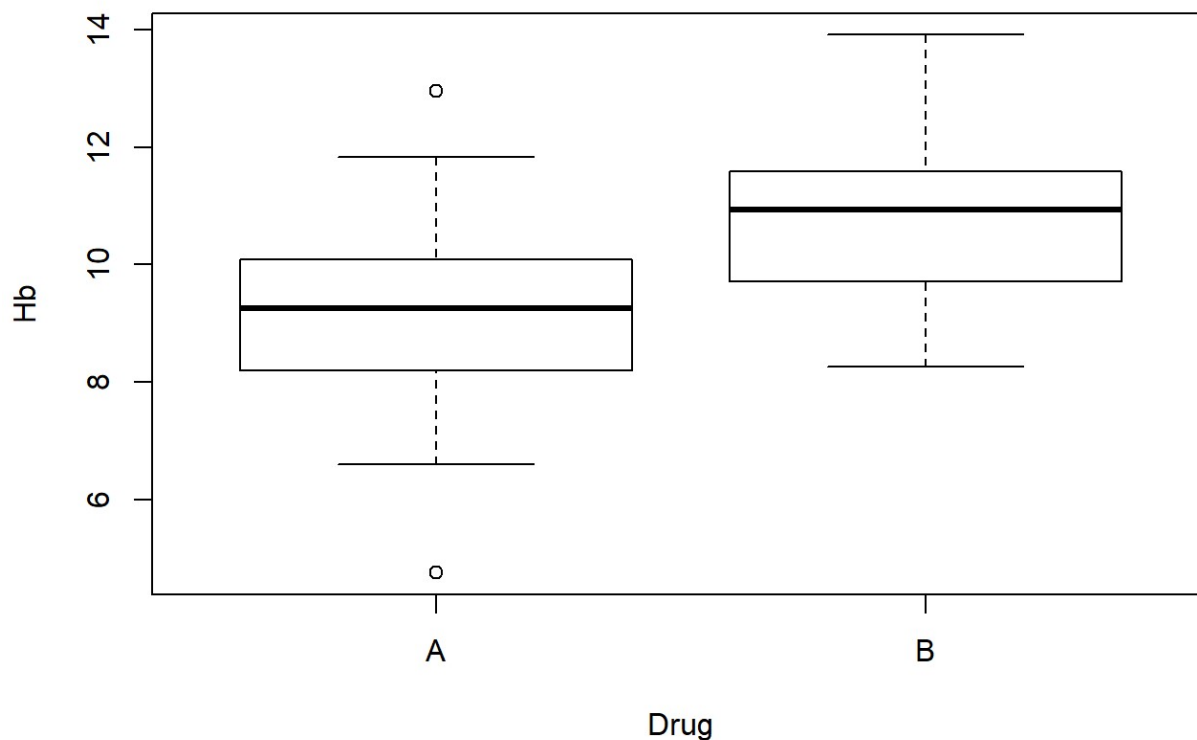
```
## [1] -0.07040083
```

```
#accepted range from -1 to +1
kurtosis(heamoglobin)
```

```
## [1] 3.091323
```

```
#accepted range from -2 to +2 may to +3
boxplot(heamoglobin ~ Drug , xlab = "Drug" , ylab = "Hb" , main = "Comparison of Drugs
& Hb")
```

Comparison of Drugs & Hb



```
#visually , data is normally distributed  
shapiro.test(heamoglobin)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  heamoglobin  
## W = 0.99259, p-value = 0.8621
```

```
## P-value > 0.05 , So data is normally distributed
```

calculate (mean , variance) :

```
DrugA_mean <- mean(heamoglobin[Drug=="A"])  
DrugB_mean <- mean(heamoglobin[Drug=="B"])  
DrugA_mean
```

```
## [1] 9.11248
```

```
DrugB_mean
```

```
## [1] 10.7686
```

```
DrugA_var <- var(heamoglobin[Drug=="A"])  
DrugB_var <- var(heamoglobin[Drug=="B"])  
DrugA_var
```

```
## [1] 2.104748
```

```
DrugB_var
```

```
## [1] 2.009903
```

```
### When we compare Variance of drug A , B >>> so we assume that var.eq = True
```

the sample contain 2 Drugs so we used independent sample t-test :

```
t.test(heamoglobin ~ Drug , mu = 0 , alternative = "two.sided" , conf.level = 0.95 , v  
ar.eq = T , paired = F)
```

```
##  
## Two Sample t-test  
##  
## data: heamoglobin by Drug  
## t = -5.7731, df = 98, p-value = 9.151e-08  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -2.225397 -1.086838  
## sample estimates:  
## mean in group A mean in group B  
## 9.11248 10.76860
```

```
#p-value < 0.05, So there is significant difference >>> reject Null Hypothesis
```