# Blatt0

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## Aufgabe 2

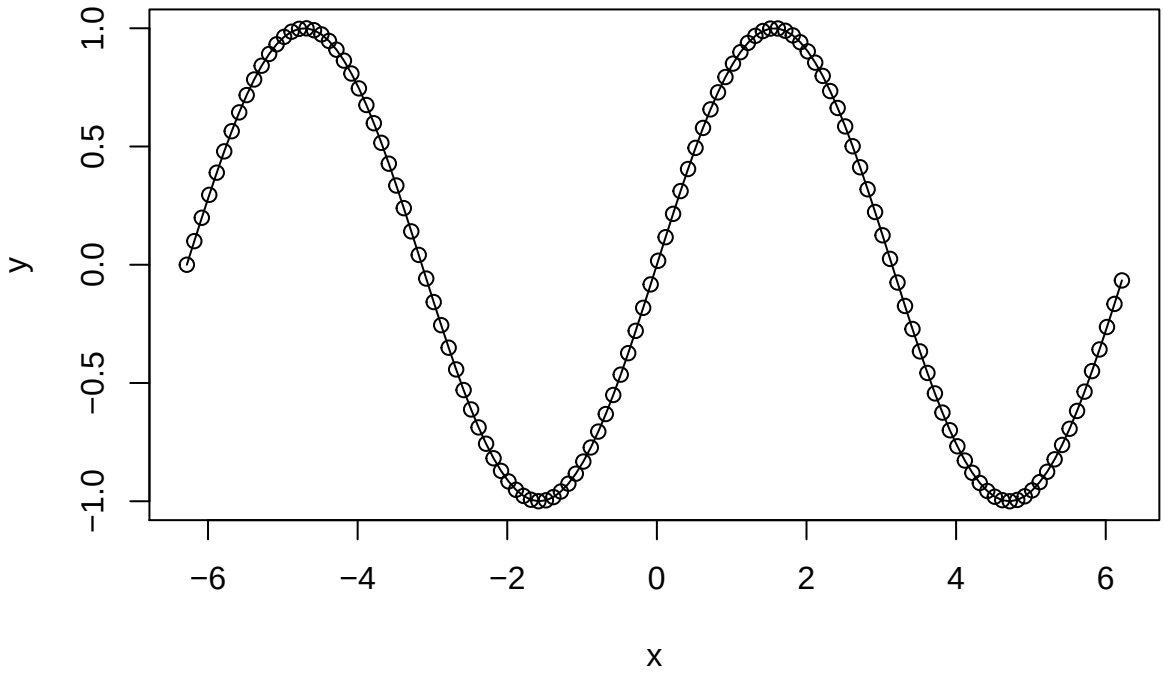
```
A <- matrix(c(1,2,3, 4,5,6, 7,8,9), nrow = 3 , ncol = 3)
B <- matrix(c(9,8,7, 6,5,4, 3,2,1), nrow = 3 , ncol = 3)

C = A%*%B
C
```

**a)**

```
##      [,1] [,2] [,3]
## [1,]   90   54   18
## [2,]  114   69   24
## [3,]  138   84   30
```

Es handelt sich nicht um eine elementweise Multiplikation sondern um eine normale Matritzenmultiplikation #### b)

```
x = seq(-2*pi,2*pi,0.1)
y = sin(x)
plot(x,y)
lines(x,y)
```




### Aufgabe 4

```
data = read.csv("epilepsy.csv",header = TRUE)
names(data)
```

```
## [1] "X"            "treatment"    "base"         "age"          "seizure.rate"
## [6] "period"       "subject"
```

```
nrow(data)
```

