

Graphics

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Introduction

- 상위수준 그림 함수는 그림을 생성한다.
- 하위수준 그림 함수는 기존의 그림에 그림을 추가한다.

상위수준 그림 함수

상위수준 그림 함수의 주요 인자 (arguments)

- main : 제목
- xlab/ylab : x축 및 y축 레이블
- xlim/ylim : x축 및 y축 범위
- col : 색깔
- lty : 선 모양
- pch : 점 모양
- cex : 그림 성분의 크기
- lwd : 선 굵기
- type : 그림 타입

```
dta <- read.csv("PK.csv")
head(dta)
```

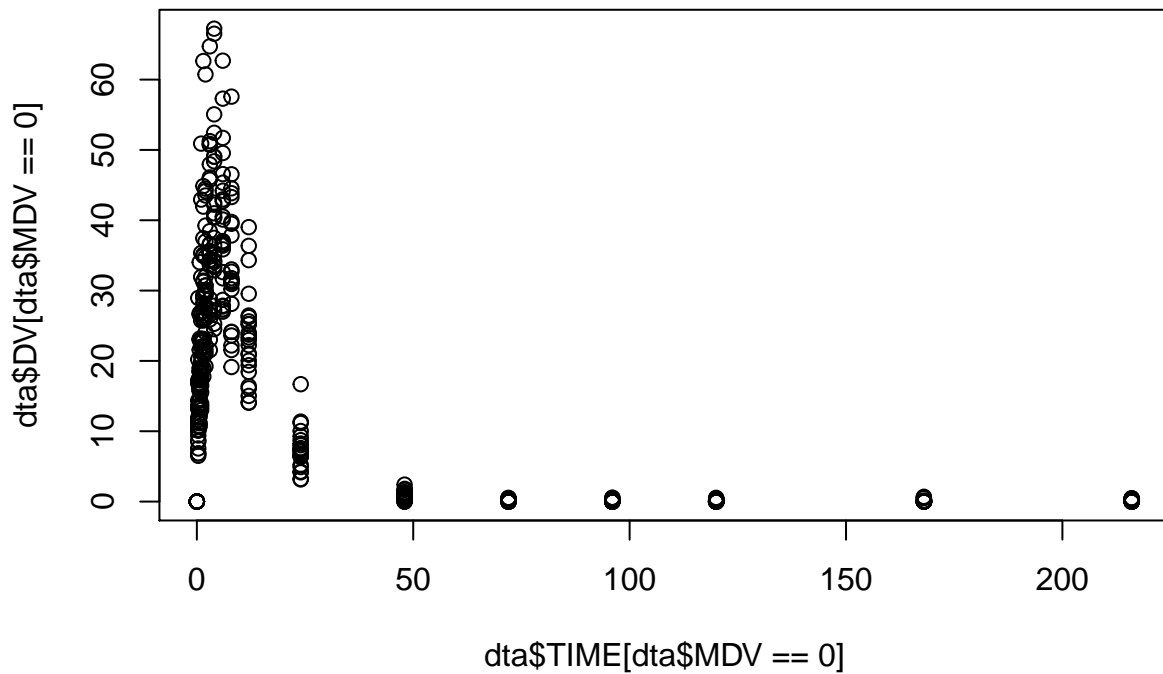
```
##   ID TIME AMT   DV MDV
## 1  1 0.00  0  0.00  0
## 2  1 0.00  4  0.00  1
## 3  1 0.33  0  9.40  0
## 4  1 0.66  0 13.71  0
## 5  1 1.00  0 16.52  0
## 6  1 1.50  0 29.36  0
```

```
str(dta)
```

```
## 'data.frame':   456 obs. of  5 variables:
## $ ID   : num  1 1 1 1 1 1 1 1 1 1 ...
## $ TIME: num  0 0 0.33 0.66 1 1.5 2 3 4 6 ...
## $ AMT  : num  0 4 0 0 0 0 0 0 0 0 ...
## $ DV   : num  0 0 9.4 13.7 16.5 ...
## $ MDV  : num  0 1 0 0 0 0 0 0 0 0 ...
```

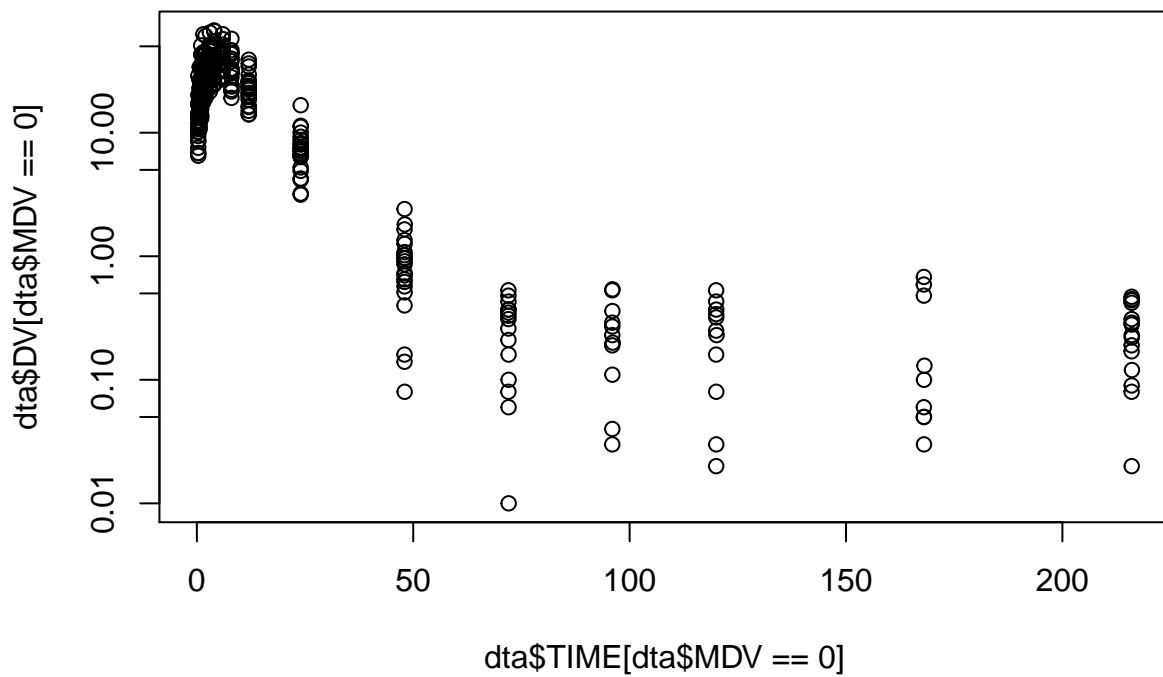
scatter plot

```
plot(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0])
```

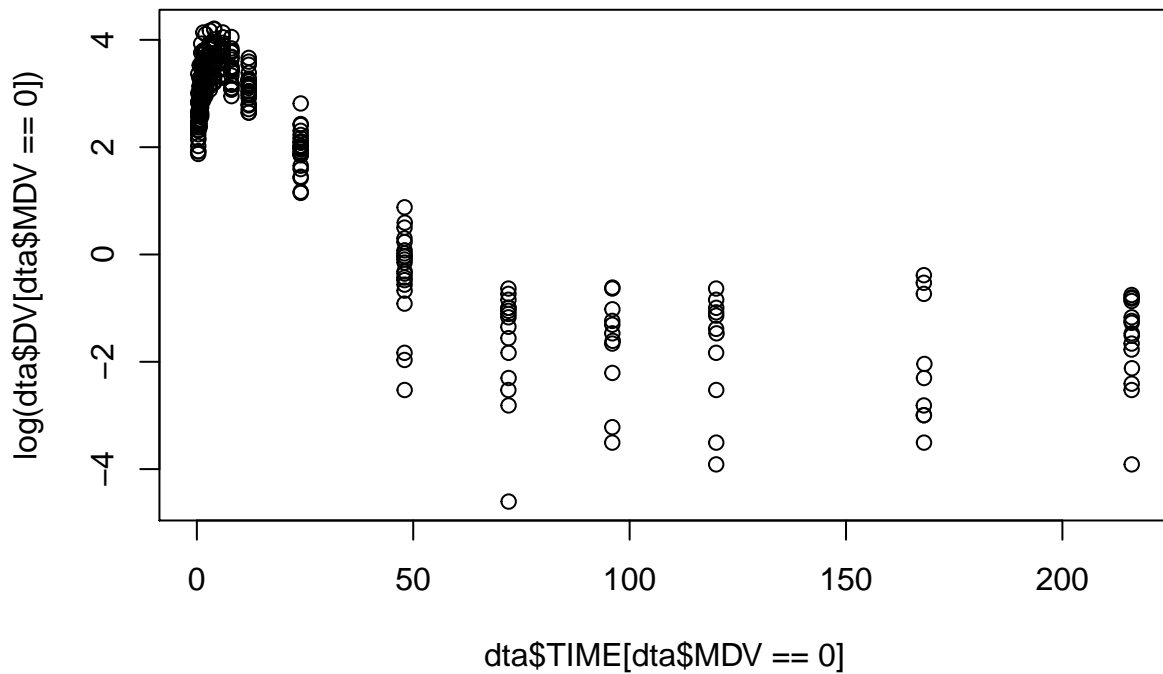


```
plot(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], log="y")
```

```
## Warning in xy.coords(x, y, xlabel, ylabel, log): 86 y values <= 0 omitted
## from logarithmic plot
```

