

Lab6

Vergil

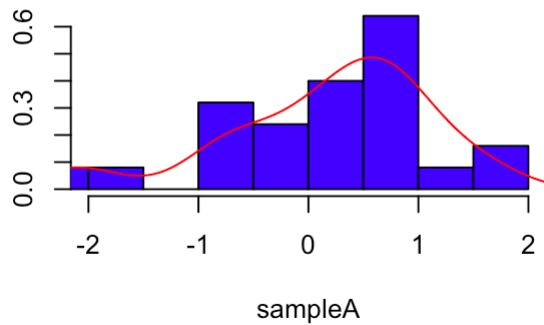
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Part 1

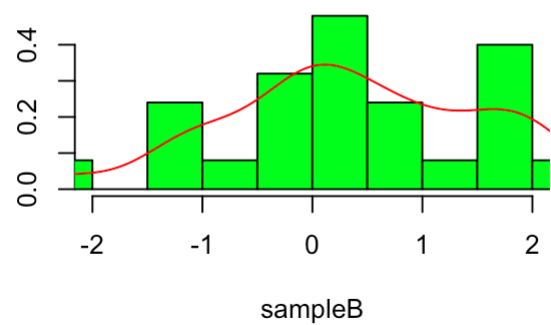
A.

```
library(MASS)
set.seed(1)
sampleA <- rnorm(25,mean=0,sd=1)
set.seed(2)
sampleB <- rnorm(25,mean=0,sd=1)
set.seed(3)
sampleC <- rnorm(25,mean=0,sd=1)
set.seed(4)
sampleD <- rnorm(25,mean=0,sd=1)
par(mfrow=c(2,2))
truehist(sampleA,col = "blue",main = "Histogram of sampleA",nbins=9,xlim = c(-2,2))
lines(density(sampleA),col="red")
truehist(sampleB,col = "green",main = "Histogram of sampleB",nbins=8,xlim = c(-2,2))
lines(density(sampleB),col="red")
truehist(sampleC,col = "yellow",main = "Histogram of sampleC",nbins=10,xlim = c(-2,2))
lines(density(sampleC),col="red")
truehist(sampleD,col = "orange",main = "Histogram of sampleD",ymax=0.5,nbins=8,xlim = c(-2,2))
lines(density(sampleD),col="red")
```

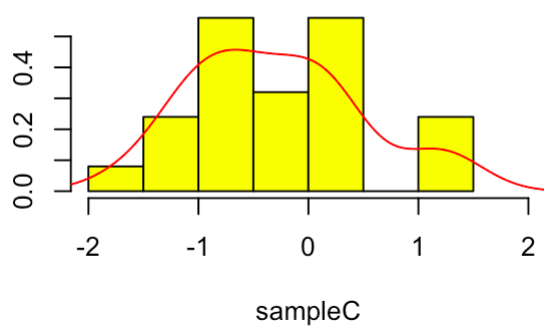
Histogram of sampleA



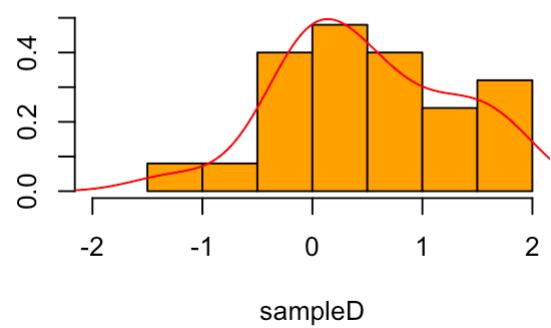
Histogram of sampleB



Histogram of sampleC



Histogram of sampleD



B.

```
set.seed(123)
sampleE <- rnorm(100000,mean=150,sd=6)
min(sampleE)
```

```
## [1] 125.2075
```

```
median(sampleE)
```

```
## [1] 150.0057
```

```
mean(sampleE)
```

```
## [1] 150.0059
```

```
max(sampleE)
```

```
## [1] 175.9369
```

```
sd(sampleE)
```