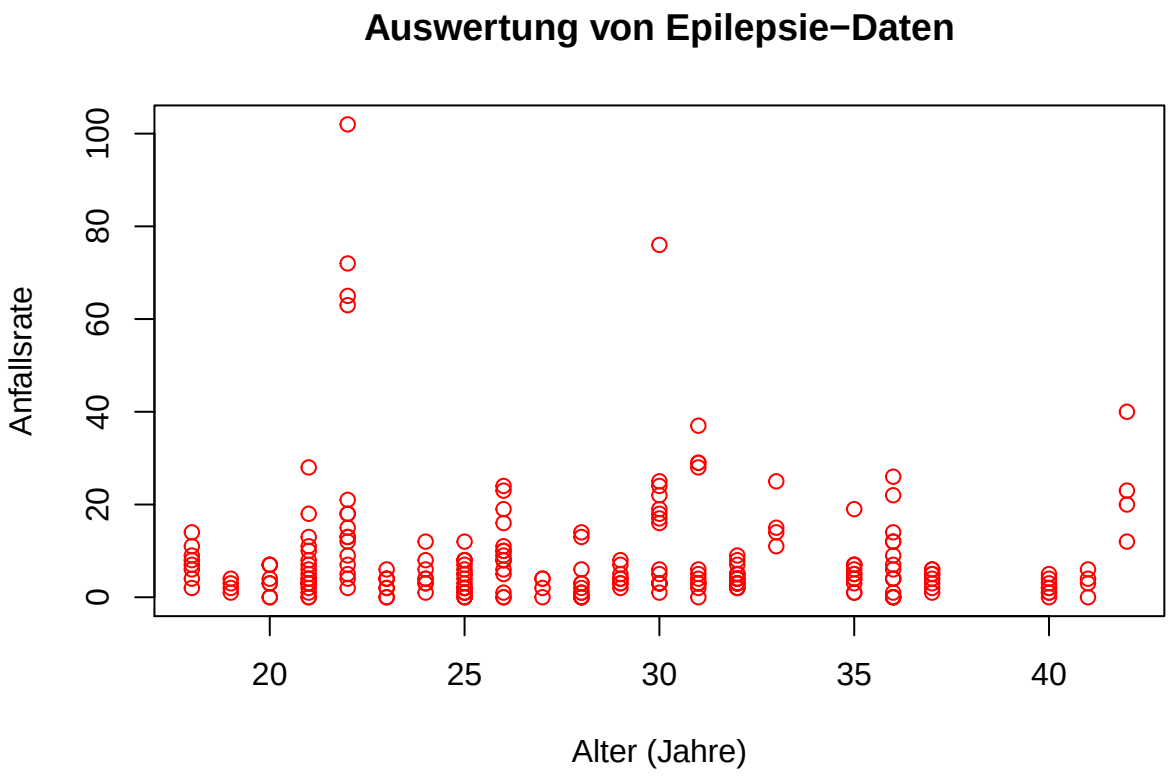
```
## [1] 236
```

```
ncol(data)
```

```
## [1] 7
```

```
#data
```

```
plot(data$age, data$seizure.rate, col = "red", main = "Auswertung von Epilepsie-Daten",
     xlab= "Alter (Jahre)", ylab = "Anfallsrate")
```