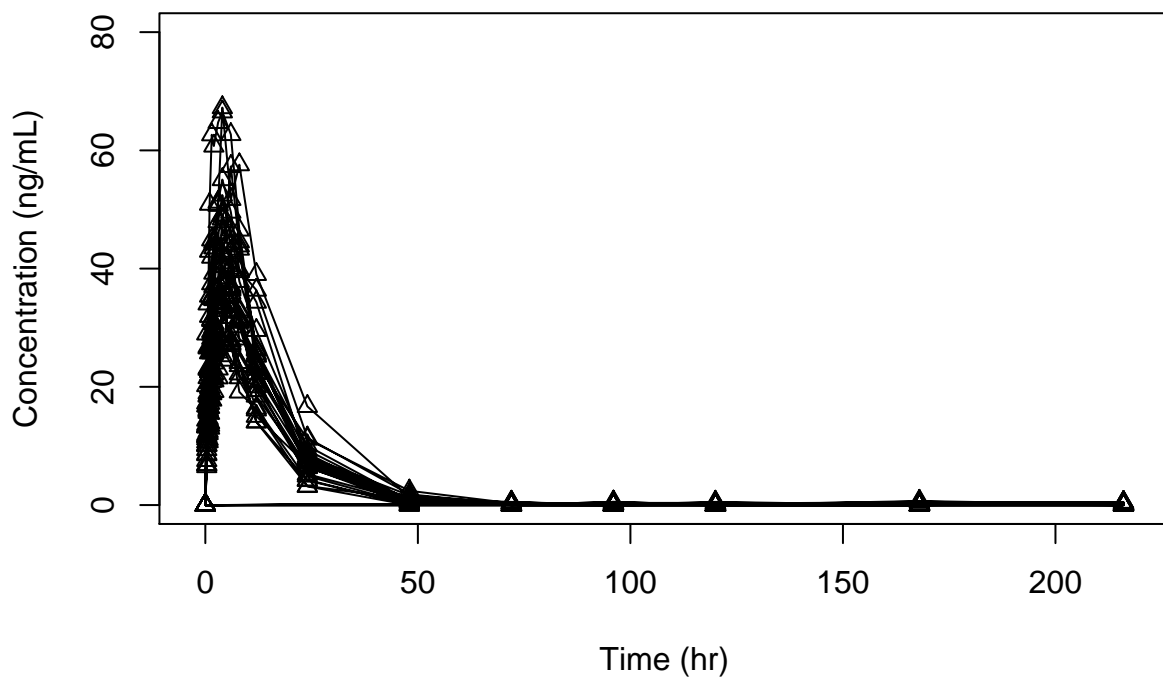


```
plot(dta$TIME[dta$MDV==0], log(dta$DV[dta$MDV==0]))
```



```
plot(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0],
     , xlab="Time (hr)", ylab="Concentration (ng/mL)"
     , type="o", pch=2, col=1, main="PK time-course of Drug X"
     , xlim =c(-2,218), ylim=c(0,80))
```

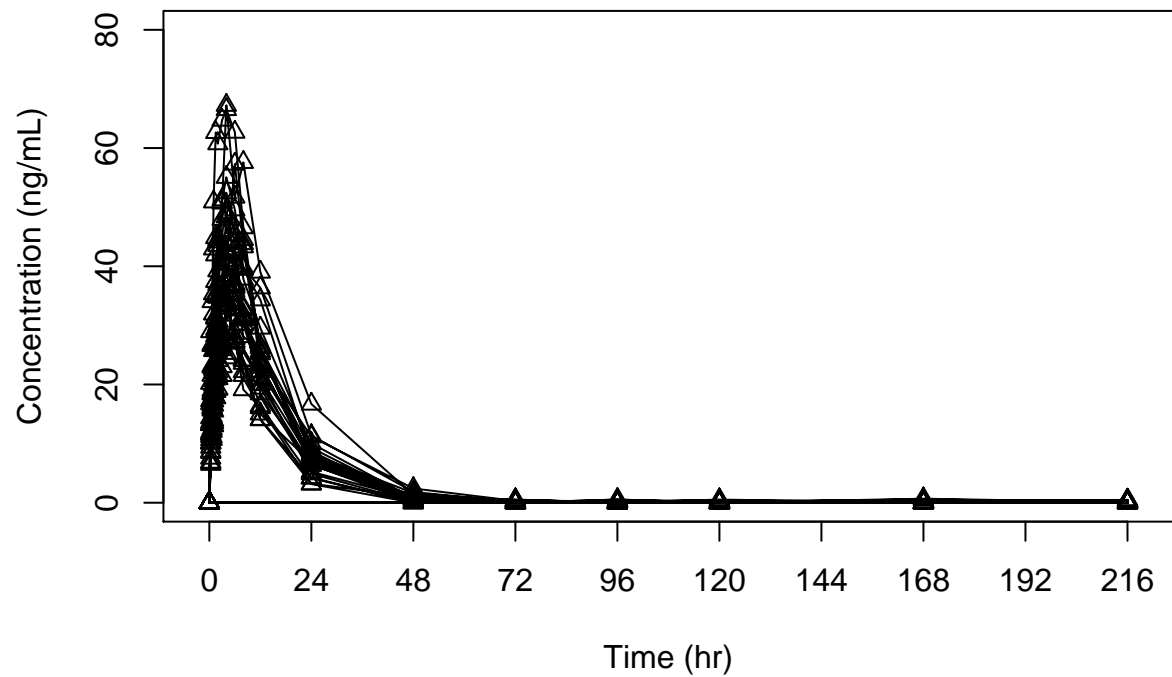
PK time-course of Drug X



```
plot(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], axes=F,
     , xlab="Time (hr)", ylab="Concentration (ng/mL)"
     , type="o", pch=2, col=1, main="PK time-course of Drug X")
```

```
, xlim =c(-2,218), ylim=c(0,80))  
axis(1, at=seq(0, 218, 24))  
axis(2)  
box()
```

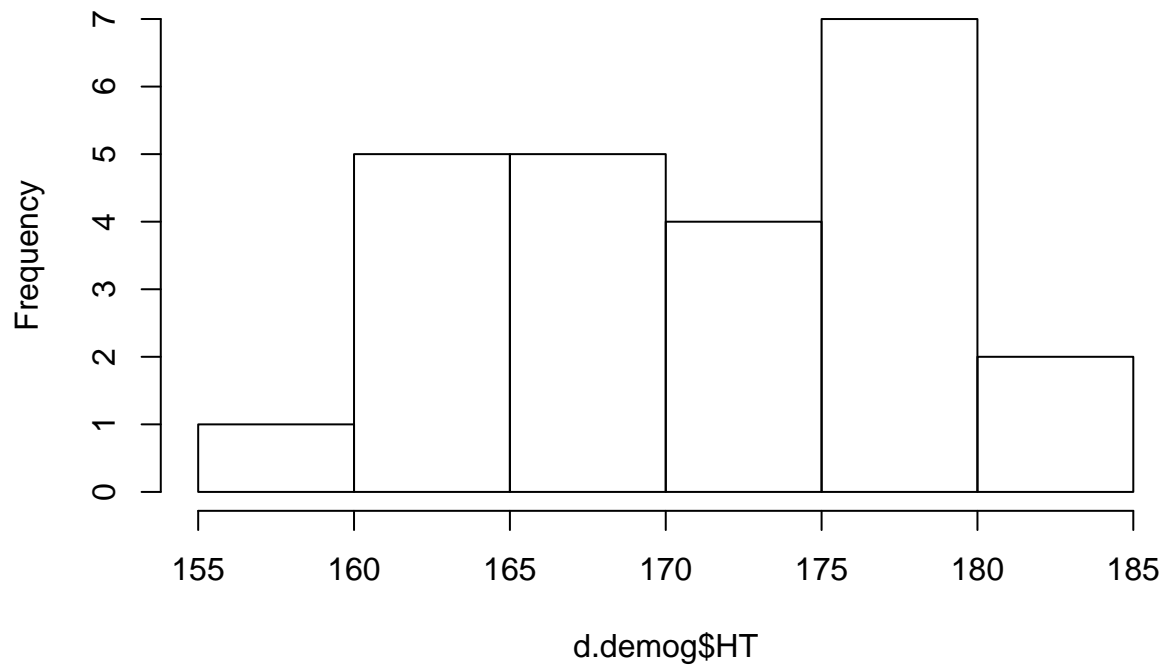
PK time-course of Drug X



Histogram

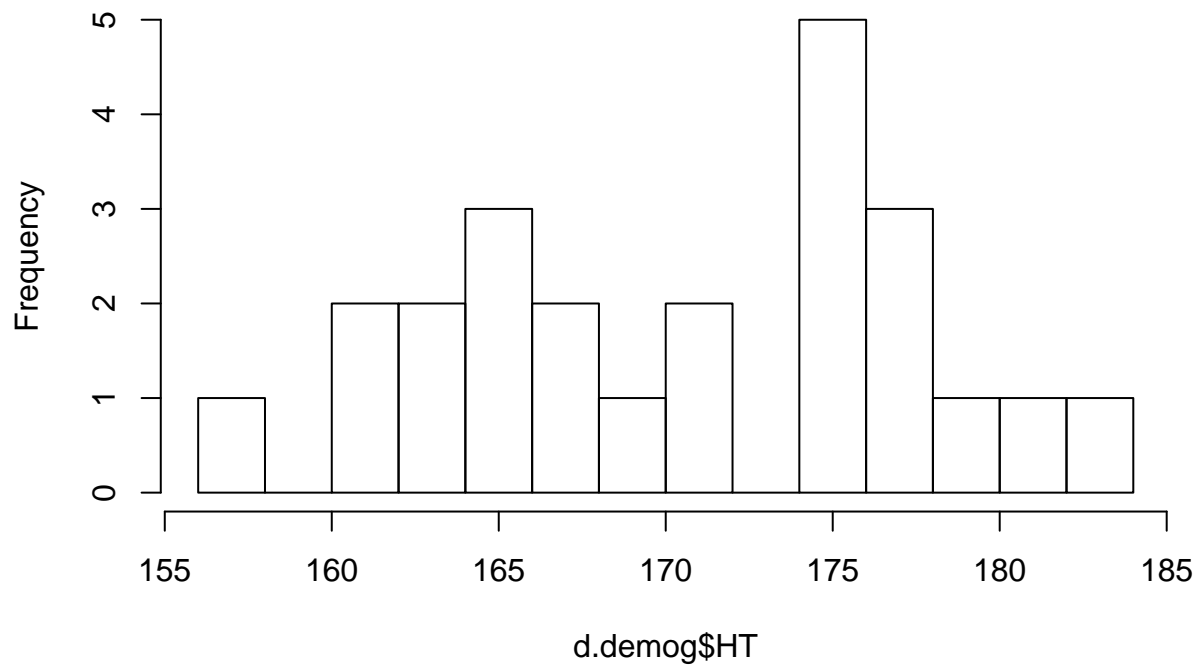
```
d.demog <- read.csv("DEMOG.csv")  
hist(d.demog$HT)
```

Histogram of d.demog\$HT



```
hist(d.demog$HT, breaks=10)  
hist(d.demog$HT, nclass=10)
```