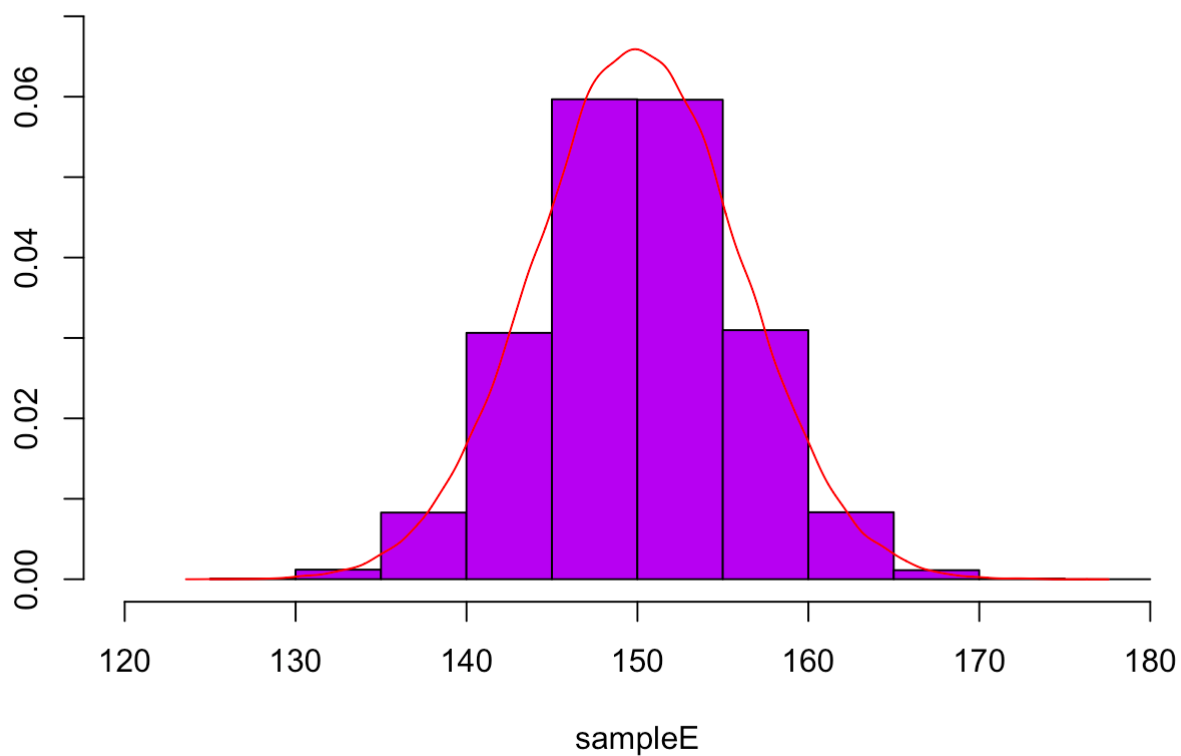
```
## [1] 5.9984
```

```
IQR(sampleE)
```

```
## [1] 8.072623
```

```
par(mfrow=c(1,1))  
truehist(sampleE,col = "purple",main = "Histogram of sampleE",nbins=8,ymax=0.07,xlim = c(120,180))  
lines(density(sampleE),col="red")
```

Histogram of sampleE



Part 2

```
library(ggplot2)  
set.seed(5551212)  
d2 <- diamonds[sample(nrow(diamonds), 25),]  
head(d2)
```

```
##          carat          cut color clarity depth table price      x      y      z
## 34497   0.32         Ideal     F   VVS1  61.7     55    867  4.38  4.43  2.72
## 25540   2.27       Premium     I    SI1  61.0     58  14362  8.42  8.40  5.19
## 42946   0.30   Very Good     F    SI2  63.5     57   506  4.25  4.22  2.69
## 40296   0.40         Ideal     G    VS1  62.8     56  1125  4.70  4.67  2.94
## 5907    0.90          Good     E    SI1  60.8     65  3933  6.14  6.17  3.74
## 25112   1.23         Ideal     D   VVS2  62.4     55  13653  6.87  6.82  4.27
```

A.

```
set.seed(123)
sampleUSArrests <- USArrests[sample(nrow(USArrests), 25),]
head(sampleUSArrests)
```

```
##          Murder Assault UrbanPop Rape
## Iowa           2.2      56      57 11.3
## Rhode Island   3.4     174      87  8.3
## Maryland       11.3     300      67 27.8
## Tennessee      13.2     188      59 26.9
## Utah            3.2     120      80 22.9
## Arizona         8.1     294      80 31.0
```