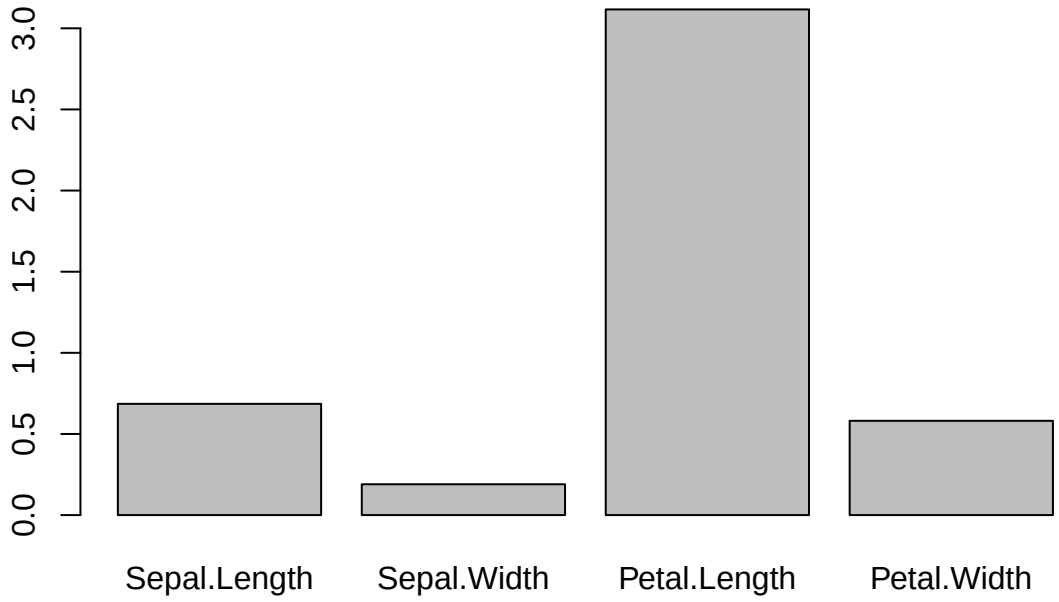



### Aufgabe 5

```
Iris = datasets::iris

names(Iris)
```

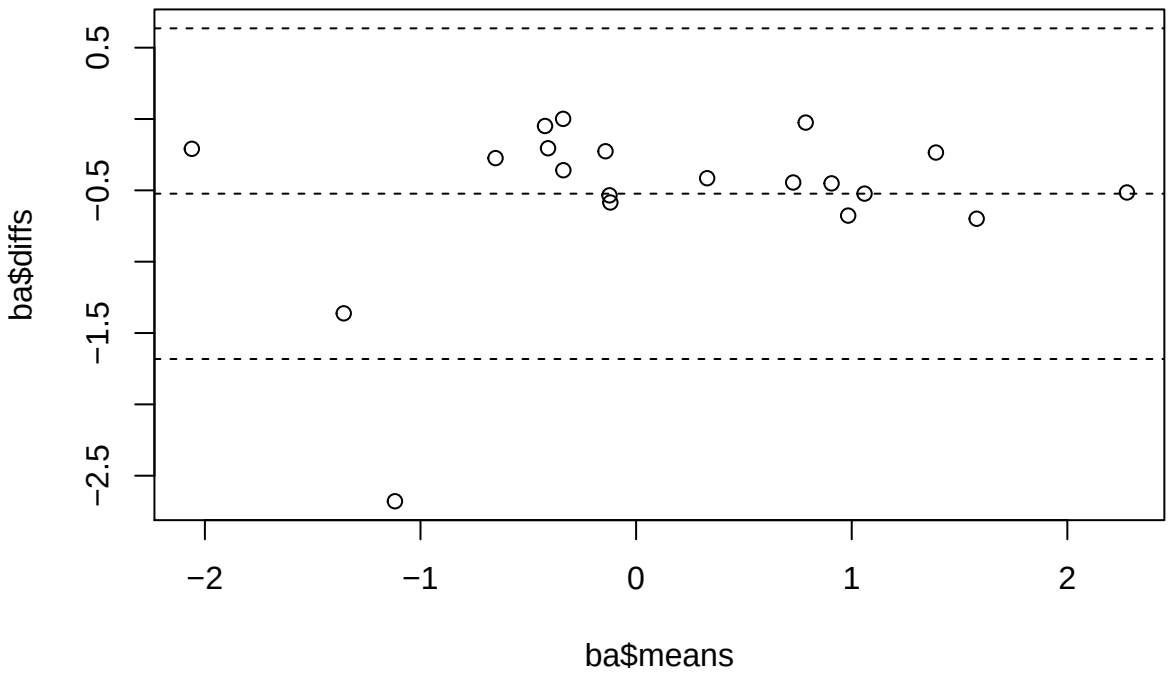
```
## [1] "Sepal.Length" "Sepal.Width"  "Petal.Length" "Petal.Width"  "Species"
```

```
#varLengthSALT = 1/(150-1)*sum((Iris$Sepal.Length-mean(Iris$Sepal.Length))^2)

varLengthS = var(Iris$Sepal.Length)
varWidthS = var(Iris$Sepal.Width)
varLengthP = var(Iris$Petal.Length)
varWidthP = var(Iris$Petal.Width)

barplot(c(varLengthS,varWidthS,varLengthP,varWidthP),names = names(Iris[,-5]))
```




### Aufgabe 6

```
library(BlandAltmanLeh)
a = c(-2.458, 0.798, 1.23, -0.338, -0.789, -0.255, 0.645, 0.506,
0.774, -0.511, -0.517, -0.391, 0.681, -2.037, 2.019, -0.447,
0.122, -0.412, 1.273, -2.165)
b = c(0.221, 1.321, 1.929, -0.339, -0.515, -0.029, 1.322, 0.951,
0.799, -0.306, -0.158, 0.144, 1.132, -0.675, 2.534, -0.398,
0.537, 0.173, 1.508, -1.956)
bland.altman.plot(a,b)
```