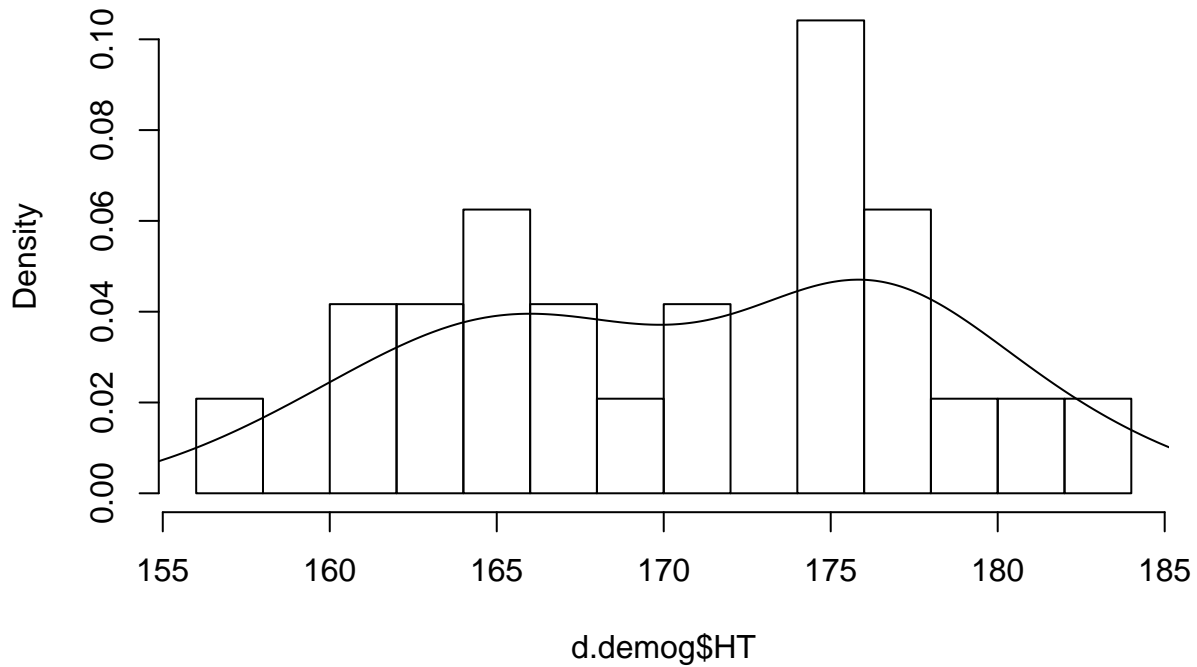
Histogram of d.demog\$HT



with density line

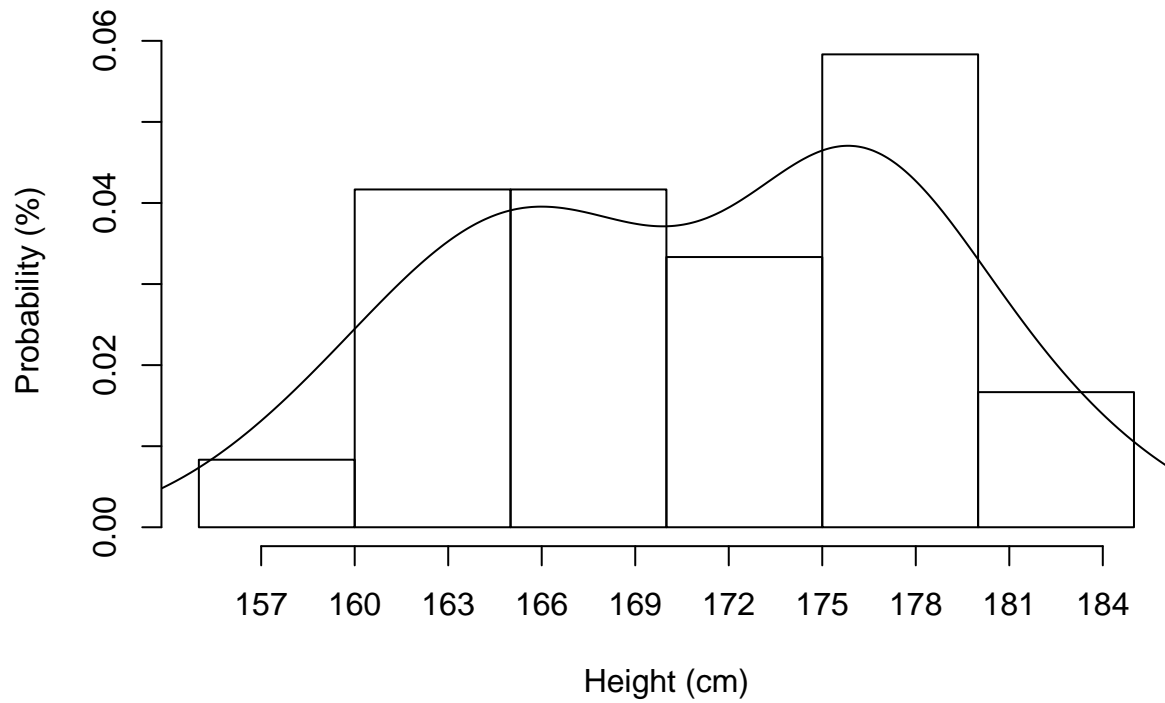
```
hist (d.demog$HT, probability=TRUE, breaks=10)  
lines(density(d.demog$HT))
```

Histogram of d.demog\$HT



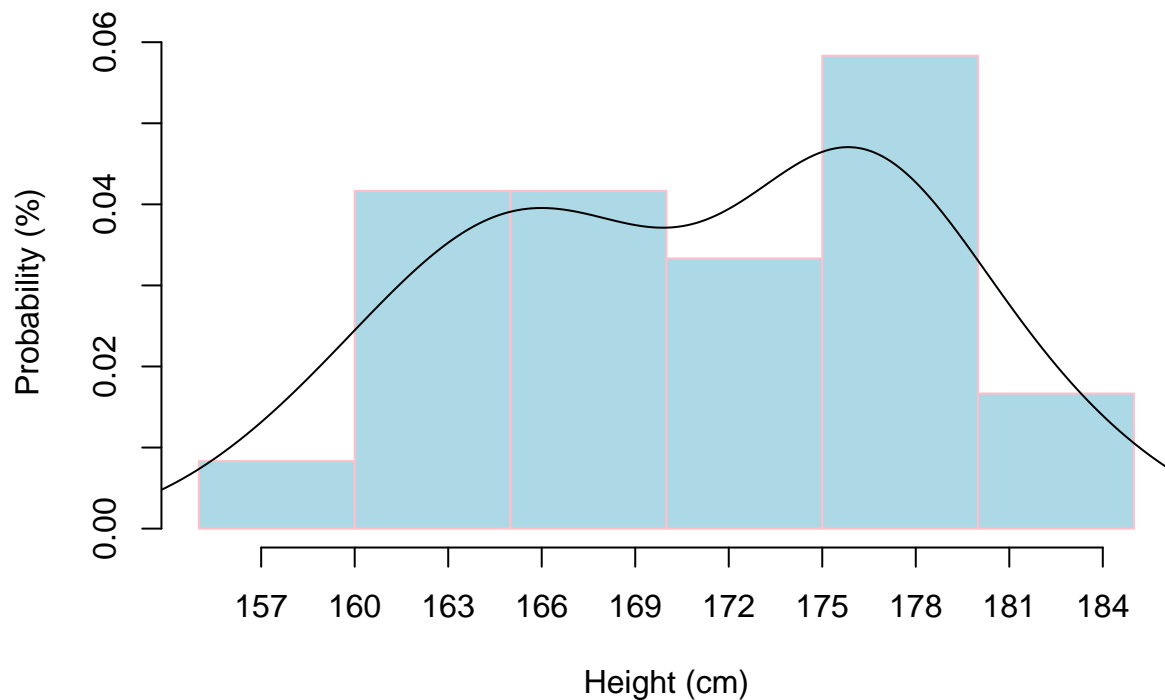
```
hist (d.demog$HT, probability=TRUE, breaks=9, xaxt="n"  
      , main="Histogram for Height", xlab="Height (cm)", ylab="Probability (%)")  
axis(1, at=seq(min(d.demog$HT), max(d.demog$HT), 3))  
lines(density(d.demog$HT))
```

Histogram for Height



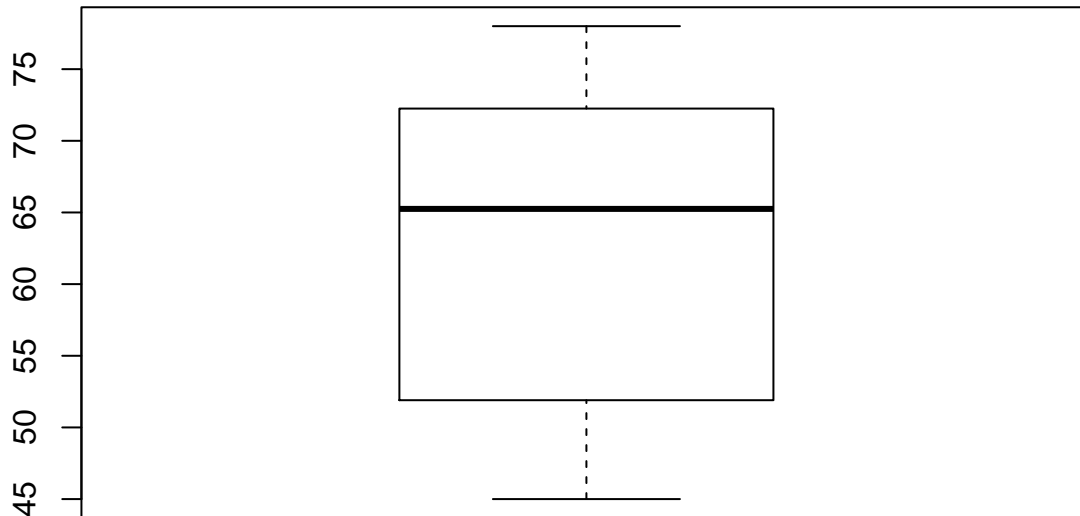
```
hist (d.demog$HT, probability=TRUE, breaks=9, xaxt="n"
      , main="Histogram for Height", xlab="Height (cm)", ylab="Probability (%)"
      , col = "lightblue", border = "pink")
axis(1, at=seq(min(d.demog$HT), max(d.demog$HT), 3))
lines(density(d.demog$HT))
```