B.

```
set.seed(123)
sampleFunction <- function(x,y) {
  sampleF <- x[sample(nrow(x), y),]
  return (sampleF)
}
sampleFunction(USArrests,10)
```

```
##          Murder Assault UrbanPop Rape
## Iowa           2.2      56      57 11.3
## Rhode Island   3.4     174      87  8.3
## Maryland       11.3     300      67 27.8
## Tennessee      13.2     188      59 26.9
## Utah            3.2     120      80 22.9
## Arizona         8.1     294      80 31.0
## Mississippi    16.1     259      44 17.1
## Wisconsin       2.6      53      66 10.8
## Virginia        8.5     156      63 20.7
## Maine           2.1      83      51  7.8
```

Part 3

A.

```
set.seed(123)
a <- rnorm(10,mean=54,sd=25)
a
```

```
## [1] 39.98811 48.24556 92.96771 55.76271 57.23219 96.87662 65.52291  
## [8] 22.37347 36.82868 42.85845
```

```
sort(a)
```

```
## [1] 22.37347 36.82868 39.98811 42.85845 48.24556 55.76271 57.23219  
## [8] 65.52291 92.96771 96.87662
```

B.

```
b <- ChickWeight[order(ChickWeight$weight),]  
head(b,n=50)
```

##	weight	Time	Chick	Diet
## 196	35	2	18	1
## 26	39	2	3	1
## 195	39	0	18	1
## 293	39	0	27	2
## 305	39	0	28	2
## 317	39	0	29	2
## 365	39	0	33	3
## 401	39	0	36	3
## 543	39	0	48	4
## 13	40	0	2	1
## 221	40	0	21	2
## 269	40	0	25	2
## 519	40	0	46	4
## 555	40	0	49	4
## 49	41	0	5	1
## 61	41	0	6	1
## 73	41	0	7	1
## 108	41	0	10	1
## 132	41	0	12	1
## 144	41	0	13	1
## 156	41	0	14	1
## 168	41	0	15	1
## 176	41	0	16	1
## 209	41	0	20	1
## 233	41	0	22	2
## 353	41	0	32	3
## 377	41	0	34	3
## 389	41	0	35	3
## 413	41	0	37	3
## 425	41	0	38	3
## 449	41	0	40	3
## 507	41	0	45	4
## 531	41	0	47	4
## 567	41	0	50	4
## 1	42	0	1	1
## 37	42	0	4	1
## 50	42	2	5	1
## 85	42	0	8	1
## 96	42	0	9	1
## 183	42	0	17	1
## 257	42	0	24	2
## 281	42	0	26	2
## 329	42	0	30	2
## 341	42	0	31	3
## 437	42	0	39	3
## 461	42	0	41	4
## 473	42	0	42	4
## 485	42	0	43	4
## 497	42	0	44	4
## 25	43	0	3	1

I ordered ChickWeight's weight from the lowest to the highest

C.

```
c <- swiss[,order(names(swiss))]  
head(c)
```

```
##           Agriculture Catholic Education Examination Fertility  
## Courtelary           17.0      9.96           12           15      80.2  
## Delemont            45.1     84.84            9            6      83.1  
## Franches-Mnt        39.7     93.40            5            5      92.5  
## Moutier             36.5     33.77            7           12      85.8  
## Neuveville          43.5       5.16           15           17      76.9  
## Porrentruy          35.3     90.57            7            9      76.1  
##           Infant.Mortality  
## Courtelary                22.2  
## Delemont                  22.2  
## Franches-Mnt              20.2  
## Moutier                   20.3  
## Neuveville                 20.6  
## Porrentruy                 26.6
```

D.

```
table(diamonds$cut)
```

```
##  
##      Fair      Good Very Good    Premium    Ideal  
##      1610      4906      12082      13791      21551
```

```
sort(table(diamonds$cut))
```

```
##  
##      Fair      Good Very Good    Premium    Ideal  
##      1610      4906      12082      13791      21551
```

```
sort(table(diamonds$cut),decreasing = T)
```

```
##  
##      Ideal    Premium Very Good      Good      Fair  
##      21551      13791      12082      4906      1610
```