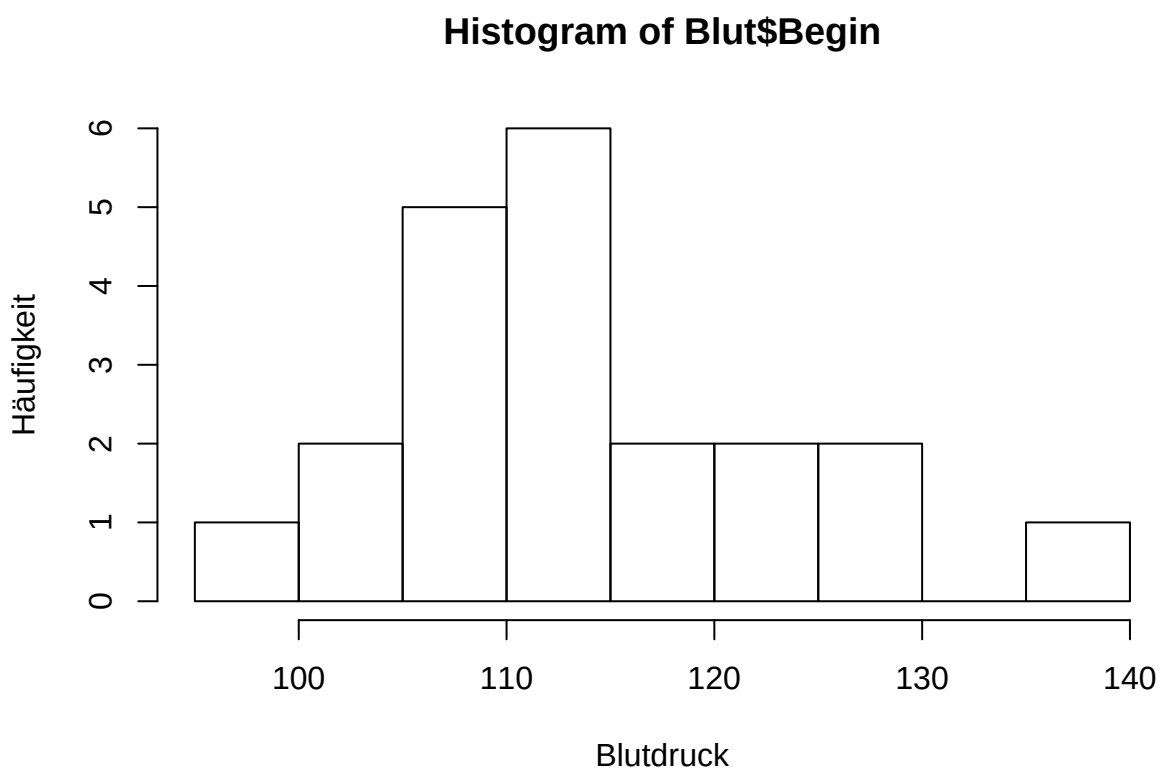

```
## NULL
```

### Aufgabe 7

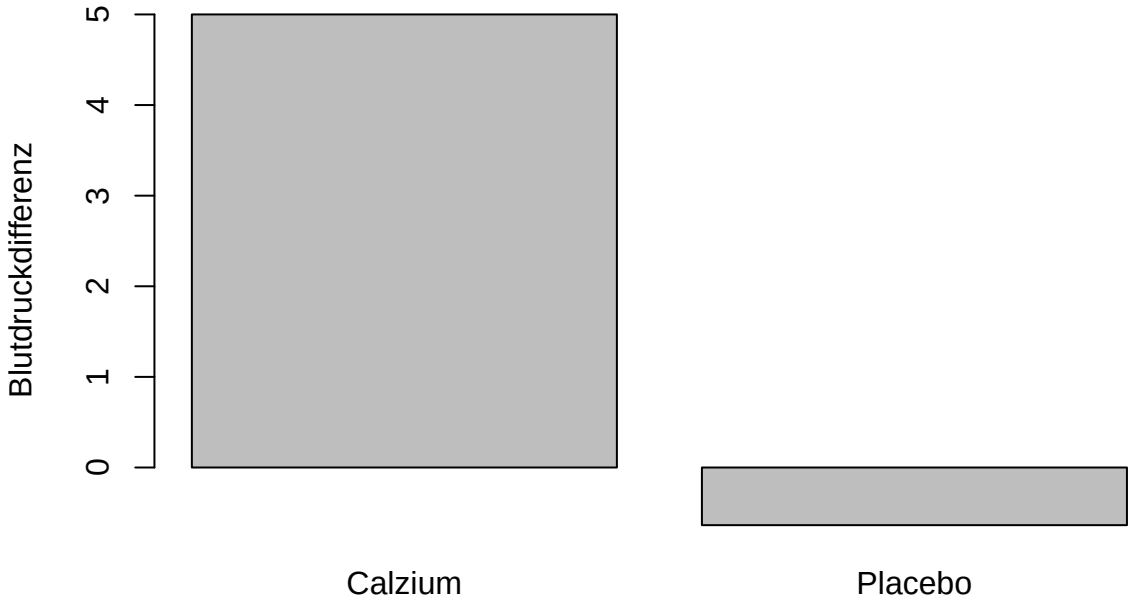
```
Blut = read.csv(file ="blutdruck.csv", sep = "")
names(Blut)
```

```
## [1] "Treatment" "Begin"     "End"       "Decrease"
```

```
hist(Blut$Begin,xlab = "Blutdruck", ylab = "Häufigkeit")
```




```
barplot(c(mean(Blut$Decrease[Blut$Treatment %in% "Calcium"]),
          mean(Blut$Decrease[Blut$Treatment %in% "Placebo"])),
        names = c("Calzium","Placebo"), ylab = "Blutdruckdifferenz")
```


Blutdruckdifferenz
0
1
2
3
4
5
Calzium
Placebo