Histogram for Height



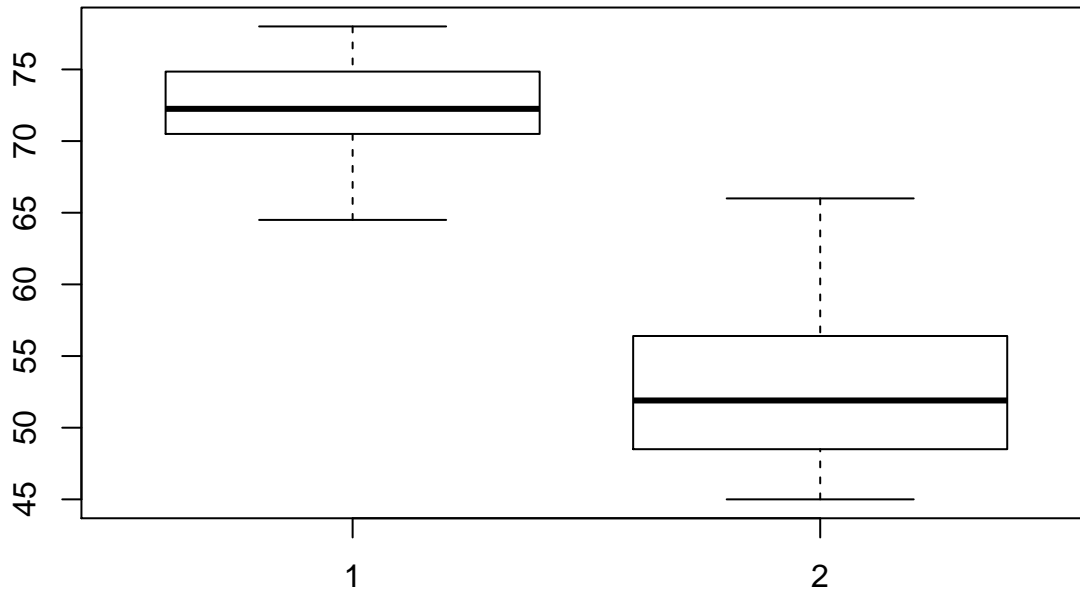
Box-Whisker Plot

```
boxplot(d.demog$WT)
```



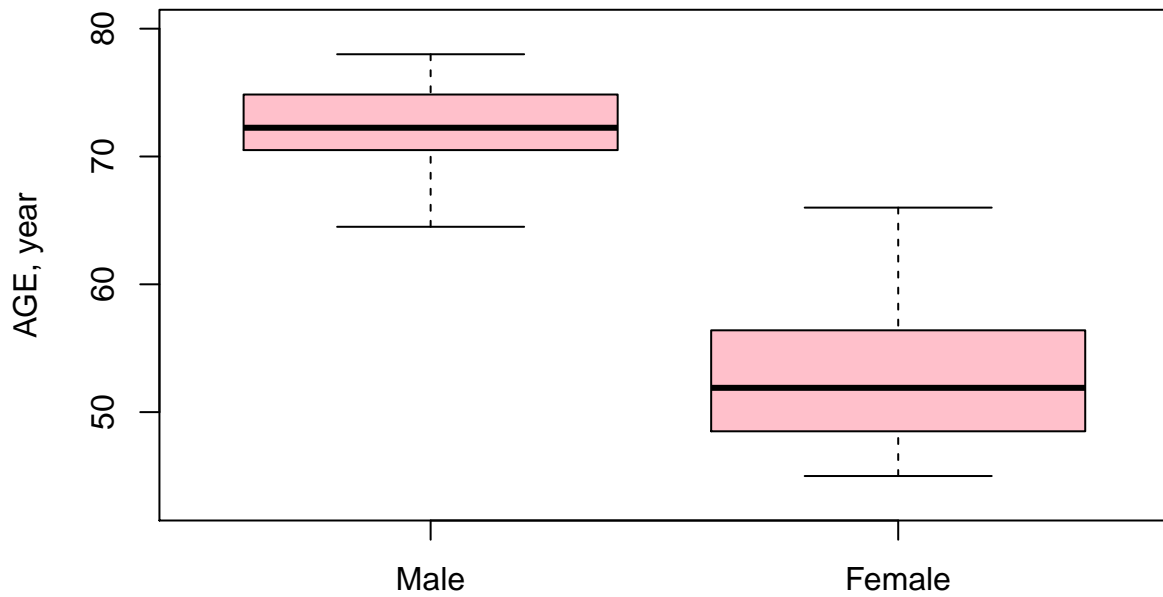
```
boxplot(d.demog$WT ~ d.demog$SEX)
```

```
boxplot(split(d.demog$WT, d.demog$SEX))
```

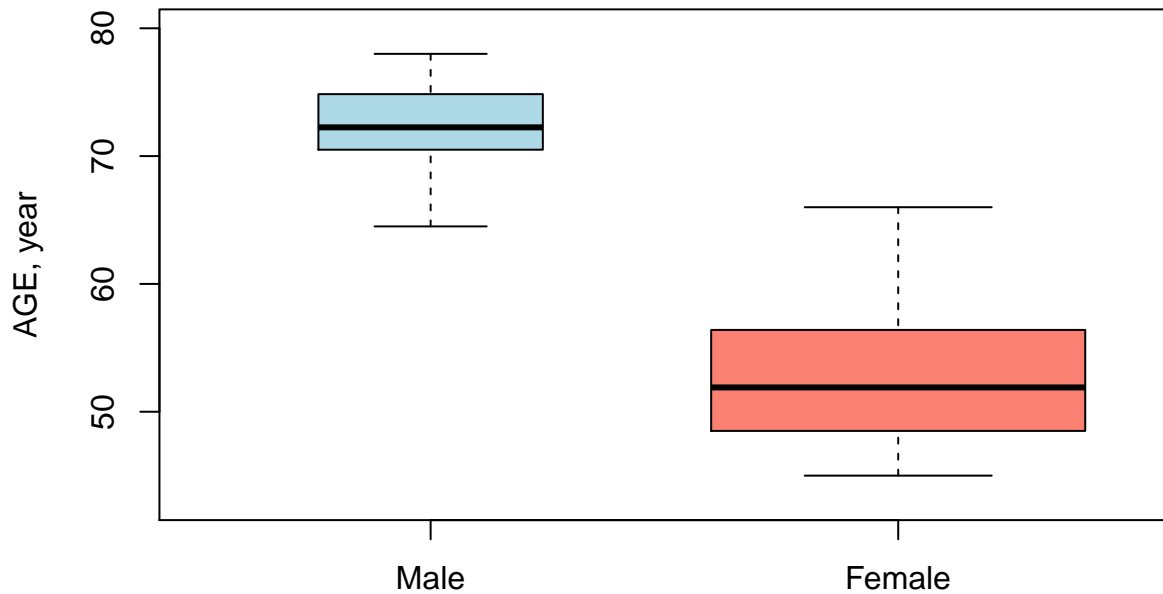


```
boxplot(WT ~ SEX, data=d.demog)
```

```
boxplot(d.demog$WT ~ d.demog$SEX  
        , names=c("Male", "Female"), ylab="AGE, year", ylim=c(min(d.demog$WT)-2, max(d.demog$WT)+2)  
        , col="pink")
```

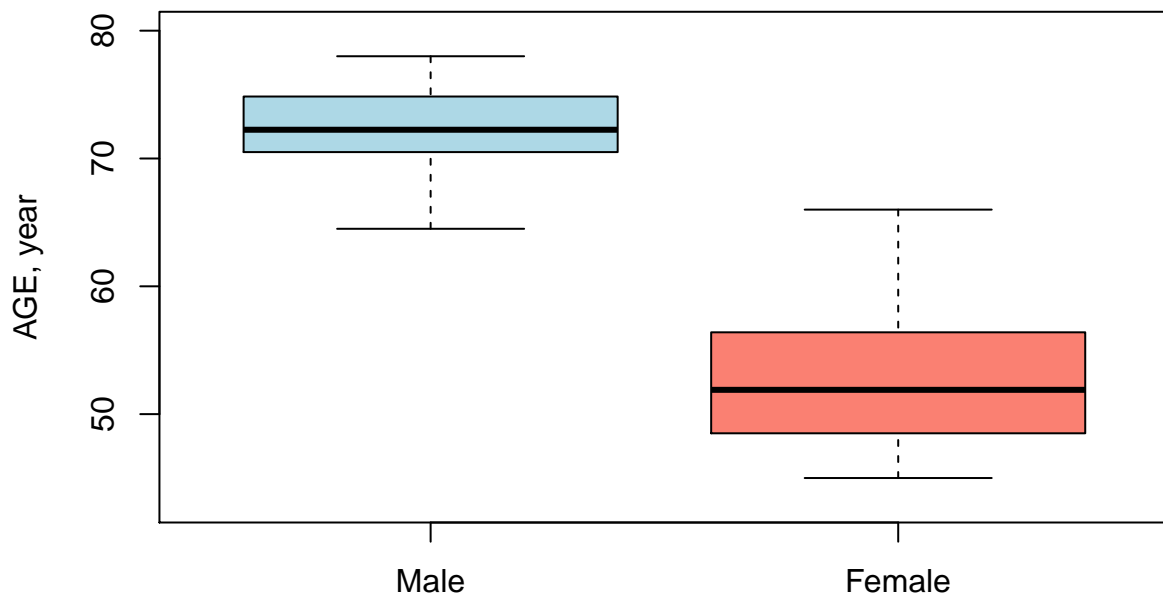



```
boxplot(d.demog$WT ~ d.demog$SEX
, names=c("Male","Female"), ylab="AGE, year", ylim=c(min(d.demog$WT)-2, max(d.demog$WT)+2)
, col=c("lightblue", "salmon"), width=c(0.6, 1))
```



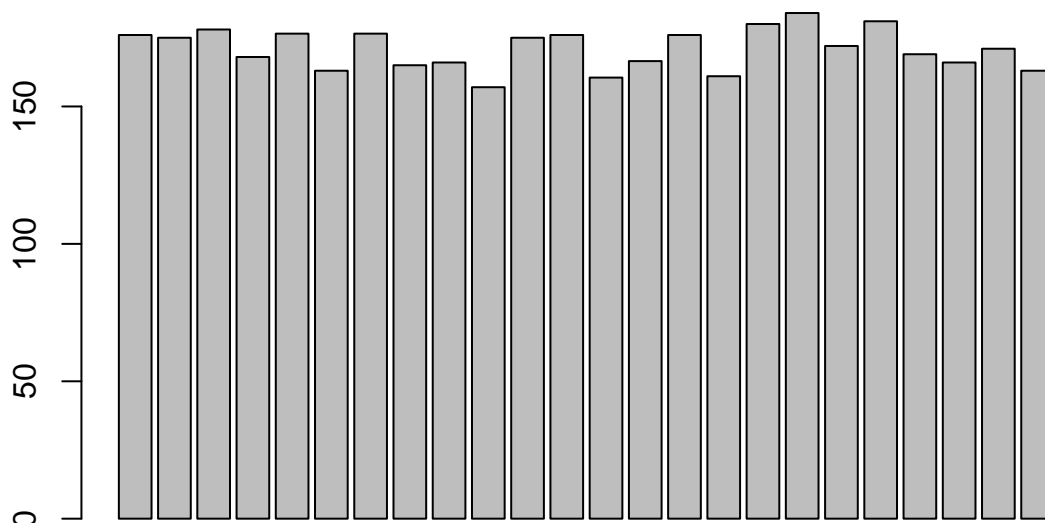
-varwidth: if varwidth is TRUE, the boxes are drawn with widths proportional to the square-roots of the number of observations in the groups.

```
boxplot(d.demog$WT ~ d.demog$SEX
, names=c("Male","Female"), ylab="AGE, year", ylim=c(min(d.demog$WT)-2, max(d.demog$WT)+2)
, col=c("lightblue", "salmon")
, varwidth=TRUE)
```



Bar Plot

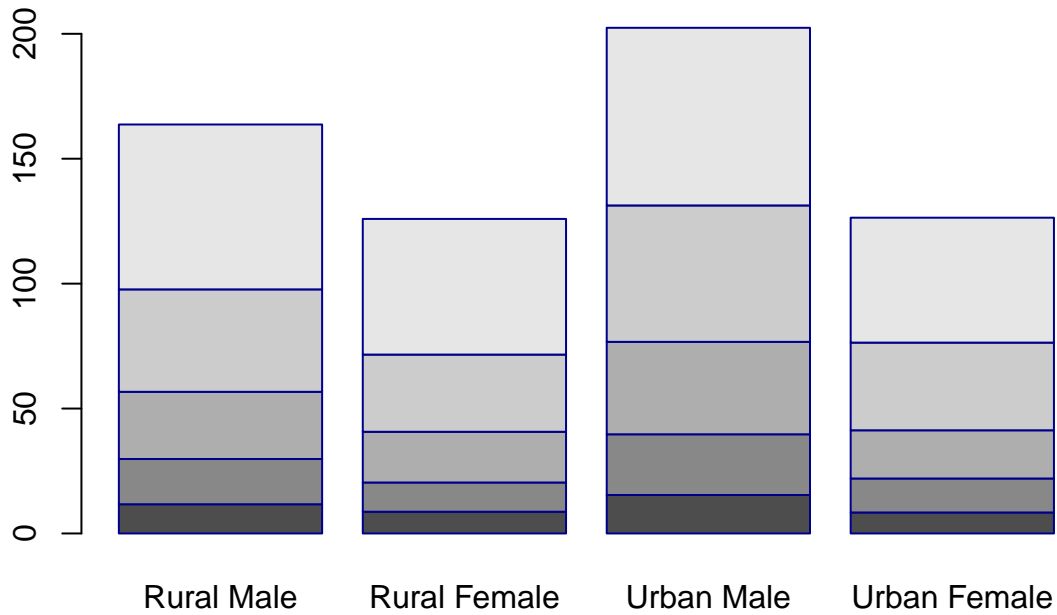
```
barplot(d.demog$HT)
```



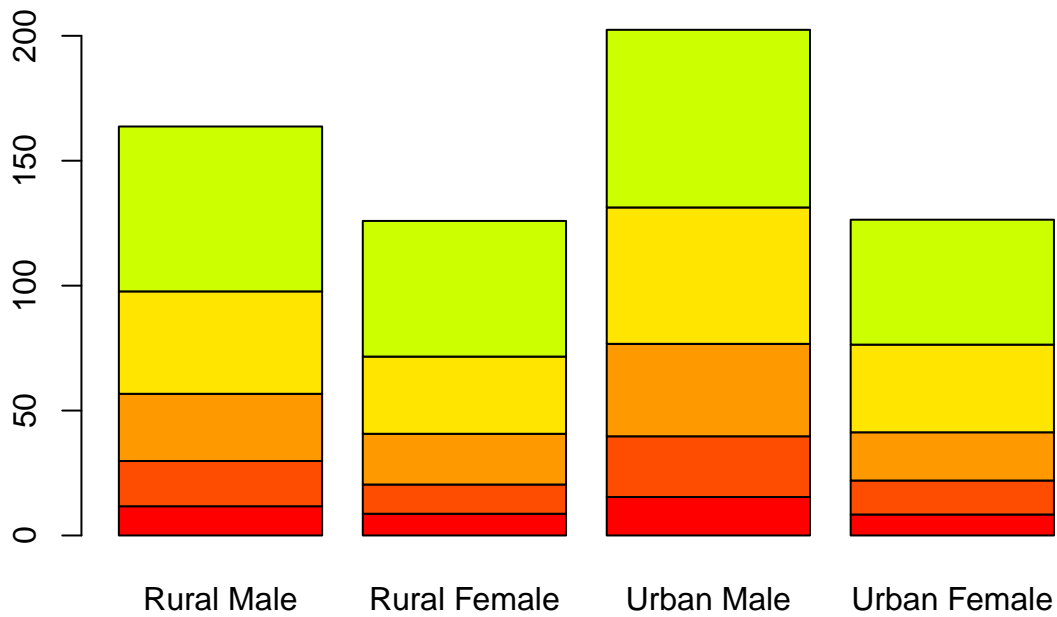
VADeaths

##	Rural	Male	Rural	Female	Urban	Male	Urban	Female
## 50-54		11.7		8.7	15.4		8.4	
## 55-59		18.1		11.7	24.3		13.6	
## 60-64		26.9		20.3	37.0		19.3	
## 65-69		41.0		30.9	54.6		35.1	
## 70-74		66.0		54.3	71.1		50.0	

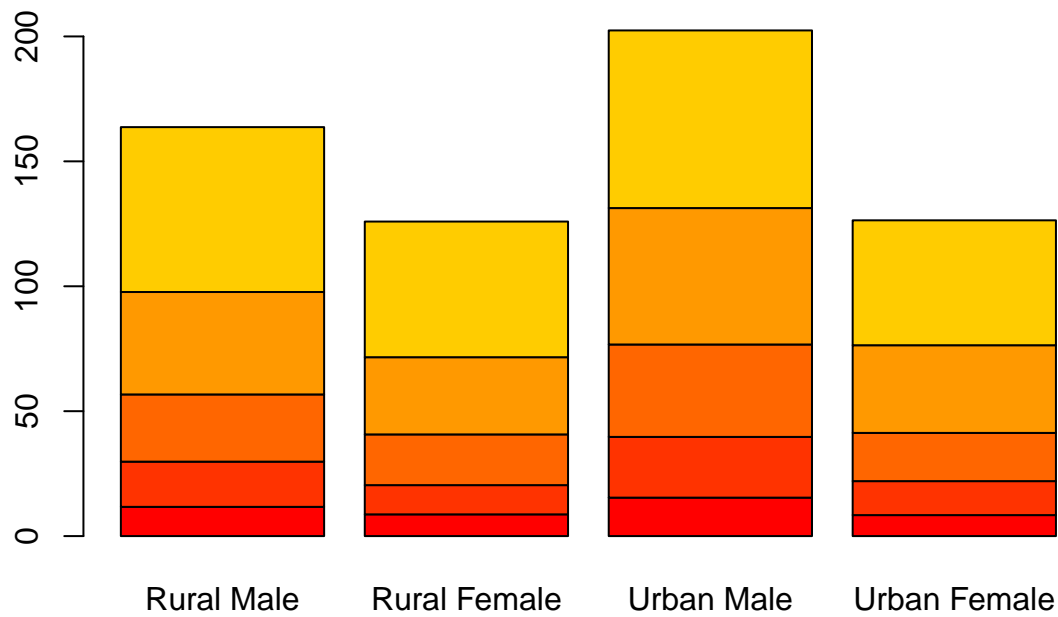
```
barplot(VADeaths, border = "dark blue")
```



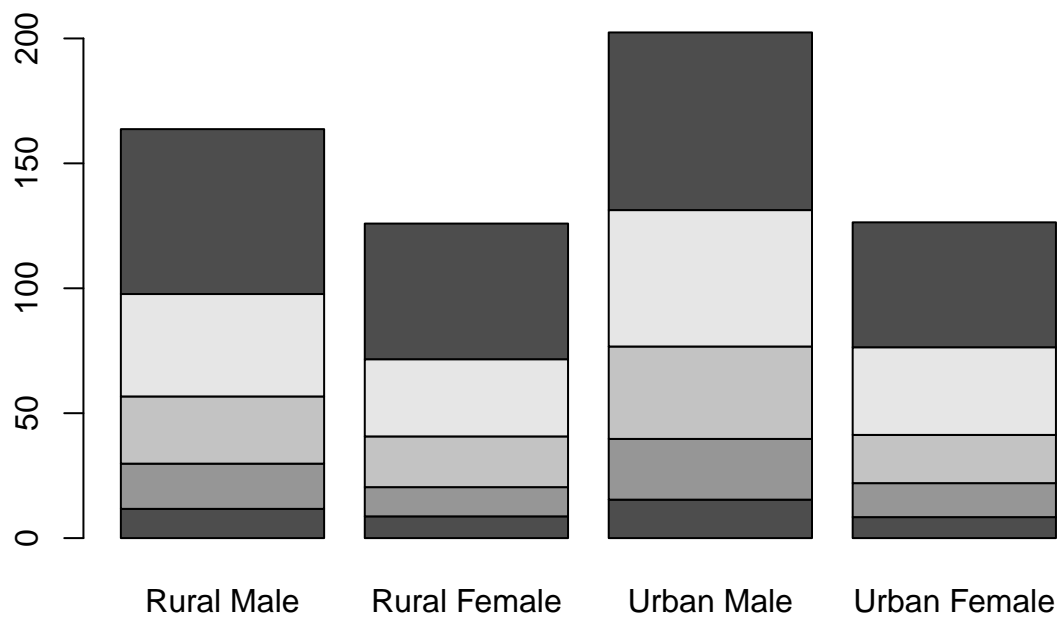
```
barplot(VADeaths, col = rainbow(20))
```



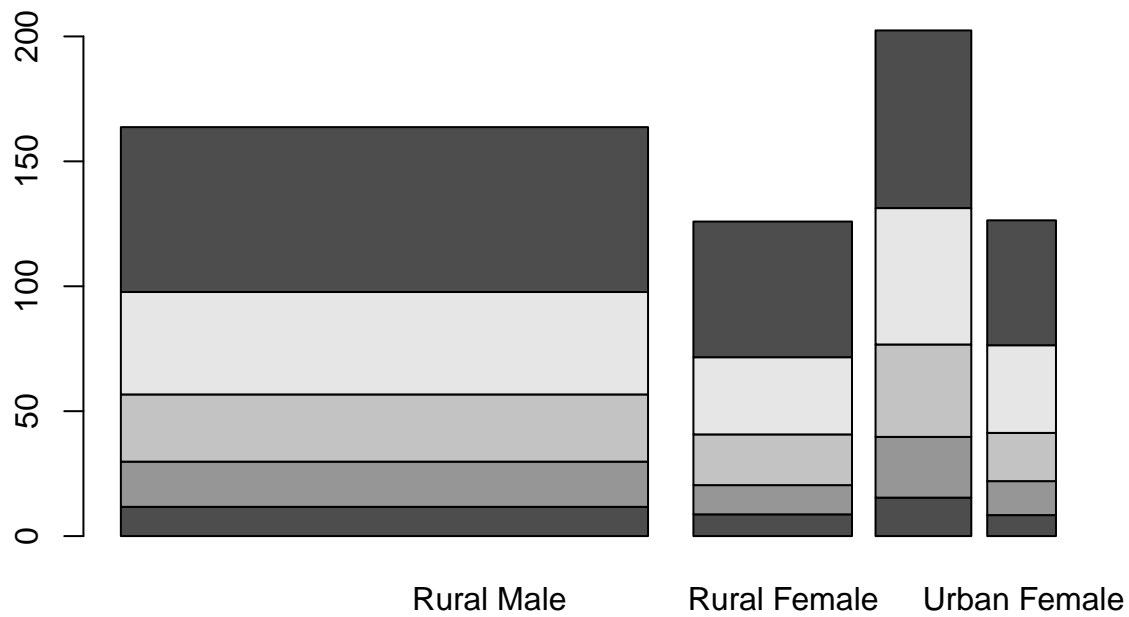
```
barplot(VADeaths, col = heat.colors(8))
```



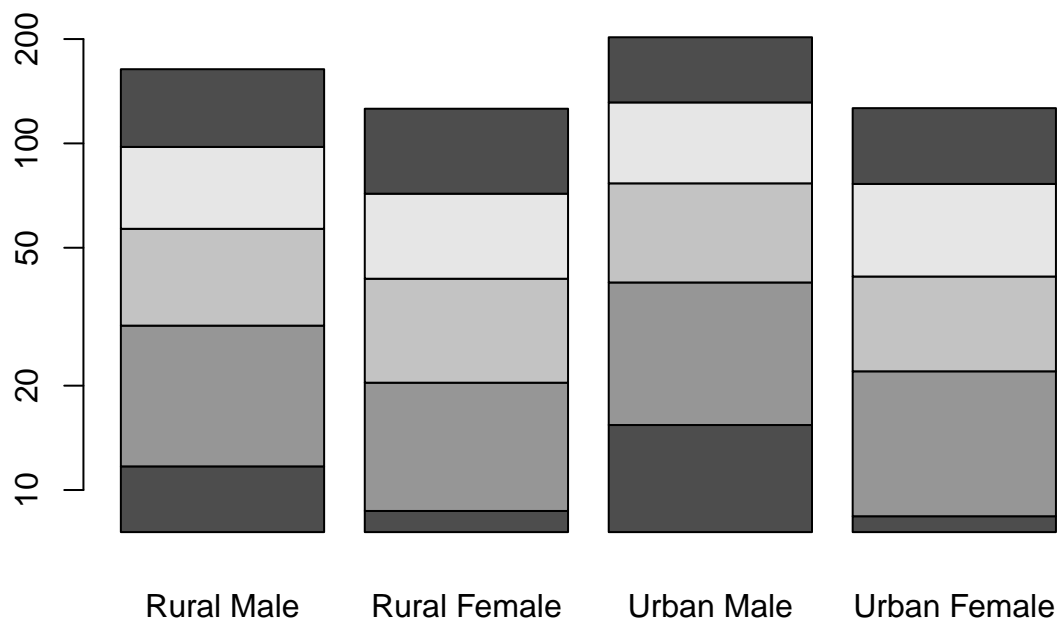
```
barplot(VADeaths, col = gray.colors(4))
```



```
barplot(VADeaths, col = gray.colors(4), log="x")
```



```
barplot(VADeaths, col = gray.colors(4), log="y")
```

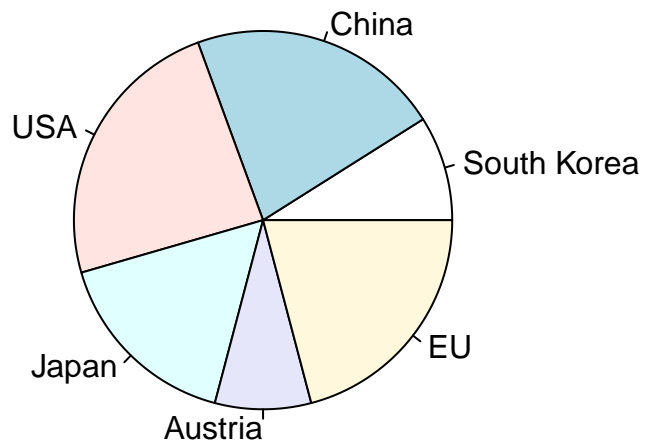


```
barplot(VADeaths, col = gray.colors(4), log="xy")
```



pie chart

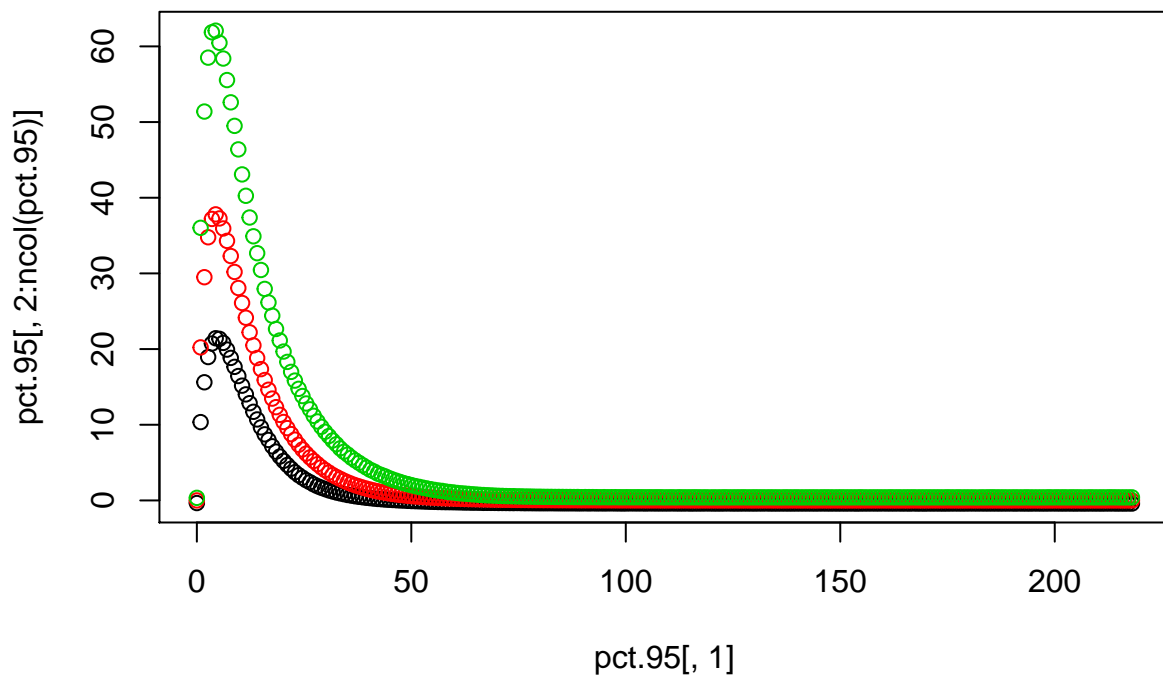
```
drug.X.market <- c(0.12, 0.29, 0.32, 0.22, 0.11, 0.28)
names(drug.X.market) <- c("South Korea", "China", "USA", "Japan", "Austria", "EU")
pie(drug.X.market)
```



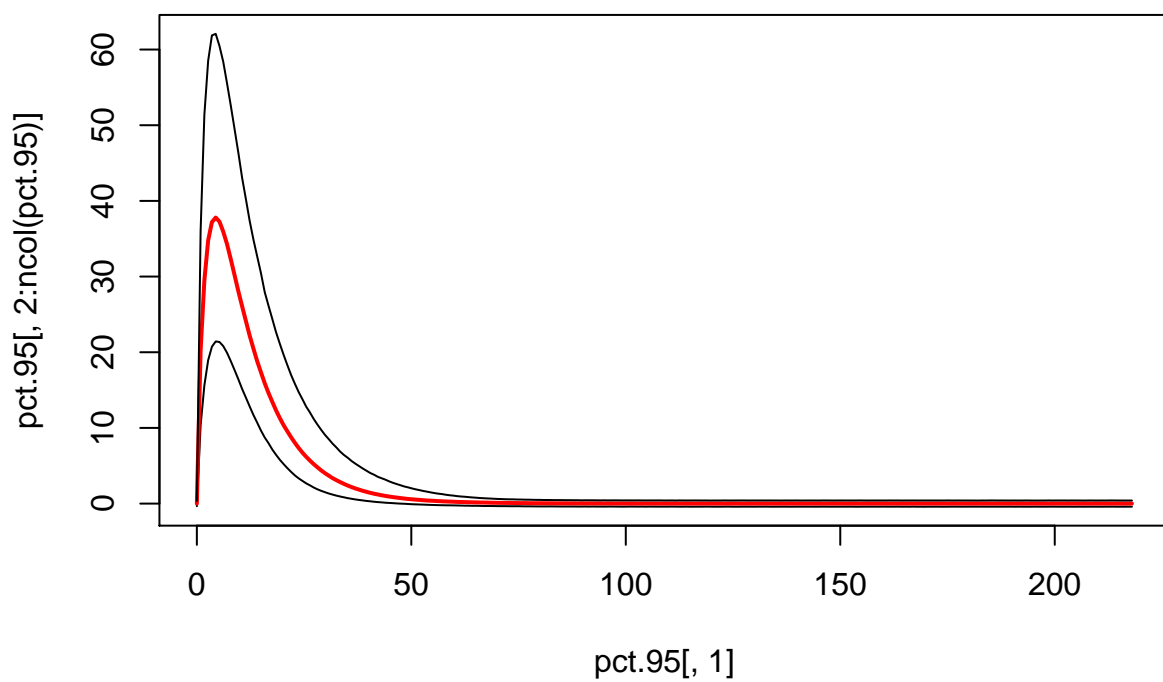
matplot 함수

matrix와 column 사이의 그림

```
pct.95 <- read.csv("pct95.csv")
matplot(pct.95[,1], pct.95[,2:ncol(pct.95)], pch=1)
```

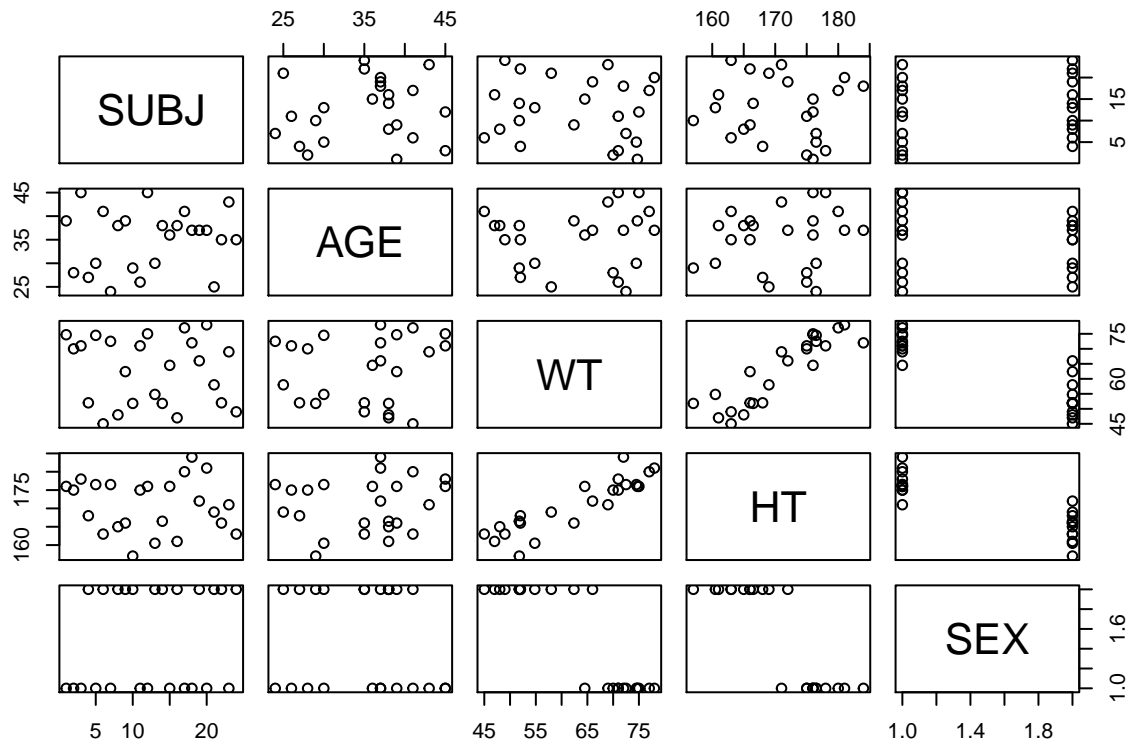


```
matplot(pct.95[,1], pct.95[,2:ncol(pct.95)], pch=1, col=c(1,2,1), type="l", lty=1, lwd=c(1,2,1))
```



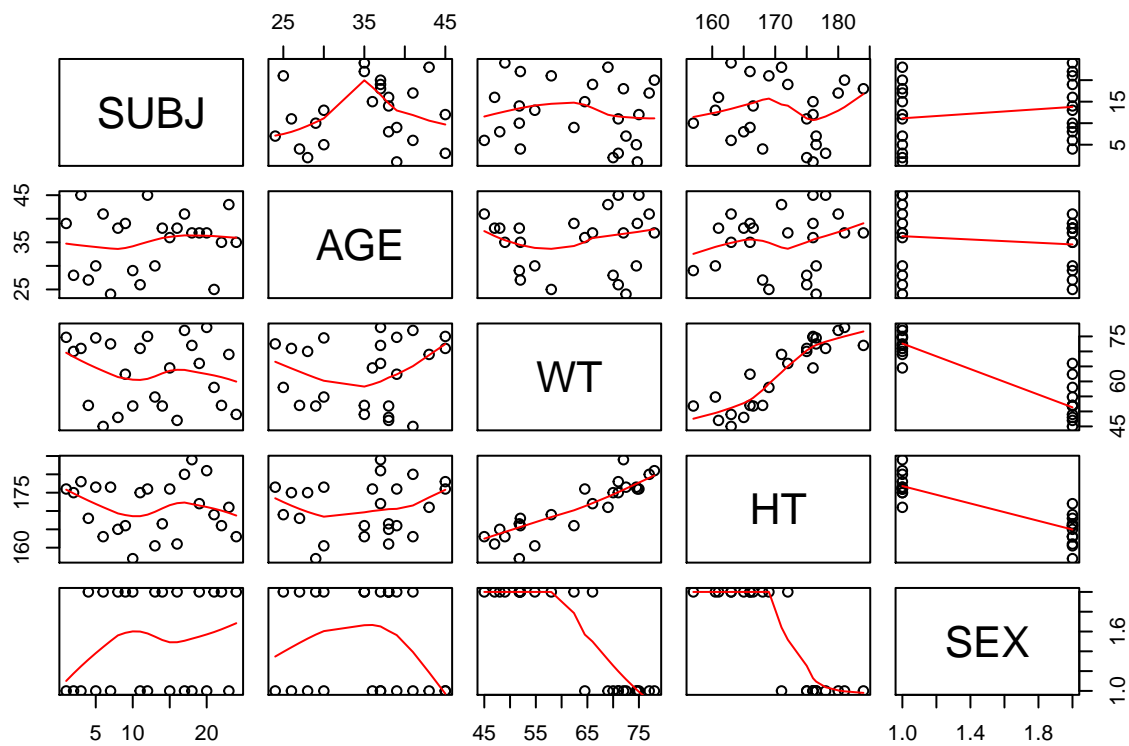
Scatter plot matrices (pairs plots)

```
pairs(d.demog)
```



add a loess smoother, type

```
pairs(d.demog, panel = panel.smooth)
```

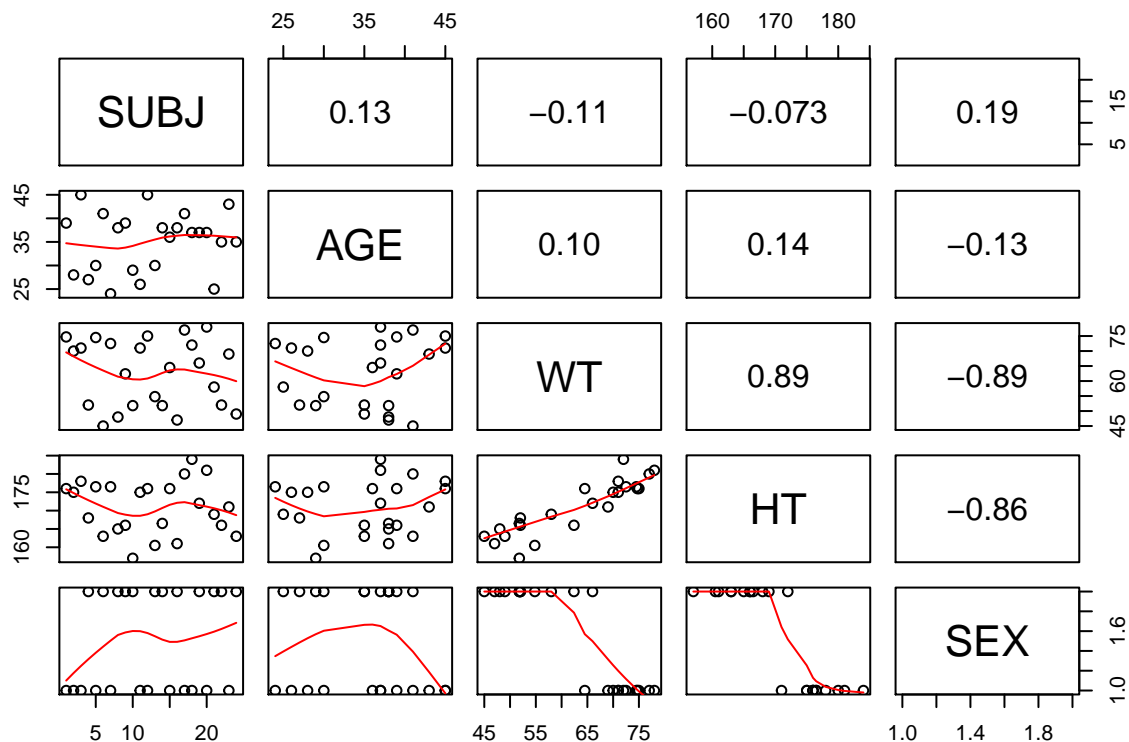



```

panel.cor <- function(x, y, digits=2, prefix="", cex.cor)
{
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  r = (cor(x, y))
  txt <- format(c(r, 0.123456789), digits=digits)[1]
  txt <- paste(prefix, txt, sep="")
  if(missing(cex.cor)) cex <- 1.5
  text(0.5, 0.5, txt, cex = 1.5)
}

pairs(d.demog, lower.panel=panel.smooth, upper.panel=panel.cor)

```



하위수준 그림 함수

- points : 점 추가
- lines : 선 추가
- abline : 기준선 추가
- mtext : 텍스트 추가
- legend : 설명(legend) 추가
- polygon : polygon 추가

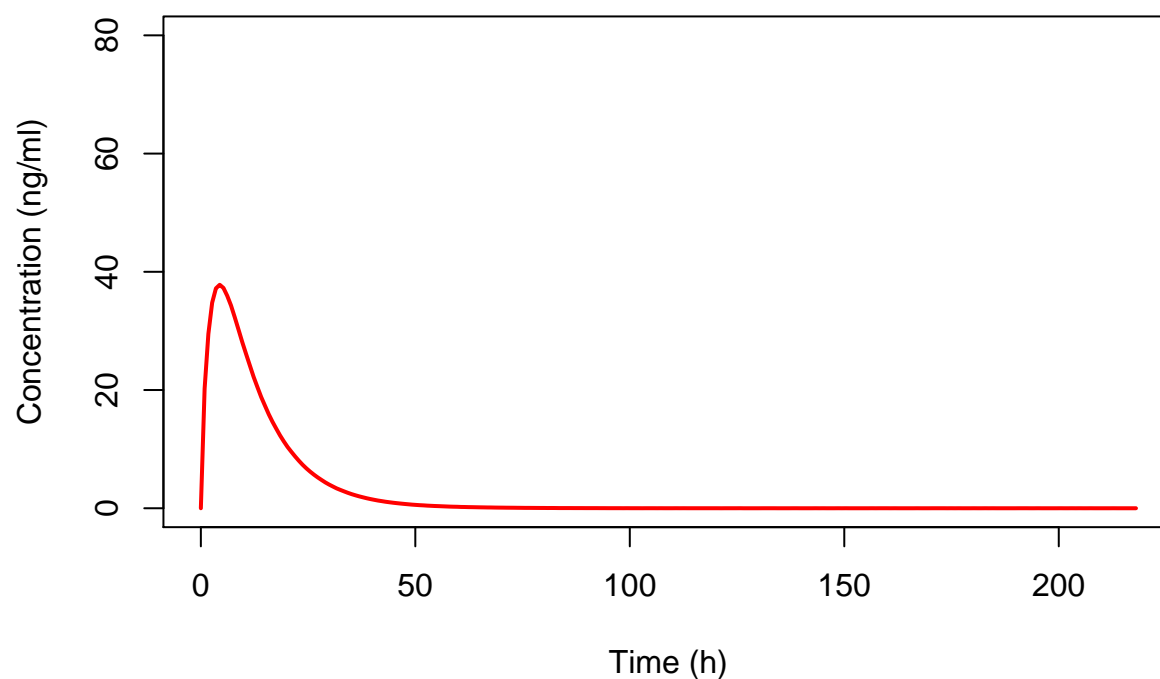
점, 선, 설명 추가 하기

```

plot(pct.95$TIME, pct.95$PCT50, main="PK of Drug X"
     , type="l", xlab="Time (h)", ylab="Concentration (ng/ml)"
     , ylim=range(0,80), lty=1, col="red", lwd=2)

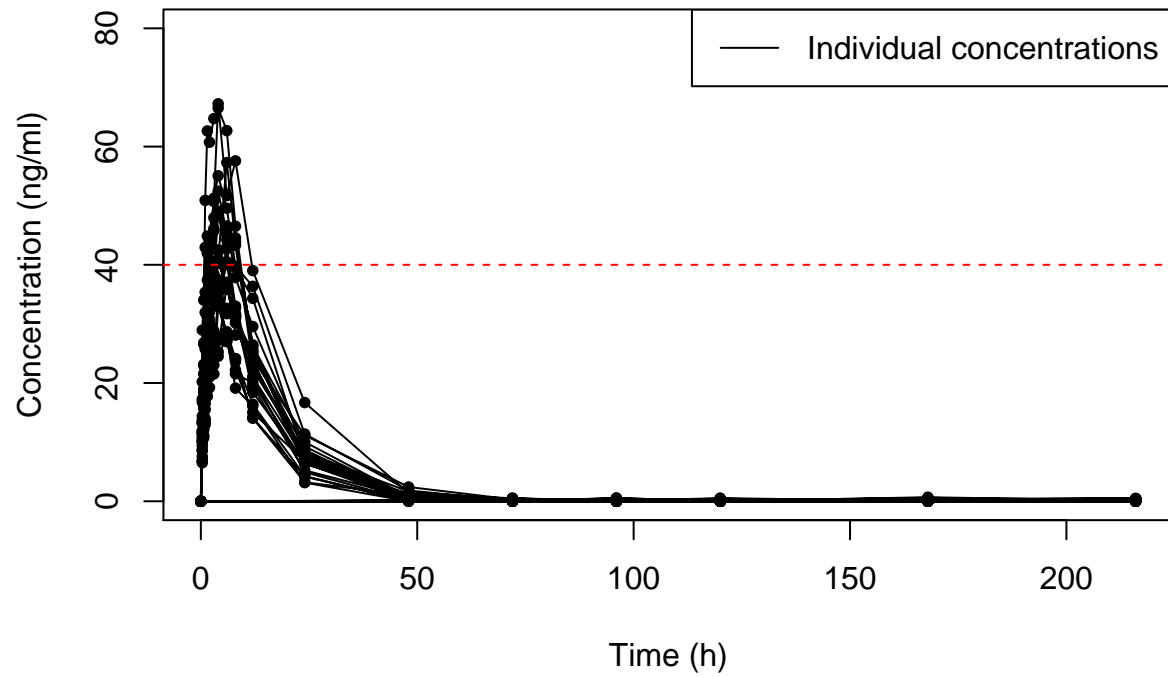
```

PK of Drug X



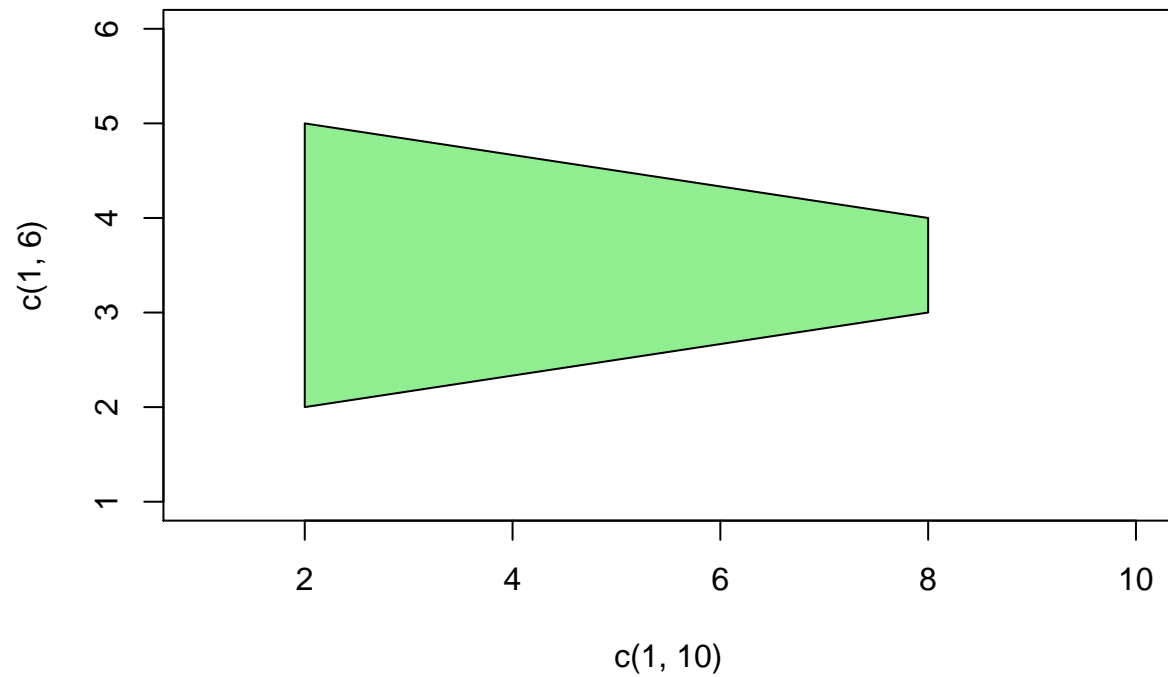
```
plot(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], main="PK of Drug X"
     , type="n", xlab="Time (h)", ylab="Concentration (ng/ml)"
     , ylim=range(0,80))
points(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], pch = 16, cex=0.8)
lines(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], col="black", lwd=1)
abline(40, 0, col="red", lty=2) # abline(a,b): y=a+b*x
legend("topright", legend=c("Individual concentrations")
      , lty=1, col="black")
```

PK of Drug X



polygon 함수

```
plot(c(1, 10), c(1, 6), type = "n")
polygon(c(2,8,8,2), c(5,4,3,2), col="lightgreen")
```



```
plot(c(1, 9), 1:2, type = "n")
polygon(1:9, c(2,1,2,1,1,2,1,2,1),
       col = c("red", "blue"),
       border = c("green", "yellow"),
       lwd = 3, lty = c("dashed", "solid"))
```

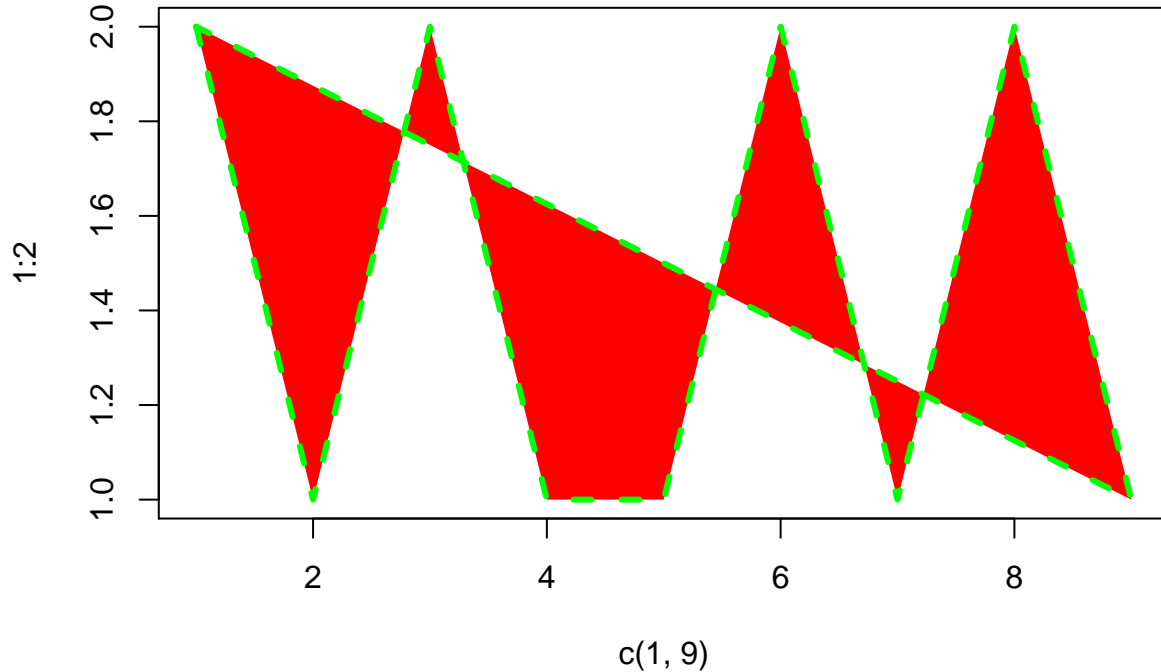


그림 출력하기

pdf graphics devices

```
pdf("PK_of_Drug_X.pdf")

plot(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], main="PK of Drug X"
     , type="n", xlab="Time (h)", ylab="Concentration (ng/ml)"
     , ylim=range(0,80))
points(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], pch = 16, cex=0.8)
lines(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], col="black", lwd=1)
abline(40, 0, col="red", lty=2) #abline(a,b): y=a+b*x
legend("topright", legend=c("Individual concentrations")
      , lty=1, col="black")

dev.off()

## pdf
## 2
```

PNG graphics devices

```
png("PK_of_Drug_X.png")

plot(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], main="PK of Drug X"
      , type="n", xlab="Time (h)", ylab="Concentration (ng/ml)"
      , ylim=range(0,80))
points(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], pch = 16, cex=0.8)
lines(dta$TIME[dta$MDV==0], dta$DV[dta$MDV==0], col="black", lwd=1)
abline(40, 0, col="red", lty=2) #abline(a,b): y=a+b*x
legend("topright", legend=c("Individual concentrations")
      , lty=1, col="black")

dev.off()

## pdf
## 2
```